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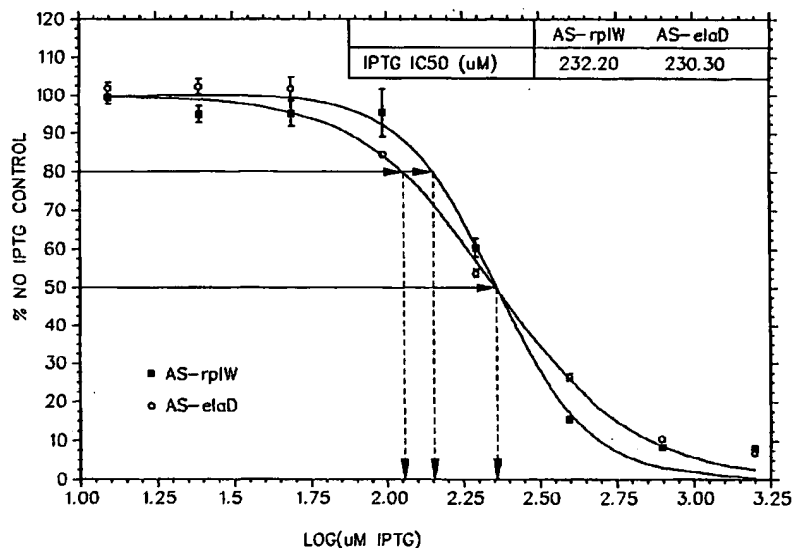
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(54) Title: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION OF E. COLI



(57) Abstract: The sequences of nucleic acids encoding proteins required for E. coli proliferation are disclosed. The nucleic acids can also be used to screen for homologous genes that are required for proliferation in microorganisms other than E. coli. The nucleic acids can also be used to design expression vectors and secretion vectors. The nucleic acids can be used to express proteins or portions thereof, to obtain antibodies capable of specifically binding to the expressed proteins, and to use those expressed proteins as a screen to isolate candidate molecules for rational drug discovery programs. The nucleic acids of the present invention can also be used in various assay systems to screen for antimicrobial agents.



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GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION OF E. COLI**BACKGROUND OF THE INVENTION**

Since the discovery of penicillin, the use of antibiotics to treat the ravages of bacterial infections has saved millions of lives. With the advent of these "miracle drugs," for a time it was popularly believed that humanity might, once and for all, be saved from the scourge of bacterial infections. In fact, during the 1980s and early 1990s, many large pharmaceutical companies cut back or eliminated antibiotics research and development. They believed that infectious disease caused by bacteria finally had been conquered and that markets for new drugs were limited. Unfortunately, this belief was overly optimistic.

The tide is beginning to turn in favor of the bacteria as reports of drug resistant bacteria become more frequent. The United States Centers for Disease Control announced that one of the most powerful known antibiotics, vancomycin, was unable to treat an infection of the common *Staphylococcus aureus* (staph). This organism is commonly found in our environment and is responsible for many nosocomial infections. The import of this announcement becomes clear when one considers that vancomycin was used for years to treat infections caused by stubborn strains of bacteria, like staph. In short, the bacteria are becoming resistant to our most powerful antibiotics. If this trend continues, it is conceivable that we will return to a time when what are presently considered minor bacterial infections are fatal diseases.

There are a number of causes for the predicament in which practitioners of medical arts find themselves. Over-prescription and improper prescription habits by some physicians have caused an indiscriminate increase in the availability of antibiotics to the public. The patient is also partly responsible, for even in instances where an antibiotic is the appropriate treatment, patients will often improperly use the drug, the result being yet another population of bacteria that is resistant, in whole or in part, to traditional antibiotics.

The bacterial scourges that have haunted humanity remain, in spite of the development of modern scientific practices to deal with the diseases that they cause. Drug resistant bacteria are now advancing on the health of humanity. A new generation of antibiotics to once again deal with the pending health threat that bacteria present is required.

Discovery of New Antibiotics

As more and more bacterial strains become resistant to the panel of available antibiotics, new compounds are required. In the past, practitioners of pharmacology would have to rely upon traditional methods of drug discovery to generate novel, safe and efficacious compounds for the treatment of disease. Traditional drug discovery methods involve blindly testing potential drug candidate-molecules, often selected at random, in the hope that one might prove to be an effective treatment for some disease. The process is painstaking and laborious, with no guarantee of success. Today, the average cost to discover and develop a new drug is nearly US \$500 million, and the

average time is 15 years from laboratory to patient. Improving this process, even incrementally, would represent a huge advance in the generation of novel antimicrobial agents.

Newly emerging practices in drug discovery utilize a number of biochemical techniques to provide for directed approaches to creating new drugs, rather than discovering them at random. For example, gene sequences and proteins encoded thereby that are required for the proliferation of an organism make for excellent targets since exposure of bacteria to compounds active against these targets would result in the inactivation of the organism. Once a target is identified, biochemical analysis of that target can be used to discover or to design molecules that interact with and alter the functions of the target. Using physical and computational techniques, to analyze structural and biochemical targets in order to derive compounds that interact with a target is called rational drug design and offers great future potential. Thus, emerging drug discovery practices use molecular modeling techniques, combinatorial chemistry approaches, and other means to produce and screen and/or design large numbers of candidate compounds.

Nevertheless, while this approach to drug discovery is clearly the way of the future, problems remain. For example, the initial step of identifying molecular targets for investigation can be an extremely time consuming task. It may also be difficult to design molecules that interact with the target by using computer modeling techniques. Furthermore, in cases where the function of the target is not known or is poorly understood, it may be difficult to design assays to detect molecules that interact with and alter the functions of the target. To improve the rate of novel drug discovery and development, methods of identifying important molecular targets in pathogenic microorganisms and methods for identifying molecules that interact with and alter the functions of such molecular targets are urgently required.

Escherichia coli represents an excellent model system to understand bacterial biochemistry and physiology. The estimated 4288 genes scattered along the 4.6×10^6 base pairs of the *Escherichia coli* (*E. coli*) chromosome offer tremendous promise for the understanding of bacterial biochemical processes. In turn, this knowledge will assist in the development of new tools for the diagnosis and treatment of bacteria-caused human disease. The entire *E. coli* genome has been sequenced, and this body of information holds a tremendous potential for application to the discovery and development of new antibiotic compounds. Yet, in spite of this accomplishment, the general functions or roles of many of these genes are still unknown. For example, the total number of proliferation-required genes contained within the *E. coli* genome is unknown, but has been variously estimated at around 200 to 700 (Armstrong, K.A. and Fan, D.P. Essential Genes in the *metB-malB* Region of *Escherichia coli* K12, 1975, J. Bacteriol. 126: 48-55).

Novel, safe and effective antimicrobial compounds are needed in view of the rapid rise of antibiotic resistant microorganisms. However, prior to this invention, the characterization of even a single bacterial gene was a painstaking process, requiring years of effort. Accordingly, there is an urgent need for more novel methods to identify and characterize bacterial genomic sequences that

encode gene products required for proliferation and for methods to identify molecules that interact with and alter the functions of such genes and gene products.

SUMMARY OF THE INVENTION

5 One embodiment of the present invention is a purified or isolated nucleic acid sequence consisting essentially of one of the sequence of nucleotides of SEQ ID NOs: 1-93, wherein expression of said nucleic acid in a microorganism is capable of inhibiting the proliferation of a microorganism. The nucleic acid sequence may have as sequence of nucleotides complementary to at least a portion of the nucleotide sequence of the coding strand of a gene whose expression is
10 required for proliferation of a microorganism. The nucleic acid may have a nucleotide sequence complementary to at least a portion of the nucleotide sequence of an RNA required for proliferation of a microorganism. The nucleotide sequence of the RNA may encode more than one gene product.

Another embodiment of the present invention is a purified or isolated nucleic acid comprising a fragment of one of the nucleotide sequences of SEQ ID NOs.: 1-93, said fragment
15 selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 and more than 50 consecutive nucleotides of the nucleotide sequence of one of SEQ ID NOs: 1-93.

Another embodiment of the present invention is a vector comprising a promoter operably linked to the nucleic acid sequences of each of the preceding paragraphs. The promoter may be
20 active in a microorganism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefir* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*,
25 *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*,
30 *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species.

Another embodiment of the present invention is a host cell containing the vectors of the preceding paragraph.

35 Another embodiment of the present invention is a purified or isolated nucleic acid consisting essentially of the coding sequence of one of SEQ ID NOs: 106-112, 119-122, 134-160, 164-171, 179-265, 271-273, 275, and 279-286.

Another embodiment of the present invention is a fragment of the nucleic acid of the preceding paragraph, said fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs: 106-112, 119-122, 134-160, 164-171, 179-265, 271-273, 275, and 279-286.

5 Another embodiment of the present invention is a vector comprising a promoter operably linked to the nucleic acid of the preceding two paragraphs.

Another embodiment of the present invention is a purified or isolated antisense nucleic acid comprising a nucleic acid sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding
10 region, or 3' noncoding region within an operon comprising a proliferation-required gene whose activity or expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93.

Another embodiment of the present invention is a purified or isolated nucleic acid comprising a nucleic acid having at least 70% identity to a sequence selected from the group
15 consisting of SEQ ID NOs.: 1-93, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 1-93, the sequences complementary to SEQ ID NOs.: 1-93 and the sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 1-93 as determined using BLASTN version 2.0 with the default parameters. The nucleic acid may be from an organism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*,
20 *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*,
25 *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas*
30 *aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species.

Another embodiment of the present invention is a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93. The polypeptide may comprise a polypeptide
35 comprising a sequence selected from the group consisting of SEQ ID NOs: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

Another embodiment of the present invention is a host cell containing the vector of the preceding paragraph.

Another embodiment of the present invention is a purified or isolated polypeptide comprising a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93, or a fragment selected from the group consisting of fragments comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the said polypeptides. The polypeptide may comprise a polypeptide comprising one of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479 or a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

Another embodiment of the present invention is a purified or isolated polypeptide comprising a polypeptide having at least 25% identity to a polypeptide whose expression is inhibited by a sequence selected from the group consisting of SEQ ID NOs.: 1-93, or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide whose expression is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-93 as determined using FASTA version 3.0t78 with the default parameters. The polypeptide may have at least 25% identity to a polypeptide comprising one of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479 or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising one of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479 as determined using FASTA version 3.0t78 with the default parameters.

Another embodiment of the present invention is an antibody capable of specifically binding one of the polypeptides of the preceding paragraph.

Another embodiment of the present invention is a method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93 into a cell and expressing said polypeptide. The method may further comprise the step of isolating said polypeptide. The polypeptide may comprise a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

Another embodiment of the present invention is a method of inhibiting proliferation of a microorganism comprising inhibiting the activity or reducing the amount of a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group

consisting of SEQ ID NOs.: 1-93 or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product. The gene product may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

5 Another embodiment of the present invention is a method for identifying a compound which influences the activity of a gene product required for proliferation, said gene product comprising a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising contacting said gene product with a candidate compound and determining whether said compound
10 influences the activity of said gene product. The gene product may be a polypeptide and said activity may be an enzymatic activity. The gene product may be a polypeptide and said activity may be a carbon compound catabolism activity. The gene product may be a polypeptide and said activity may be a biosynthetic activity. The gene product may be a polypeptide and said activity may be a transporter activity. The gene product may be a polypeptide and said activity may be a
15 transcriptional activity. The gene product may be a polypeptide and said activity may be a DNA replication activity. The gene product may be a polypeptide and said activity may be a cell division activity. The gene product may be a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

20 Another embodiment of the present invention is a compound identified using the methods of the preceding paragraph.

Another embodiment of the present invention is a method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited
25 by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising:

- (a) providing a target that is a gene or RNA, wherein said target comprises a nucleic acid encoding said gene product;
- (b) contacting said target with a candidate compound or nucleic acid; and
- 30 (c) measuring an activity of said target.

The target may be a messenger RNA molecule and said activity may be translation of said messenger RNA. The target may be a messenger RNA molecule and said activity may be transcription of a gene encoding said messenger RNA. The target may be a gene and said activity may be transcription of said gene. The target may be a nontranslated RNA and said activity may be
35 processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex. The target gene or RNA may encode a polypeptide comprising a sequence

selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

Another embodiment of the present invention is a compound or nucleic acid identified using the methods of the preceding paragraph.

5 Another embodiment of the present invention is a method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a microorganism, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising the steps of:

10 (a) expressing a sub-lethal level of an antisense nucleic acid complementary to a nucleic acid encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;

(b) contacting said sensitized cell with a compound; and

(c) determining whether said compound inhibits the growth of said sensitized cell.

15 The determining step may comprise determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell. The cell may be selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells. The cell may be a Gram negative bacterium. The cell may be an *E. coli* cell. The cell may be from an organism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*,
20 *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,
25 *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species. The antisense nucleic acid may be transcribed from an inducible promoter. The method may further comprise the step of contacting said cell with a concentration of inducer which induces said antisense nucleic acid to a sub-lethal level. Growth inhibition may be measured by monitoring
30 optical density of a culture growth solution. The gene product may be a polypeptide. The polypeptide may comprise a sequence selected from the group consisting of SEQ ID NOs.: 299-

305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479. The gene product may be an RNA.

Another embodiment of the present invention is a compound identified using the methods of the preceding paragraph.

5 Another embodiment of the present invention is a method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93 or a compound with activity against the product of said gene into a population of cells expressing said gene. The compound may be an antisense nucleic acid
10 comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, or a proliferation-inhibiting portion thereof. The proliferation inhibiting portion of one of SEQ ID NOs.: 1-93 may be a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive nucleotides of one of SEQ ID NOs.: 1-93. The population may be a population selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells. The
15 population may be a population of Gram negative bacteria. The population may be a population of *E. coli* cells. The population may be a population selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*),
20 *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*,
25 *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species. The gene may encode a polypeptide comprising a sequence selected from the
30 group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

Another embodiment of the present invention is a preparation comprising an effective concentration of an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable
35 carrier. The proliferation-inhibiting portion of one of SEQ ID NOs.: 1-93 may comprise at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-93.

Another embodiment of the present invention is a method for inhibiting the activity or expression of a gene in an operon required for proliferation wherein the activity or expression of at least one gene in said operon is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising contacting a cell in a cell population with an antisense nucleic acid comprising at least a proliferation-inhibiting portion of said operon. The antisense nucleic acid comprises a sequence selected from the group consisting of SEQ ID NOs.: 1-93 or a proliferation inhibiting portion thereof.

The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population. The cell may be contacted with said antisense nucleic acid by introducing a phage which expresses said antisense nucleic acid into said cell population. The cell may be contacted with said antisense nucleic acid by expressing said antisense nucleic acid from the chromosome of cells in said cell population. The cell may be contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the synthesis of said antisense nucleic acid. The cell may be contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population. The cell may be contacted with said antisense nucleic acid by introducing a ribozyme into said cell population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide. The cell may be contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell. The cell may be contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid. The antisense nucleic acid may be a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-93. The antisense nucleic acid may be an oligonucleotide.

Another embodiment of the present invention is a method for identifying a gene which is required for proliferation of a microorganism comprising:

(a) contacting a microorganism other than *E. coli* with a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-93;

(b) determining whether said nucleic acid inhibits proliferation of said microorganism;
and

(c) identifying the gene in said microorganism which is inhibited by said nucleic acid.

The microorganism may be a Gram negative bacterium. The microorganism may be selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*,

Enterobacter cloacae, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species. The method may further comprise introducing said nucleic acid into a vector functional in said microorganism prior to introducing said inhibitory nucleic acid into said microorganism.

Another embodiment of the present invention is a method for identifying a compound having the ability to inhibit proliferation of a microorganism comprising:

- (a) identifying in a first microorganism a homolog of a gene or gene product present in a second microorganism which is different than said first microorganism, wherein the activity or level of said gene or gene product is inhibited by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 1-93 ;
- (b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said first microorganism;
- (c) contacting said first microorganism with a sub-lethal level of said inhibitory nucleic acid, thus sensitizing said first microorganism;
- (d) contacting the sensitized microorganism of step (c) with a compound; and
- (e) determining whether said compound inhibits proliferation of said sensitized microorganism.

The determining step may comprise determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism. Step (a) may comprise identifying a homologous nucleic acid to a gene or gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-93 or a nucleic acid encoding a homologous polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-93 by using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database. Step (a) may comprise identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying nucleic acids which hybridize to said first gene. Step (a) may comprise expressing a nucleic acid selected from the group consisting of SEQ ID NOs. 1-93 in said microorganism. The inhibitory nucleic acid may be an antisense nucleic acid. The inhibitory nucleic acid may comprise an antisense nucleic acid to a portion of

said homolog. The inhibitory nucleic acid may comprise an antisense nucleic acid to a portion of the operon encoding said homolog. The step of contacting the first microorganism with a sub-lethal level of said inhibitory nucleic acid may comprise directly contacting said microorganism with said inhibitory nucleic acid. The step of contacting the first microorganism with a sub-lethal level of said inhibitory nucleic acid may comprise expressing an antisense nucleic acid to said homolog in said microorganism. The gene product may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

Another embodiment of the present invention is a compound identified using the method of the preceding paragraph.

Another embodiment of the present invention is a method of identifying a compound having the ability to inhibit proliferation comprising:

(a) contacting a microorganism other than *E. coli* with a sub-lethal level of a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 1-93 or a portion thereof which inhibits the proliferation of *E. coli*, thus sensitizing said microorganism;

(b) contacting the sensitized microorganism of step (a) with a compound; and

(c) determining whether said compound inhibits proliferation of said sensitized microorganism.

The determining step may comprise determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism.

Another embodiment of the present invention is a compound identified using the methods of the preceding paragraph.

Another embodiment of the present invention is a method for identifying a compound having activity against a biological pathway required for proliferation comprising:

(a) sensitizing a cell by expressing a sub-lethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, in said cell to reduce the activity or amount of said gene product;

(b) contacting the sensitized cell with a compound; and

(c) determining whether said compound inhibits the growth of said sensitized cell.

The determining step may comprise determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

The cell may be selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells. The cell may be a Gram negative bacterium. The Gram negative bacterium may be *E. coli*. The cell may be selected from the group consisting of *Aspergillus fumigatus*, *Bacillus*

anthracis, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*,
 5 *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*,
 10 *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species. The antisense nucleic acid may be transcribed from an inducible promoter. The method may further comprise contacting the cell with an agent which induces expression of said antisense nucleic acid
 15 from said inducible promoter, wherein said antisense nucleic acid is expressed at a sub-lethal level. The inhibition of proliferation may be measured by monitoring the optical density of a liquid culture. The gene product may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

20 Another embodiment of the present invention is a compound identified using the methods of the preceding paragraph.

Another embodiment of the present invention is a method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product
 25 required for proliferation of said cell, wherein said gene product is a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93;

(b) contacting said cell with a compound; and

(c) determining whether said compound reduces proliferation of said contacted cell.

30 The determining step may comprise determining whether said compound reduces proliferation of said contacted cell to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent. The agent which reduces the activity or level of a gene product required for proliferation of said cell may comprise an antisense nucleic acid to a gene or operon required for proliferation. The agent which reduces the activity or level of a gene product required
 35 for proliferation of said cell may comprise a compound known to inhibit growth or proliferation of a microorganism. The cell may contain a mutation which reduces the activity or level of said gene product required for proliferation of said cell. The mutation may be a temperature sensitive

mutation. The gene product may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

5 Another embodiment of the present invention is a compound identified using the method of the preceding paragraph.

Another embodiment of the present invention is a method for identifying the biological pathway in which a proliferation-required gene or its gene product lies, wherein said gene or gene product comprises a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said
10 method comprising:

- (a) expressing a sub-lethal level of an antisense nucleic acid which inhibits the activity of said proliferation-required gene or gene product in a cell;
- (b) contacting said cell with a compound known to inhibit growth or proliferation of a microorganism, wherein the biological pathway on which said compound acts is known; and
- 15 (c) determining whether said cell is sensitive to said compound.

The determining step may comprise determining whether said cell has a substantially greater sensitivity to said compound than a cell which does not express said sub-lethal level of said antisense nucleic acid and wherein said gene or gene product lies in the same pathway on which said compound acts if said cell expressing said sub-lethal level of said antisense nucleic acid has a
20 substantially greater sensitivity to said compound than said cell which does not express said sub-lethal level of said antisense nucleic acid.

The gene product may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

25 Another embodiment of the present invention is a method for determining the biological pathway on which a test compound acts comprising:

- (a) expressing a sub-lethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a cell, wherein the activity or expression of said proliferation-required nucleic acid is inhibited by an antisense nucleic acid comprising a sequence selected from
30 the group consisting of SEQ ID NOs.: 1-93 and wherein the biological pathway in which said proliferation-required nucleic acid or a protein encoded by said proliferation-required polypeptide lies is known,
- (b) contacting said cell with said test compound; and
- (c) determining whether said cell is sensitive to said test compound.

35 The determining step may comprise determining whether said cell has a substantially greater sensitivity to said test compound than a cell which does not express said sub-lethal level of said antisense nucleic acid. The method may further comprise:

(d) expressing a sub-lethal level of a second antisense nucleic acid complementary to a second proliferation-required nucleic acid in a second cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

5 (e) determining whether said second cell does not have a substantially greater sensitivity to said test compound than a cell which does not express said sub-lethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological pathway against which the antisense nucleic acid of step (a) acts if said second cell does not have substantially greater sensitivity to said test compound.

10 Another embodiment of the present invention is a purified or isolated nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93.

Another embodiment of the present invention is a compound which interacts with a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93 to inhibit proliferation.

15 Another embodiment of the present invention is a compound which interacts with a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93 to inhibit proliferation.

Another embodiment of the present invention is a method for manufacturing an antibiotic comprising the steps of screening one or more candidate compounds to identify a compound that
20 reduces the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93 and manufacturing the compound so identified.

The screening step may comprise performing any one of the methods of identifying a compound
25 described above.

Another embodiment of the present invention is a method for inhibiting proliferation of a microorganism in a subject comprising administering a compound that reduces the activity or level of a gene product required for proliferation of said microorganism, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a
30 sequence selected from the group consisting of SEQ ID NOs.: 1-93 to said subject. The method of subject may be selected from the group consisting of vertebrates, mammals, avians, and human beings. The gene product may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

35

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is an IPTG dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing either an antisense clone to the *E. coli rplW* gene (AS-*rplW*) which encodes a ribosomal protein required for protein synthesis and essential for cell proliferation, or an antisense clone to the *elaD* gene (AS-*elaD*) which is not known to be involved in protein synthesis and which is also essential for proliferation.

Figure 2A is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to the *rplW* gene (AS-*rplW*) which was carried out in the presence of 0, 20 or 50 μ M IPTG.

Figure 2B is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to the *elaD* gene (AS-*elaD*) which was carried out in the presence of 0, 20 or 50 μ M IPTG.

Figure 3 is a graph showing the fold increase in tetracycline sensitivity of *E. coli* transfected with antisense clones to essential ribosomal protein genes *L23* (AS-*rplW*) and *L7/L12* and *L10* (AS-*rplLrplJ*). Antisense clones to genes known not to be involved in protein synthesis (*atpB/E*(AS-*atpB/E*), *visC* (AS-*visC*), *elaD* (AS-*elaD*), *yohH* (AS-*yohH*) are much less sensitive to tetracycline.

Definitions

By "biological pathway" is meant any discrete cell function or process that is carried out by a gene product or a subset of gene products. Biological pathways include enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such as cell walls. Biological pathways that are usually required for proliferation of microorganisms include, but are not limited to, cell division, DNA synthesis and replication, RNA synthesis (transcription), protein synthesis (translation), protein processing, protein transport, fatty acid biosynthesis, cell wall synthesis, cell membrane production, synthesis and maintenance, and the like.

By "inhibit activity of a gene or gene product" is meant having the ability to interfere with the function of a gene or gene product in such a way as to decrease expression of the gene or to reduce the level or activity of a product of the gene. Agents which inhibit the activity of a gene include agents that inhibit transcription of the gene, agents that inhibit processing of the transcript of the gene, agents that reduce the stability of the transcript of the gene, and agents that inhibit translation of the mRNA transcribed from the gene. In microorganisms, agents which inhibit the activity of a gene can act to decrease expression of the operon in which the gene resides or alter the folding or processing of operon RNA so as to reduce the level or activity of the gene product. The gene product can be a non-translated RNA such as ribosomal RNA, a translated RNA (mRNA) or

the protein product resulting from translation of the gene mRNA. Of particular utility to the present invention are antisense RNAs that have activities against the operons or genes to which they specifically hybridize.

By "activity against a gene product" is meant having the ability to inhibit the function or to
5 reduce the level or activity of the gene product in a cell.

By "activity against a protein" is meant having the ability to inhibit the function or to reduce the level or activity of the protein in a cell.

By "activity against a nucleic acid" is meant having the ability to inhibit the function or to reduce the level or activity of the nucleic acid in a cell.

10 By "activity against a gene" is meant having the ability to inhibit the function or expression of the gene in a cell.

By "activity against an operon" is meant having the ability to inhibit the function or reduce the level of one or more products of the operon in a cell.

By "antibiotic" is meant an agent which inhibits the proliferation of a microorganism.

15 By "*E. coli* or *Escherichia coli*" is meant *Escherichia coli* or any organism previously categorized as a species of *Shigella* including *Shigella boydii*, *Shigella flexneri*, *Shigella dysenteriae*, *Shigella sonnei*, *Shigella 2A*.

By "identifying a compound" is meant to screen one or more compounds in a collection of compounds such as a combinatorial chemical library or other library of chemical compounds or to
20 characterize a single compound by testing the compound in a given assay and determining whether it exhibits the desired activity.

By "inducer" is meant an agent or solution which, when placed in contact with a microorganism, increases transcription from a desired promoter.

As used herein, "nucleic acid" means DNA, RNA, or modified nucleic acids. Thus, the
25 terminology "the nucleic acid of SEQ ID NO: X" includes both the DNA sequence of SEQ ID NO: X and an RNA sequence in which the thymidines in the DNA sequence have been substituted with uridines in the RNA sequence and in which the deoxyribose backbone of the DNA sequence has been substituted with a ribose backbone in the RNA sequence. Modified nucleic acids are nucleic acids having nucleotides or structures which do not occur in nature, such as nucleic acids in which
30 the internucleotide phosphate residues with methylphosphonates, phosphorothioates, phosphoramidates, and phosphate esters. Nonphosphate internucleotide analogs such as siloxane bridges, carbonate bridges, thioester bridges, as well as many others known in the art may also be used in modified nucleic acids. Modified nucleic acids may also comprise, α -anomeric nucleotide units and modified nucleotides such as 1,2-dideoxy-d-ribofuranose, 1,2-dideoxy-1-
35 phenylribofuranose, and N^4 , N^4 -ethano-5-methyl-cytosine are contemplated for use in the present invention. Modified nucleic acids may also be peptide nucleic acids in which the entire

deoxyribose-phosphate backbone has been exchanged with a chemically completely different, but structurally homologous, polyamide (peptide) backbone containing 2-aminoethyl glycine units.

As used herein, "sub-lethal" means a concentration of an agent below the concentration required to inhibit all cell growth.

5

DETAILED DESCRIPTION OF THE INVENTION

The present invention describes a group of *E. coli* genes and gene families required for growth and/or proliferation. A proliferation-required gene or gene family is one where, in the absence of a gene transcript and/or gene product, growth or viability of the microorganism is reduced or eliminated. Thus, as used herein the terminology "proliferation-required" or "required for proliferation" encompasses instances where the absence of a gene transcript and/or gene product completely eliminates cell growth as well as instances where the absence of a gene transcript and/or gene product merely reduces cell growth. These proliferation-required genes can be used as potential targets for the generation of new antimicrobial agents. To achieve that goal, the present invention also encompasses novel assays for analyzing proliferation-required genes and for identifying compounds which interact with the gene products of the proliferation-required genes. In addition, the present invention contemplates the expression of genes and the purification of the proteins encoded by the nucleic acid sequences identified as required proliferation genes and reported herein. The purified proteins can be used to generate reagents and screen small molecule libraries or other candidate compound libraries for compounds that can be further developed to yield novel antimicrobial compounds. The present invention also describes methods for identification of homologous genes or polypeptides in organisms other than *E. coli*.

The present invention utilizes a novel method to identify proliferation-required *E. coli* sequences. Generally, a library of nucleic acid sequences from a given source are subcloned or otherwise inserted into an inducible expression vector, thus forming an expression library. Although the insert nucleic acids may be derived from the chromosome of the organism into which the expression vector is to be introduced, because the insert is not in its natural chromosomal location, the insert nucleic acid is an exogenous nucleic acid for the purposes of the discussion herein. The term expression is defined as the production of an RNA molecule from a gene, gene fragment, genomic fragment, or operon. Expression can also be used to refer to the process of peptide or polypeptide synthesis. An expression vector is defined as a vehicle by which a ribonucleic acid (RNA) sequence is transcribed from a nucleic acid sequence carried within the expression vehicle. The expression vector can also contain features that permit translation of a protein product from the transcribed RNA message expressed from the exogenous nucleic acid sequence carried by the expression vector. Accordingly, an expression vector can produce an RNA molecule as its sole product or the expression vector can produce a RNA molecule that is ultimately translated into a protein product.

Once generated, the expression library containing the exogenous nucleic acid sequences is introduced into an *E. coli* population to search for genes that are required for bacterial proliferation.

Because the library molecules are foreign to the population of *E. coli*, the expression vectors and the nucleic acid segments contained therein are considered exogenous nucleic acid.

Expression of the exogenous nucleic acid fragments in the test population of *E. coli* containing the expression vector library is then activated. Activation of the expression vectors consists of
5 subjecting the cells containing the vectors to conditions that result in the expression of the exogenous nucleic acid sequences carried by the expression vector library. The test population of *E. coli* cells is then assayed to determine the effect of expressing the exogenous nucleic acid fragments on the test population of cells. Those expression vectors that, upon activation and expression, negatively impact the growth of the *E. coli* screen population are identified, isolated, and purified for further study.

10 A variety of assays are contemplated to identify nucleic acid sequences that negatively impact growth upon expression. In one embodiment, growth in *E. coli* cultures expressing exogenous nucleic acid sequences is compared to growth in cultures not expressing these sequences. Optical density is used to monitor the extent of growth. Alternatively, enzymatic assays can be used to determine bacterial growth rates to identify exogenous nucleic acid sequences of interest. Colony size, colony
15 morphology, and cell morphology are additional factors used to evaluate growth of the host cells. Those cultures that fail to grow or grow at a reduced rate under expression conditions are identified as containing an expression vector encoding a nucleic acid fragment that negatively affects a proliferation-required gene.

Once exogenous nucleic acid sequences of interest are identified, they are analyzed. The first
20 step of the analysis is to acquire the nucleic acid sequence of the nucleic acid fragment of interest. To achieve this end, the insert in those expression vectors identified as containing a sequence of interest is sequenced, using standard techniques well known in the art. The next step of the process is to determine the source of the nucleic acid sequence.

Determination of sequence source is achieved by comparing the obtained sequence data with
25 known sequences in various genetic databases. The sequences identified are used to probe these gene databases. The result of this procedure is a list of exogenous nucleic acid sequences corresponding to a list that includes novel bacterial genes required for proliferation as well as genes previously identified as required for proliferation.

The number of DNA and protein sequences available in database systems has been growing
30 exponentially for years. For example, at the end of 1998, the complete sequences of *Caenorhabditis elegans*, *Saccharomyces cerevisiae* and nineteen bacterial genomes, including *E. coli* were available. This sequence information is stored in a number of databanks, such as GenBank (the National Center for Biotechnology Information (NCBI), and is publicly available for searching.

A variety of computer programs are available to assist in the analysis of the sequences stored
35 within these databases. FASTA, (W. R. Pearson (1990) "Rapid and Sensitive Sequence Comparison with FASTP and FASTA" Methods in Enzymology 183:63- 98), Sequence Retrieval System (SRS), (Etzold & Argos, SRS an indexing and retrieval tool for flat file data libraries. Comput. Appl.

Biosci. 9:49-57, 1993) are two examples of computer programs that can be used to analyze sequences of interest. In one embodiment of the present invention, the BLAST family of computer programs, which includes BLASTN version 2.0 with the default parameters, or BLASTX version 2.0 with the default parameters, is used to analyze nucleic acid sequences. BLAST, an acronym for "Basic Local Alignment Search Tool," is a family of programs for database similarity searching. The BLAST family of programs includes: BLASTN, a nucleotide sequence database searching program, BLASTX, a protein database searching program where the input is a nucleic acid sequence; and BLASTP, a protein database searching program where the input is an amino acid sequence. BLAST programs embody a fast algorithm for sequence matching, rigorous statistical methods for judging the significance of matches, and various options for tailoring the program for special situations. Assistance in using the program can be obtained by e-mail at blast@ncbi.nlm.nih.gov.

Bacterial genes are often transcribed in polycistronic groups. These groups comprise operons, which are a collection of genes and intergenic sequences. The genes of an operon are co-transcribed and often have related functions. Given the nature of the screening protocol, it is possible that the identified exogenous nucleic acid sequence corresponds to a gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual sequence that is required for bacterial proliferation. Accordingly, determining which gene(s) that is encoded within the operons is individually required for proliferation is often desirable.

In one embodiment of the present invention, an operon is dissected to determine which gene or genes are required for proliferation. For example, the RegulonDB DataBase described by Huerta et al. (*Nucl. Acids Res.* 26:55-59, 1998), which may also be found on the website http://www.cifn.unam.mx/Computational_Biology/regulondb/, may be used to identify the boundaries of operons encoded within microbial genomes. A number of techniques that are well known in the art can then be used to dissect the operon. In one aspect of this embodiment, gene disruption by homologous recombination is used to individually inactivate the genes of an operon that is thought to contain a gene required for proliferation.

Several gene disruption techniques have been described for the replacement of a functional gene with a mutated, non-functional (null) allele. These techniques generally involve the use of homologous recombination. The method described by Link et al. (*J. Bacteriol* 1997 179:6228) serves as an excellent example of these methods as applicable to disruption of genes in *E. coli*. This technique uses crossover PCR to create a null allele with an in-frame deletion of the coding region of a target gene. The null allele is constructed in such a way that sequences adjacent to the wild type gene (ca. 500 bp) are retained. These homologous sequences surrounding the deletion null

allele provide targets for homologous recombination so that the wild type gene on the *E. coli* chromosome can be replaced by the constructed null allele.

The crossover PCR amplification product is subcloned into the vector pKO3, the features of which include a chloramphenicol resistance gene, the counter-selectable marker *sacB*, and a temperature sensitive autonomous replication function. Following transformation of an *E. coli* cell population with such a vector, selection for cells that have undergone homologous recombination of the vector into the chromosome is achieved by growth on chloramphenicol at the non-permissive temperature of 43°C. Under these conditions, autonomous replication of the plasmid cannot occur and cells are resistant to chloramphenicol only if the chloramphenicol resistance gene has been integrated into the chromosome. Usually a single crossover event is responsible for this integration event such that the *E. coli* chromosome now contains a tandem duplication of the target gene consisting of one wild type allele and one deletion null allele separated by vector sequence.

This new *E. coli* strain containing the tandem duplication can be maintained at permissive temperatures in the presence of drug selection (chloramphenicol). Subsequently, cells of this new strain are cultured at the permissive temperature 30°C without drug selection. Under these conditions, the chromosome of some of the cells within the population will have undergone an internal homologous recombination event resulting in removal of the plasmid sequences. Subsequent culturing of the strain in growth medium lacking chloramphenicol but containing sucrose is used to select for such recombinative resolutions. In the presence of the counter-selectable marker *sacB*, sucrose is rendered into a toxic metabolite. Thus, cells that survive this counter-selection have lost both the plasmid sequences from the chromosome and the autonomously replicating plasmid that results as a byproduct of recombinative resolution.

There are two possible outcomes of the above recombinative resolution via homologous recombination. Either the wild type copy of the targeted gene is retained on the chromosome or the mutated null allele is retained on the chromosome. In the case of an essential gene, a single copy of the null allele would be lethal and such cells should not be obtained by the above procedure when applied to essential genes. In the case of a non-essential gene, roughly equal numbers of cells containing null alleles and cells containing wild type alleles should be obtained. Thus, the method serves as a test for essentiality of the targeted gene: when applied to essential genes, only cells with a wild type allele on the chromosome will be obtained.

Other techniques have also been described for the creation of disruption mutations in *E. coli*. For example, Link et al. also describe inserting an in-frame sequence tag concomitantly with an in-frame deletion in order to simplify analysis of recombinants obtained. Further, Link et al. describe disruption of genes with a drug resistance marker such as a kanamycin resistance gene. Arigoni et al., (Arigoni, F. et al. A Genome-based Approach for the Identification of Essential Bacterial Genes, *Nature Biotechnology* 16: 851-856) describe the use of gene disruption combined with engineering a second copy of a test gene such that the expression of the gene is regulated by

and inducible promoter such as the arabinose promoter to test the essentiality of the gene. Many of these techniques result in the insertion of large fragments of DNA into the gene of interest, such as a drug selection marker. An advantage of the technique described by Link et al. is that it does not rely on an insertion into the gene to cause a functional defect, but rather results in the precise removal of the coding region. This insures the lack of polar effects on the expression of genes downstream from the target gene.

Recombinant DNA techniques can be used to express the entire coding sequences of the gene identified as required for proliferation, or portions thereof. The over-expressed proteins can be used as reagents for further study. The identified exogenous sequences are isolated, purified, and cloned into a suitable expression vector using methods well known in the art. If desired, the nucleic acids can contain the sequences encoding a signal peptide to facilitate secretion of the expressed protein.

Expression of fragments of the bacterial genes identified as required for proliferation is also contemplated by the present invention. The fragments of the identified genes can encode a polypeptide comprising at least 5, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 75, or more than 75 consecutive amino acids of a gene complementary to one of the identified sequences of the present invention. The nucleic acids inserted into the expression vectors can also contain sequences upstream and downstream of the coding sequence.

When expressing the coding sequence of an entire gene identified as required for bacterial proliferation or a fragment thereof, the nucleic acid sequence to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector can be any of the bacterial, insect, yeast, or mammalian expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon usage and codon bias of the sequence can be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, et al., U.S. Patent No. 5,082,767. Fusion protein expression systems are also contemplated by the present invention.

Following expression of the protein encoded by the identified exogenous nucleic acid sequence, the protein is purified. Protein purification techniques are well known in the art. Proteins encoded and expressed from identified exogenous nucleic acid sequences can be partially purified using precipitation techniques, such as precipitation with polyethylene glycol. Alternatively, epitope tagging of the protein can be used to allow simple one step purification of the protein. Chromatographic methods usable with the present invention can include ion-exchange chromatography, gel filtration, use of hydroxyapatite columns, immobilized reactive dyes, chromatofocusing, and use of high-performance liquid chromatography. Electrophoretic methods such one-dimensional gel electrophoresis, high-resolution two-dimensional polyacrylamide electrophoresis,

isoelectric focusing, and others are contemplated as purification methods. Also, affinity chromatographic methods, comprising antibody columns, ligand presenting columns and other affinity chromatographic matrices are contemplated as purification methods in the present invention.

The purified proteins produced from the gene coding sequences identified as required for proliferation can be used in a variety of protocols to generate useful antimicrobial reagents. In one embodiment of the present invention, antibodies are generated against the proteins expressed from the identified exogenous nucleic acid sequences. Both monoclonal and polyclonal antibodies can be generated against the expressed proteins. Methods for generating monoclonal and polyclonal antibodies are well known in the art. Also, antibody fragment preparations prepared from the produced antibodies discussed above are contemplated.

In addition, the purified protein, fragments thereof, or derivatives thereof may be administered to an individual in a pharmaceutically acceptable carrier to induce an immune response against the protein. Preferably, the immune response is a protective immune response which protects the individual. Methods for determining appropriate dosages of the protein and pharmaceutically acceptable carriers are familiar to those skilled in the art.

Another application for the purified proteins of the present invention is to screen small molecule libraries for candidate compounds active against the various target proteins of the present invention. Advances in the field of combinatorial chemistry provide methods, well known in the art, to produce large numbers of candidate compounds that can have a binding, or otherwise inhibitory effect on a target protein. Accordingly, the screening of small molecule libraries for compounds with binding affinity or inhibitory activity for a target protein produced from an identified gene sequence is contemplated by the present invention.

The present invention further contemplates utility against a variety of other pathogenic organisms in addition to *E. coli*. For example, the invention has utility in identifying genes required for proliferation in prokaryotes and eukaryotes. For example, the invention has utility with protists, such as *Plasmodium* spp. and as *Entamoeba* spp.; plants; animals, such as *Contracaecum* spp.; and fungi including *Candida* spp., ((e.g., *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*)), *Saccharomyces cerevisiae*, *Cryptococcus neoformans*, and *Aspergillus fumigatus*. In one embodiment of the present invention, monera, specifically bacteria are probed in search of novel gene sequences required for proliferation. This embodiment is particularly important given the rise of drug resistant bacteria.

The numbers of bacterial species that are becoming resistant to existing antibiotics are growing. A partial list of these organisms includes: *Staphylococcus* spp., such as *S. aureus*; *Enterococcus* spp., such as *E. faecalis*; *Pseudomonas* spp., such as *P. aeruginosa*, *Clostridium* spp., such as *C. botulinum* or *C. difficile*, *Haemophilus* spp., such as *H. influenzae*, *Enterobacter* spp., such as *E. cloacae*, *Vibrio* spp., such as *V. cholera*; *Moraxella* spp., such as *M. catarrhalis*;

Streptococcus spp., such as *S. pneumoniae*, *Neisseria* spp., such as *N. gonorrhoeae*; *Mycoplasma* spp., such as *Mycoplasma pneumoniae*; *Salmonella typhimurium*; *Helicobacter pylori*; *Escherichia coli*; and *Mycobacterium tuberculosis*. The sequences identified as required for proliferation in the present invention can be used to probe these and other organisms to identify homologous required proliferation genes contained therein.

In one embodiment of the present invention, the nucleic acid sequences disclosed herein are used to screen genomic libraries generated from bacterial species of interest other than *E. coli*. For example, the genomic library may be from *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* or any species falling within the genera of any of the above species. Standard molecular biology techniques are used to generate genomic libraries from various microorganisms. In one aspect, the libraries are generated and bound to nitrocellulose paper. The identified exogenous nucleic acid sequences of the present invention can then be used as probes to screen the libraries for homologous sequences. The homologous sequences identified can then be used as targets for the identification of new, antimicrobial compounds with activity against more than one organism.

For example, the preceding methods may be used to isolate nucleic acids having a sequence with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% identity to a nucleic acid sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 1-93, 106-112, 119-122, 134-160, 164-171, 179-265, 271-273, 275, and 279-286, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, and the sequences complementary thereto. Identity may be measured using BLASTN version 2.0 with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, *Nucleic Acid Res.* 25: 3389-3402 (1997)). For example, the homologous polynucleotides may have a coding sequence which is a naturally occurring allelic variant of one of the coding sequences described herein. Such allelic variants may have a substitution, deletion or addition of one or more nucleotides when compared to

the nucleic acids of SEQ ID NOs: 1-93, 106-112, 119-122, 134-160, 164-171, 179-265, 271-273, 275, and 279-286 or the sequences complementary thereto.

Additionally, the above procedures may be used to isolate nucleic acids which encode polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, or at least 40% identity or similarity to a polypeptide having the sequence of one of SEQ ID NOs: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479 or to a polypeptide whose expression is inhibited by a nucleic acid of one of SEQ ID NOs.: 1-93, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of the preceding polypeptides as determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, or TBLASTN with the default parameters. (Alschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997)).

Alternatively, homologous nucleic acids or polypeptides may be identified by searching a database to identify sequences having a desired level of homology to a nucleic acid or a polypeptide involved in proliferation or an antisense nucleic acid to a nucleic acid involved in microbial proliferation. A variety of such databases are available to those skilled in the art, including GenBank and GenSeq. In some embodiments, the databases are screened to identify nucleic acids or polypeptides having at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, or at least 50%, at least 40% identity or similarity to a nucleic acid or polypeptide involved in proliferation or an antisense nucleic acid involved in proliferation. For example, the database may be screened to identify nucleic acids homologous to one of SEQ ID Nos. 1-93, 106-112, 119-122, 134-160, 164-171, 179-265, 271-273, 275, and 279-286, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, or homologous to the sequences complementary to any of the preceding nucleic acids. In other embodiments, the databases are screened to identify polypeptides having at least 99%, 95%, 90%, 85%, 80%, 70%, 60%, 50%, 40%, or at least 25% identity or similarity to a polypeptide involved in proliferation or a portion thereof. For example, the database may be screened to identify polypeptides homologous to a polypeptide comprising one of SEQ ID NOs. 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479, a polypeptide whose expression is inhibited by a nucleic acid of one of SEQ ID NOs: 1-93, or homologous to fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of any of the preceding polypeptides. In some embodiments, the database may be screened to identify homologous nucleic acids or polypeptides from organisms other than *E. coli*, including organisms such as *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr*

(also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* or any species falling within the genera of any of the above species.

In another embodiment, gene expression arrays and microarrays can be employed. Gene expression arrays are high density arrays of DNA samples deposited at specific locations on a glass chip, nylon membrane, or the like. Such arrays can be used by researchers to quantify relative gene expression under different conditions. Gene expression arrays are used by researchers to help identify optimal drug targets, profile new compounds, and determine disease pathways. An example of this technology is found in U.S. Patent No. 5807522.

It is possible to study the expression of all genes in the genome of a particular microbial organism using a single array. For example, the arrays from Genosys consist of 12 x 24 cm nylon filters containing PCR products corresponding to 4290 ORFs from *E. coli*. 10 ngs of each are spotted every 1.5 mm on the filter. Single stranded labeled cDNAs are prepared for hybridization to the array (no second strand synthesis or amplification step is done) and placed in contact with the filter. Thus the labeled cDNAs are of "antisense" orientation. Quantitative analysis is done by phosphorimager.

Hybridization of cDNA made from a sample of total cell mRNA to such an array followed by detection of binding by one or more of various techniques known to those in the art results in a signal at each location on the array to which cDNA hybridized. The intensity of the hybridization signal obtained at each location in the array thus reflects the amount of mRNA for that specific gene that was present in the sample. Comparing the results obtained for mRNA isolated from cells grown under different conditions thus allows for a comparison of the relative amount of expression of each individual gene during growth under the different conditions.

Gene expression arrays may be used to analyze the total mRNA expression pattern at various time points after induction of an antisense nucleic acid complementary to a proliferation-required gene. Analysis of the expression pattern indicated by hybridization to the array provides

information on whether or not the target gene of the antisense nucleic acid is being affected by antisense induction, how quickly the antisense is affecting the target gene, and for later timepoints, what other genes are affected by antisense expression. For example, if the antisense is directed against a gene for ribosomal protein L7/L12 in the 50S subunit, its targeted mRNA may disappear first and then other mRNAs may be observed to increase, decrease or stay the same. Similarly, if the antisense is directed against a different 50S subunit ribosomal protein mRNA (e.g. L25), that mRNA may disappear first followed by changes in mRNA expression that are similar to those seen with the L7/L12 antisense expression. Thus, the mRNA expression pattern observed with an antisense nucleic acid complementary to a proliferation required gene may identify other proliferation-required nucleic acids in the same pathway as the target of the antisense nucleic acid. In addition, the mRNA expression patterns observed with candidate drug compounds may be compared to those observed with antisense nucleic acids against a proliferation-required nucleic acid. If the mRNA expression pattern observed with the candidate drug compound is similar to that observed with the antisense nucleic acid, the drug compound may be a promising therapeutic candidate. Thus, the assay would be useful in assisting in the selection of candidate drug compounds for use in screening methods such as those described below.

In cases where the source of nucleic acid deposited on the array and the source of the nucleic acid being hybridized to the array are from two different organisms, gene expression arrays can identify homologous genes in the two organisms.

The present invention also contemplates additional methods for screening other microorganisms for proliferation-required genes. In this embodiment, the conserved portions of sequences identified as proliferation-required can be used to generate degenerate primers for use in the polymerase chain reaction (PCR). The PCR technique is well known in the art. The successful production of a PCR product using degenerate probes generated from the sequences identified herein would indicate the presence of a homologous gene sequence in the species being screened. This homologous gene is then isolated, expressed, and used as a target for candidate antibiotic compounds. In another aspect of this embodiment, the homologous gene is expressed in an autologous organism or in a heterologous organism in such a way as to alter the level or activity of a homologous gene required for proliferation in the autologous or heterologous organism. In still another aspect of this embodiment, the homologous gene or portion is expressed in an antisense orientation in such a way as to alter the level or activity of a nucleic acid required for proliferation of an autologous or heterologous organism.

The homologous sequences to proliferation-required genes identified using the techniques described herein may be used to identify proliferation-required genes of organisms other than *E. coli*, to inhibit the proliferation of organisms other than *E. coli* by inhibiting the activity or reducing the amount of the identified homologous nucleic acid or polypeptide in the organism other than *E. coli*, or to identify compounds which inhibit the growth of organisms other than *E. coli* as described below.

In another embodiment of the present invention, *E. coli* sequences identified as required for proliferation are transferred to expression vectors capable of function within non-*E. coli* species. As would be appreciated by one of ordinary skill in the art, expression vectors must contain certain elements that are species specific. These elements can include promoter sequences, operator sequences, repressor genes, origins of replication, selectable marker genes, ribosomal binding sequences, termination sequences, and others. To use the identified exogenous sequences of the present invention, one of ordinary skill in the art would know to use standard molecular biology techniques to isolate vectors containing the sequences of interest from cultured bacterial cells, isolate and purify those sequences, and subclone those sequences into an expression vector adapted for use in the species of bacteria to be screened.

Expression vectors for a variety of other species are known in the art. For example, Cao et al. report the expression of steroid receptor fragments in *Staphylococcus aureus*. J. Steroid Biochem Mol Biol. 44(1):1-11 (1993). Also, Pla et al. have reported an expression vector that is functional in a number of relevant hosts including: *Salmonella typhimurium*, *Pseudomonas putida*, and *Pseudomonas aeruginosa*. J. Bacteriol. 172(8):4448-55 (1990). These examples demonstrate the existence of molecular biology techniques capable of constructing expression vectors for the species of bacteria of interest to the present invention.

Following the subcloning of the identified nucleic acid sequences into an expression vector functional in the microorganism of interest, the identified nucleic acid sequences are conditionally transcribed to assay for bacterial growth inhibition. Those expression vectors found to contain sequences that, when transcribed, inhibit bacterial growth are compared to the known genomic sequence of the pathogenic microorganism being screened or, if the homologous sequence from the organism being screened is not known, it may be identified and isolated by hybridization to the proliferation-required *E. coli* sequence of interest or by amplification using primers based on the proliferation-required *E. coli* sequence of interest as described above.

The antisense sequences from the second organism which are identified as described above may then be operably linked to a promoter, such as an inducible promoter, and introduced into the second organism. The techniques described herein for identifying *E. coli* genes required for proliferation may thus be employed to determine whether the identified sequences from a second organism inhibit the proliferation of the second organism.

Antisense nucleic acids required for the proliferation of organisms other than *E. coli* or the genes corresponding thereto, may also be hybridized to a microarray containing the *E. coli* ORFs to gauge the homology between the *E. coli* sequences and the proliferation-required nucleic acids from other organisms. For example, the proliferation-required nucleic acid may be from *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*),

Candida dubliniensis, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* or any species falling within the genera of any of the above species. The proliferation-required nucleic acids from an organism other than *E. coli* may be hybridized to the array under a variety of conditions which permit hybridization to occur when the probe has different levels of homology to the sequence on the microarray. This would provide an indication of homology across the organisms as well as clues to other possible essential genes in these organisms.

In still another embodiment, the exogenous nucleic acid sequences of the present invention that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. The antisense sequences can be complementary to the proliferation-required genes whose sequence corresponds to the exogenous nucleic acid probes identified here (i.e. the antisense nucleic acid may hybridize to the gene or a portion thereof). Alternatively, antisense therapeutics can be complementary to operons in which proliferation-required genes reside (i.e. the antisense nucleic acid may hybridize to any gene in the operon in which the proliferation-required genes reside). Further, antisense therapeutics can be complementary to a proliferation-required gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual sequence that is required for bacterial proliferation or an operon containing a proliferation-required gene.

In addition to therapeutic applications, the present invention encompasses the use of nucleic acid sequences complementary to sequences required for proliferation as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. This utility provides a rapid and dependable method by which to identify the causative agent or agents of a bacterial infection. This utility would provide clinicians the ability to prescribe species specific antimicrobial compounds to treat such infections. In an extension of this utility, antibodies generated against proteins translated from mRNA transcribed from proliferation-required sequences can also be used to screen for specific microorganisms that produce such proteins in a species-specific manner.

The following examples teach the genes of the present invention and a subset of uses for the *E. coli* genes identified as required for proliferation. These examples are illustrative only and are not intended to limit the scope of the present invention.

EXAMPLES

- 5 The following examples are directed to the identification and exploitation of *E. coli* genes required for proliferation. Methods of gene identification are discussed as well as a variety of methods to utilize the identified sequences.

Genes Identified as Required for Proliferation of *E. coli*

- 10 Exogenous nucleic acid sequences were cloned into an inducible expression vector and assayed for growth inhibition activity. Example 1 describes the examination of a library of exogenous nucleic acid sequences cloned into the IPTG-inducible expression vector pLEX5BA (Krause et al., J. Mol. Biol. 274: 365 (1997)) or a modified version of pLEX5BA, pLEX5BA-3' in which a synthetic linker containing a T7 terminator was ligated between the PstI and HindIII sites
15 of pLEX5BA. In particular, to construct pLEX5BA-3', the following oligonucleotides were annealed and inserted into the PstI and HindIII sites of pLEX5BA:

5' -GTCTAGCATAACCCCTTGGGGCCTCTAAACGGGTCCTTGAGGGGTTTTTTGA-3' (SEQ ID NO: 480)

- 20 5' -AGCTTCAAAAAACCCCTCAAGGACCCGTTTAGAGGCCCAAGGGGTTAT
GCTAGACTGCA-3' (SEQ ID NO: 481)

- Random fragments of *E. coli* genomic DNA were generated by DNaseI digestion or sonication, filled in with T4 polymerase, and cloned into the SmaI site of pLEX5BA or
25 pLEX5BA-3'. Upon activation or induction, the expression vectors produced an RNA molecule corresponding to the subcloned exogenous nucleic acid sequences. The RNA product was in an antisense orientation with respect to the *E. coli* genes from which it was originally derived. This antisense RNA then interacted with sense mRNA produced from various *E. coli* genes and interfered with or inhibited the translation of the sense messenger RNA (mRNA) thus preventing
30 protein production from these sense mRNA molecules. In cases where the sense mRNA encoded a protein required for the proliferation, bacterial cells containing an activated expression vector failed to grow or grew at a substantially reduced rate. Similar results have also been obtained in cases where the gene encodes a non-translated RNA, such as a ribosomal RNA.

- It will be appreciated that vectors other than pLEX5BA or pLEX5BA-3' may be used to
35 transcribe the genomic DNA inserts. In addition, it will be appreciated that, if desired, pLEX5BA or pLEX5BA-3' may be modified to introduce features such as stop codons in all three reading frames downstream of the genomic DNA inserts to ensure that if the genomic DNA insert encodes a polypeptide (i.e. the insert is in the sense orientation rather than the antisense orientation or the

insert is in the antisense orientation but contains a cryptic ORF) translation of the polypeptide will terminate shortly after the genomic insert.

EXAMPLE 1

Inhibition of Bacterial Proliferation after IPTG induction

5 To study the effects of transcriptional induction in liquid medium, growth curves were carried out by back diluting cultures 1:200 into fresh media with or without 1 mM IPTG and measuring the OD₄₅₀ every 30 minutes (min). To study the effects of transcriptional induction on solid medium, 10², 10³, 10⁴, 10⁵, 10⁶, 10⁷ and 10⁸ fold dilutions of overnight cultures were prepared. Aliquots of from 0.5 to 3 µl of these dilutions were spotted on selective agar plates with or without 1 mM IPTG. After 10 overnight incubation, the plates were compared to assess the sensitivity of the clones to IPTG.

Of the numerous clones tested, some clones were identified as containing a sequence that inhibited *E. coli* growth after IPTG induction. Accordingly, the gene to which the inserted nucleic acid sequence corresponds, or a gene within the operon containing the inserted nucleic acid, may be required for proliferation in *E. coli*.

15 **Characterization of Isolated Clones Negatively Affecting *E. coli* Proliferation**

Following the identification of those inserts that, upon expression, negatively impacted *E. coli* growth or proliferation, the inserts were isolated and subjected to nucleic acid sequence determination.

EXAMPLE 2

Nucleic Acid Sequence Determination of Identified Clones Expressing Nucleic Acid Fragments with

20 Detrimental Effects of *E. coli* Proliferation

The nucleotide sequences for the exogenous identified sequences were determined using plasmid DNA isolated using QIAPREP (Qiagen, Valencia, CA) and methods supplied by the manufacturer. The primers used for sequencing the inserts were 5' - TGTTTATCAGACCGCTT - 3' (SEQ ID NO: 1) and 5' - ACAATTTACACAGCCTC - 3' (SEQ ID NO: 2). These sequences flank 25 the polylinker in pLEX5BA. Sequence identification numbers (SEQ ID NOs) for the identified inserts are listed in Table I and discussed below.

EXAMPLE 3

Comparison Of Isolated Sequences to Known Sequences

The nucleic acid sequences of the subcloned fragments obtained from the expression vectors 30 discussed above were compared to known *E. coli* sequences in GenBank using BLAST version 1.4 or version 2.0.6 using the following default parameters: Filtering off, cost to open a gap=5, cost to extend a gap=2, penalty for a mismatch in the blast portion of run=-3, reward for a match in the blast portion of run=1, expectation value (e)=10.0, word size=11, number of one-line descriptions=100, number of alignments to show (B)=100. BLAST is described in Altschul, J Mol Biol. 215:403-10 (1990). 35 Expression vectors were found to contain nucleic acid sequences in both the sense and antisense orientations. The presence of known genes, open reading frames, and ribosome binding sites was determined by comparison to public databases holding genetic information and various computer

programs such as the Genetics Computer Group programs FRAMES and CODONPREFERENCE. Clones were designated as "antisense" if the cloned fragment was oriented to the promoter such that the RNA transcript produced was complementary to the expressed mRNA (or non-translated RNA) from a chromosomal locus. Clones were designated as "sense" if they coded for an RNA fragment that was identical to a portion of a wild type mRNA from a chromosomal locus.

The sequences described in Examples 1-2 that inhibited bacterial proliferation and contained gene fragments in an antisense orientation are listed in Table I. This table lists each identified sequence by: a sequence identification number, a Molecule Number, a gene to which the identified sequence corresponds, listed according to the National Center for Biotechnology Information (NCBI), Blattner (Science 277:1453-1474(1997); also contains the *E. coli* K-12 genome sequence), or Rudd (Micro. and Mol. Rev. 62:985-1019 (1998)), nomenclatures. The CONTIG numbers for each identified sequence is shown, as well as the location of the first and last base pairs located on the *E. coli* chromosome. A Molecule Number with a "***" indicates a clone corresponding to an intergenic sequence.

TABLE I

Identified Clones with Corresponding Genes and Operons

SeqID	Molecule Number	Clone name	Contig	start	stop	Gene name (Blattner)	Gene name (NCBI)
1	EcXA118a	E1M10000131C06	AE000408	5299	5440	b3310	rpIN
2	EcXA118b	E1M10000152F04	AE000408	5300	5452	b3310	rpIN
3	EcXA118c	E1M10000152H04	AE000408	5311	5450	b3310	rpIN
4	EcXA118d	E1M10000153H03	AE000408	5299	5475	b3310	rpIN
5	EcXA119	E1M10000129F10	AE000372	2407	2153	b2883	b2883
6	EcXA120	E1M10000129G04	AE000248	2494	2888	b1509	b1509
7	EcXA121	E1M10000119D03	AE000491	1722	2001	b4191	yjfQ
8	EcXA122a	1029-M5	AE000300	232	1	b2108	yehA
			AE000299	10036	9848	b2107	b2107
9	EcXA122b	X3S208-17	AE000300	186	1	b2108	yehA
			AE000299	10036	9870	b2107	b2107
10	EcXA122c	E1M10000124C07	AE000299	10036	9896	b2107	b2107
			AE000300	78	1	b2108	yehA
11	EcXA122d	E1M10000125D06	AE000300	203	1	b2108	yehA
			AE000299	10036	9892	b2107	b2107
12	EcXA123	E1M10000106A08	AE000410	7832	7968	b3343	yheL
13	EcXA124	E1M10000106D02	AE000408	5951	6225	b3311	rpsQ
			AE000408	5951	6225	b3312	rpmC
14	EcXA125	E1M10000124D09	AE000465	7071	7309	b3901	yiiL
15	EcXA126	E1M10000124E02	AE000441	9429	9316	b3644	yicC
16	EcXA127a	E1M10000124E06	AE000369	1145	856	b2851	b2851
17	EcXA127b	E1M10000159A11	AE000369	1145	763	b2851	b2851
18	EcXA128	E1M10000124G04	AE000171	6676	6427	b0679	nagE
19	EcXA129	E1M10000127C09	AE000123	1270	1506	b0135, b0136	yadC, yadK
20	EcXA130	E1M10000146E05	AE000450	9592	9828	b3737, b3738	atpE, atpB
21	EcXA131	E1M10000162C01	AE000383	11211	11350	b3016	b3016

SeqID	Molecule Number	Clone name	Contig	start	stop	Gene name (Blattner)	Gene name (NCBI)
22	EcXA132	E1M10000163A04	AE000243	5440	5650	b1465	narV
23	EcXA133a	E1M10000120F06	AE000408	5273	5425	b3309, b3310	rplX, rplN
24	EcXA133b	E1M10000132H04	AE000408	5263	5422	b3309, b3310	rplX, rplN
25	EcXA133c	E1M10000172C05	AE000408	5190	5433	b3309, b3310	rplX, rplN
26	EcXA134	E1M10000162H06	AE000402	4689	4795	b3229	sspA
27	EcXA136a	E1M10000147B03	AE000373	1	251	b2892	recJ
			AE000372	11967	12144	b2891	prfB
28	EcXA136b	E1M10000155F04	AE000373	1	372	b2892	recJ
			AE000372	12002	12144	b2891	prfB
29	EcXA137	E1M10000142F12	AE000132	9172	8451	b0243, b0244	proA, thrW
30	EcXA138	E1M10000148B09	AE000393	10354	10051	b3121	yhaC
31	EcXA139	E1M10000143A12	AE000189	3600	4024	b0874	b0874
32	EcXA139b	E1M10000169H02	AE000189	3646	4026	b0874	b0874
33	EcXA140a	E1M10000143C10	AE000445	1	260	b3672	b3672
			AE000444	12573	12697	b3671	ilvB
34	EcXA140b	E1M10000151F10	AE000445	1	378	b3672	b3672
			AE000444	12576	12697	b3671	ilvB
35	EcXA141	E1M10000143G09	AE000294	9227	9498	b2035	rfc
36	EcXA142	E1M10000159C10	AE000408	1	199	b3299	rpmJ
			AE000407	10488	10601	b3298	rpsM
37	EcXA143	E1M10000159F03	AE000368	7705	7317	b2846	b2846
38	EcXA144a	E1M10000160A03	AE000257	545	368	b1613	manA
39	EcXA144b	E1M10000132F02	AE000257	585	395	b1613	manA
40	EcXA144c	E1M10000153E04	AE000257	552	395	b1613	manA
41	EcXA145	E1M10000160A06	AE000366	5350	5533	b2827	thyA
42	EcXA146	E1M10000160C02	AE000449	9694	9815	b3725	pstB
43	EcXA147	E1M10000160C03	AE000211	6964	7126	b1111	b1111
44	EcXA148	E1M10000160E10	AE000455	10737	10577	b3794	rffM
45	EcXA149a	E1M10000160F11	AE000374	7930	7680	b2912	ygfA
46	EcXA149b	E1M10000153F05	AE000374	7910	7625	b2912	ygfA
47	EcXA150	E1M10000160H03	AE000442	5556	5377	b3650	spoT
48	EcXA151	E1M10000144E03	AE000429	8099	8352	b3528	dctA
49	EcXA152	E1M10000144G07	AE000308	1086	1385	b2182	bcr
50	EcXA153	E1M10000144B01	AE000477	4261	4055	b4038	yjbI
51	EcXA154	E1M10000150E02	AE000290	5618	5406	b1983	b1983
52	EcXA155	E1M10000150E06	AE000339	116	496	b2522	sseB
53	EcXA156	E1M10000156B08	AE000463	2852	2699	b3874	yihN
54	EcXA157	E1M10000156D07	AE000408	7274	7464	b3314, b3315	rpsC, rplV
55	EcXA158	E1M10000156G12	AE000338	5181	5370	b2519	b2519
56	EcXA159	E1M10000151G10	AE000154	7217	7618	b0482	b0482
57	EcXA160	E1M10000166G06	AE000269	4488	5074	b1744	b1744
58	EcXA161	869.A23	AE000146	3702	3950	b0398	sbcD
59	EcXA162	E1M10000112F05	AE000497	7921	8156	b4267	yjgV
60	EcXA163	E1M10000118B05	AE000447	8832	8741	b3705	yidC
61	EcXA164	E1M10000118C04	AE000314	6749	6688	b2243	glpC
62	EcXA165	E1M10000118C05	AE000170	219	290	b0655	ybeJ
63	EcXA166	E1M10000118G06	AE000461	5835	5770	b3859	yihE
64	EcXA167	E1M10000119A05	AE000298	9388	9521	b2093	gatB
65	EcXA168	E1M10000123E09	AE000267	4622	4413	b1721	b1721
66	EcXA169	E1M10000123F11	AE000408	2650	2767	b3303	rpsE
67	EcXA170	E1M10000129G01	AE000143	3523	3913	b0363	b0363
68	EcXA171	E1M10000132G08	AE000189	6799	6699	b0876	b0876
69	EcXA172	E1M10000139B11	AE000323	3697	3531	b2345	b2345
70	EcXA173	E1M10000153A09	AE000424	6886	6968	b3485	yhhJ

SeqID	Molecule Number	Clone name	Contig	start	stop	Gene name (Blattner)	Gene name (NCBI)
71	EcXA174	E1M10000153C04	AE000377	8932	8832	b2945	endA
72	EcXA175	E1M10000154F03	AE000279	7957	7837	b1854	pykA
73	EcXA176	E1M10000157B02	AE000485	4932	5094	b4125	yjdH
74	EcXA177	E1M10000160H05	AE000326	3140	3035	b2378	b2378
75	EcXA178	E1M10000163H01	AE000113	1	266	b0023	rpsT
76	EcXA179	E1M10000164G04	AE000262	233	1	b1665	valV
77	EcXA180	E1M10000168F02	AE000480	3110	3350	b4066	yjcF
78	EcXA181	E1M10000169D08	AE000469	10535	10604	b3956	ppc
79	EcXA182	E1M10000169H07	AE000376	10447	10586	b2935	tktA
80	EcXA183	E1M10000169H08	AE000118	8416	8228	b0084	ftsI
81	EcXA184	E1M10000172C01	AE000358	8498	8844	b2750	cysC
82	EcXA185	E1M10000176C01	AE000407	10053	10119	b3297	rpsK
83	EcXA186	E1M10000176F01	AE000135	987	812	b0270	yagG
84	EcXA187	P319-3.M16	AE000317	2279	1872	b2271	b2271
85	EcXA188	P347.2	AE000211	7845	8005	b1113	b1113
86	EcXA189a	E1M10000168A04	AE000277	2048	1861	b1828	b1828
87	EcXA189b	E1M10000125F09	AE000277	2042	1868	b1828	b1828
88	EcXA189c	E1M10000113F02	AE000277	2050	1857	b1828	b1828
89	EcXA190a	E1M10000161D04	AE000387	49	312	b3052	b3052
90	EcXA190b	E1M10000155B11	AE000387	49	285	b3052	b3052
91	EcXA191a	E1M10000167H09	AE000451	18	220	b3740	gidB
92	EcXA191b	E1M10000120H05	AE000451	1	188	b3740	gidB
93	EcXA192	E1M10000154H07	AE000452	3326	3106	b3750, b3751	rbsC, rpsB

EXAMPLE 4

Identification of Genes and their Corresponding Operons Affected by Antisense Inhibition

5 The sequencing of the entire *E. coli* genome is described in Blattner et al., Science 277:1453-1474(1997) and the sequence of the genome is listed in GenBank Accession No.U00096. The operons to which the proliferation-inhibiting nucleic acids correspond were identified using RegulonDB and information in the literature. The coordinates of the boundaries of these operons on the *E. coli* genome are listed in Table III. Table II lists the molecule numbers of the inserts containing the growth inhibiting nucleic acid fragments, the genes in the operons corresponding to the inserts, the SEQ ID NOs of the genes containing the inserts, the SEQ ID NOs of the proteins encoded by the genes, the start and stop points of the genes on the *E. coli* genome, the orientation of the genes on the genome, whether the operons are predicted or documented, and the predicted functions of the genes. The identified operons, their putative functions, and whether or not the genes are presently thought to be required for proliferation are discussed below.

Functions for the identified genes were determined by using either Blattner functional class designations or by comparing identified sequence with known sequences in various databases. A variety of biological functions were noted for the genes to which the clones of the present invention correspond. The functions for the genes of interest appear in Table II.

20 The proteins that are listed in Table II are involved in a wide range of biological functions.

TABLE II
All Operon Data with Whole Chromosome Coordinates

Molecule Number	Gene	Seq ID (Gene)	Seq ID (Protein)	Start	Stop	Orientation	operon prediction	Predicted function
EcXA118a-d	<i>rpmJ</i>	94	287	3440255	3440371	<	documented	50S ribosomal subunit protein X (L36)
	<i>prlA</i>	95	288	3440403	3441734	<		<i>SecY</i> : multispinning membrane protein, translocator of proteins
	<i>rpLO</i>	96	289	3441742	3442176	<		50S ribosomal subunit protein L15
	<i>rpmD</i>	97	290	3442180	3442359	<		50S ribosomal subunit protein L30
	<i>rpsE</i>	98	291	3442363	3442866	<		eps, spc, spcA; 30S ribosomal subunit protein S5
	<i>rplR</i>	99	292	3442881	3443234	<		50S ribosomal subunit protein L18
	<i>rplF</i>	100	293	3443244	3443777	<		50S ribosomal subunit protein L6; gentamicin sensitivity
	<i>rpsH</i>	101	294	3443790	3444182	<		30S ribosomal subunit protein S8
	<i>rpsN</i>	102	295	3444216	3444521	<		30S ribosomal subunit protein S14
	<i>rplE</i>	103	296	3444536	3445075	<		50S ribosomal subunit protein L5
	<i>rplX</i>	104	297	3445090	3445404	<		50S ribosomal subunit protein L24
	<i>rplN</i>	105	298	3445415	3445786	<		50S ribosomal subunit protein L14
EcXA119	<i>b2882</i>	106	299	3022315	3023772	>	predicted	Unknown
	<i>b2883</i>	107	300	3023787	3025106	>		Unknown
	<i>b2884</i>	108	301	3025142	3025711	>		Unknown
	<i>b2885</i>	109	302	3025678	3026508	>		Unknown
EcXA120	<i>b1509</i>	110	303	1590689	1592089	<	predicted	Unknown
	<i>ydeK</i>	111	304	1592133	1596110	<		Unknown
EcXA121	<i>yjfQ</i>	112	305	4415276	4416031	<	predicted	Unknown
EcXA122	<i>b2106</i>	113	306	2183937	2184761	>	predicted	Unknown
	<i>b2107</i>	114	307	2184800	2185318	>		Unknown
	<i>yehA</i>	115	308	2185400	2186434	<	predicted	Unknown
	<i>yehB</i>	116	309	2186450	2188930	<		Unknown

Molecule Number	Gene	Seq ID (Gene)	Seq ID (Protein)	Start	Stop	Orientation	operon prediction	Predicted function
	<i>yehC</i>	117	310	2188946	2189665	<		Unknown
	<i>yehD</i>	118	311	2189700	2190242	<		Unknown
EcXA123	<i>yheL</i>	119	312	3472315	3472602	<	predicted	Unknown
	<i>b3344</i>	120	313	3472610	3472969	<		Unknown
	<i>yheN</i>	121	314	3472969	3473355	<		Unknown
	<i>b3346</i>	122	315	3473355	3474089	<		Unknown
EcXA124	<i>rpsQ</i>	123	316	3445951	3446205	<	documented	neaA; 30S ribosomal subunit protein S17
	<i>rpmC</i>	124	317	3446205	3446396	<		50S ribosomal subunit protein L29
	<i>rplP</i>	125	318	3446396	3446806	<		50S ribosomal subunit protein L16
	<i>rpsC</i>	126	319	3446819	3447520	<		30S ribosomal subunit protein S3
	<i>rplV</i>	127	320	3447538	3447870	<		eryB; erythromycin sensitivity; 50S ribosomal subunit protein L22
	<i>rpsS</i>	128	321	3447885	3448163	<		30S ribosomal subunit protein S19
	<i>rplB</i>	129	322	3448180	3449001	<		50S ribosomal subunit protein L2
	<i>rplW</i>	130	323	3449019	3449321	<		50S ribosomal subunit protein L23
	<i>rplD</i>	131	324	3449318	3449923	<		eryA; 50S ribosomal subunit protein L4; erythromycin sensitivity
	<i>rplC</i>	132	325	3449934	3450563	<		50S ribosomal subunit protein L3
	<i>rpsJ</i>	133	326	3450596	3450907	<		nusE; 30S ribosomal subunit protein S10
EcXA125	<i>yilL</i>	134	327	4090705	4091019	<	predicted	Unknown
EcXA126	<i>yicC</i>	135	328	3814303	3815166	>	predicted	Unknown
EcXA127a-b	<i>b2851</i>	136	329	2989290	2989781	>	predicted	Unknown
EcXA128	<i>nagE</i>	137	330	703167	705113	>	documented	pstN; N-acetylglucosamine-specific enzyme II of phosphotransferase system
EcXA129	<i>yadC</i>	138	331	149715	150953	<	predicted	Unknown
	<i>yadK</i>	139	332	151003	151599	<		Unknown
	<i>yadL</i>	140	333	151626	152231	<		Unknown
	<i>yadM</i>	141	334	152243	152854	<		Unknown

Molecule Number	Gene	Seq ID (Gene)	Seq ID (Protein)	Start	Stop	Orientation	operon prediction	Predicted function
EcXA130	<i>atpC</i>	142	335	3913181	3913600	<	documented	papG, uncC; membrane-bound ATP synthase, F1 sector, -subunit (EC 3.6.1.3)
	<i>atpD</i>	143	336	3913621	3915003	<		papB, uncD; membrane-bound ATP synthase, F1 sector, -subunit (EC 3.6.1.3)
	<i>atpG</i>	144	337	3915030	3915893	<		papC, uncG; membrane-bound ATP synthase, F1 sector, -subunit (EC 3.6.1.3)
	<i>atpA</i>	145	338	3915944	3917485	<		papA, uncA; membrane-bound ATP synthase, F1 sector, -subunit (EC 3.6.1.3)
	<i>atpH</i>	146	339	3917498	3918031	<		papE, uncH; membrane-bound ATP synthase, F1 sector, -subunit (EC 3.6.1.3)
	<i>atpF</i>	147	340	3918046	3918516	<		papF, uncF; membrane-bound ATP synthase, F0 sector, subunit b (EC 3.6.1.3)
	<i>atpE</i>	148	341	3918578	3918817	<		papH, uncE; membrane-bound ATP synthase, F0 sector, subunit c; DCCD (EC 3.6.1.3)
	<i>atpB</i>	149	342	3918864	3919679	<		papD, uncB; membrane-bound ATP synthase, F0 sector, subunit a (EC 3.6.1.3)
	<i>atpI</i>	150	343	3919688	3920080	<		uncI; membrane-bound ATP synthase subunit, F1-F0-type proton-ATPase (EC 3.6.1.34)
	<i>b3015</i>	151	344	3156944	3158185	<	predicted	Unknown
EcXA132	<i>b3016</i>	152	345	3158185	3159162	<		Unknown
	<i>narV</i>	153	346	1533961	1534641	<	documented	regulationCryptic nitrate reductase II, -subunit
	<i>narW</i>	154	347	1534638	1535333	<		regulationCryptic nitrate reductase II, -subunit
	<i>narY</i>	155	348	1535333	1536877	<		regulationCryptic NR II, -subunit
EcXA133a-c	<i>narZ</i>	156	349	1536874	1540614	<		regulationCryptic NR II, -subunit
							Same operon as EcXA118	

Molecule Number	Gene	Seq ID (Gene)	Seq ID (Protein)	Start	Stop	Orientation	operon prediction	Predicted function
EcXA134	<i>sspB</i>	157	350	3373914	3374411	<	documented	Stress response protein
	<i>sspA</i>	158	351	3374417	3375055	<		pog; stress response protein
EcXA136a-b	<i>lysS</i>	159	352	3031677	3033194	<	documented	asuD herC; lysyl tRNA synthetase, constitutive
	<i>prfB</i>	160	353	3033204	3034302	<		supK; peptide chain release factor 2
	<i>recJ</i>	161	354	3034393	3036126	<	predicted	Single-stranded DNA-specific exonuclease, 5-3
	<i>dsbC</i>	162	355	3036132	3036842	<		xprA; periplasmic disulfide oxidoreductase, protein disulfide isomerase
	<i>xerD</i>	163	356	3036867	3037763	<		xprB; recombinase, site specific
EcXA137	<i>proB</i>	164	357	259612	260715	>	documented	pro2; -glutamyl kinase (EC 2.7.2.11)
	<i>proA</i>	165	358	260727	261980	>		pro1; -glutamyl phosphate reductase (EC 1.2.1.41)
EcXA138	<i>yhaB</i>	166	359	3265474	3266034	>	predicted	
	<i>yhaC</i>	167	360	3266056	3267243	>		
EcXA139a-b	<i>b0874</i>	168	361	913181	914128	<	predicted	
EcXA140a-b	<i>ilvN</i>	169	362	3848429	3848719	<	documented	Acetohydroxy acid synthase I, small subunit (EC 4.1.3.18); valine sensitive small subunit; positive regulator for thr and ilv
	<i>ilvB</i>	170	363	3848723	3850411	<		Acetolactate synthase I, valine sensitive (EC 4.1.3.18)
	<i>b3672</i>	171	364	3850517	3850615	<		
EcXA141	<i>y152_7</i>	172	365	2099917	2100933	<	predicted	nucleotide sequence and phylogenetic relationships of a new E. coli insertion element. Schwartz E
	<i>yefJ</i>	173	366	2100938	2101411	<		Unknown
	<i>yefI</i>	174	367	2101413	2102531	<		Unknown
	<i>yefH</i>	175	368	2102516	2103106	<		Unknown

Molecule Number	Gene	Seq ID (Gene)	Seq ID (Protein)	Start	Stop	Orientation	operon prediction	Predicted function
	<i>yefG</i>	176	369	2103087	2104079	<		Unknown
	<i>yfc</i>	177	370	2104082	2105248	<		O-antigen polymerase
	<i>yefE</i>	178	371	2105248	2106351	<		Unknown
EcXA142							Same operon as EcXA118	
EcXA143	<i>b2846</i>	179	372	2985498	2986190	>	predicted	Unknown
EcXA144a-c	<i>manA</i>	180	373	1686600	1687775	>	predicted	pmi; mannosephosphate isomerase (EC 5.3.1.8)
EcXA145	<i>thpA</i>	181	374	2962383	2963177	<	documented	Aminopterin, trimethoprim resistance; thymidylate synthetase (EC 2.1.1.45)
	<i>lgt</i>	182	375	2963184	2964059	<		transferaseumpA; phosphatidylglycerol:prolipoprotein diacylglycerol transferase
EcXA146	<i>phoU</i>	183	376	3904481	3905206	<	documented	phoT; P uptake, high-affinity P-specific transport system, regulatory gene
	<i>pstB</i>	184	377	3905221	3905994	<		phoT; high-affinity P-specific transport; cytoplasmic ATP-binding protein
	<i>pstA</i>	185	378	3906177	3907067	<		R2pho, phoR2b, phoT; high-affinity P-specific transport
	<i>pstC</i>	186	379	3907067	3908026	<		phoW; high-affinity P-specific transport; cytoplasmic membrane component
	<i>pstS</i>	187	380	3908113	3909153	<		phoR2, umpA, phoR2a, phoS, R2pho; high-affinity P-specific transport; periplasmic P-binding
EcXA147	<i>b1111</i>	188	381	1167423	1168133	<	predicted	Unknown
EcXA148	<i>yifH</i>	189	382	3972208	3972753	>	predicted	Unknown
	<i>yifI</i>	190	383	3972758	3973888	>		Unknown
	<i>yifJ</i>	191	384	3973890	3975140	>		Unknown
	<i>rffT</i>	192	385	3976214	3977566	>		Synthesis of enterobacterial common antigen; Fuc4NAc transferase

Molecule Number	Gene	Seq ID (Gene)	Seq ID (Protein)	Start	Stop	Orientation	operon prediction	Predicted function
	<i>rffM</i>	193	386	3977569	3978309	>		UDP-MannAcA transferase
	<i>b4404</i>	194	387	3975137	3975361	>		Unknown
	<i>b4405</i>	195	388	3975603	3976217	>		Unknown
EcXA149a-b	<i>ygfA</i>	196	389	3054261	3054809	>	predicted	Unknown
EcXA150	<i>rpoZ</i>	197	390	3819733	3820008	>	documented	spoS; RNA polymerase,
	<i>spoT</i>	198	391	3820027	3822135	>		Guanosine 5'-diphosphate, 3'-diphosphate pyrophosphatase, ppGpp synthetase II activity
	<i>spoU</i>	199	392	3822142	3822831	>		
	<i>recG</i>	200	393	3822837	3824918	>		spoV? branch migration of Holliday junctions, junction-specific DNA helicase (see ruvABC)
EcXA151	<i>dctA</i>	201	394	3679791	3681077	<	predicted	Uptake of C-4 dicarboxylic acids; 3-fluoromaleate resistance, D-tartrate resistant
EcXA152	<i>bcr</i>	202	395	2276590	2277780	<	predicted	bicA, bicR, sur, suxA; transmembrane; affects sulfathiazole-sulfonamide resistance
	<i>yejD</i>	203	396	2277808	2278503	<		Unknown
EcXA153	<i>yjbI</i>	204	397	4248534	4249862	>	predicted	Unknown
EcXA154	<i>b1983</i>	205	398	2054880	2055596	>	predicted	Unknown
EcXA155	<i>sseB</i>	206	399	2652177	2652962	<	predicted	Enhances serine sensitivity (inhibits homoserine deHase) on lactate; weaker than sseA
EcXA156	<i>yihN</i>	207	400	4059826	4061091	>	predicted	Unknown
EcXA157							Same operon as EcXA124	Unknown
EcXA158	<i>b2519</i>	208	401	2643033	2645345	<	predicted	Unknown
	<i>b2520</i>	209	402	2645346	2650307	<		Unknown
EcXA159	<i>b0482</i>	210	403	506510	507304	<	predicted	Unknown

Molecule Number	Gene	Seq ID (Gene)	Seq ID (Protein)	Start	Stop	Orientation	operon prediction	Predicted function
EcXA160	<i>b1744</i>	211	404	1823979	1824947	<	predicted	Unknown
	<i>b1745</i>	212	405	1824940	1826283	<		Unknown
	<i>b1746</i>	213	406	1826280	1827758	<		Unknown
	<i>b1747</i>	214	407	1827755	1828789	<		Unknown
	<i>b1748</i>	215	408	1828786	1830006	<		Unknown
EcXA161	<i>sbcC</i>	216	409	411831	414977	<	predicted	Cosuppressor with <i>sbcB</i> of <i>recB</i> <i>recC</i> mutations
	<i>sbcD</i>	217	410	414974	416176	<		Cosuppressor with <i>sbcB</i> of <i>recB</i> <i>recC</i> mutations
EcXA162	<i>yigU</i>	218	411	4490155	4490919	<	predicted	Unknown
	<i>yigV</i>	219	412	4490943	4491974	<		Unknown
EcXA163	<i>yidC</i>	220	413	3882705	3884351	>	predicted	Unknown
EcXA164	<i>glpA</i>	221	414	2350667	2352295	>	documented	Glycerol-3-phosphate dehydrogenase (anaerobic) large subunit (EC 1.1.99.5)
	<i>glpB</i>	222	415	2352285	2353544	>		sn-Glycerol-3-phosphate dehydrogenase (anaerobic) subunit (EC 1.1.99.5); membrane anchor
	<i>glpC</i>	223	416	2353541	2354731	>		sn-Glycerol-3-phosphate dehydrogenase (anaerobic) small subunit (EC 1.1.99.5)
EcXA165	<i>ybeJ</i>	224	417	686062	686970	<	predicted	Unknown
EcXA166	<i>yihE</i>	225	418	4039996	4040982	>	predicted	Unknown
	<i>dsbA</i>	226	419	4040999	4041625	>		iarA, ppfA; disulfide oxidoreductase, periplasmic protein disulfide-isomerase; role in cytochrome c synthesis (EC 5.3.4.1)
EcXA167	<i>gatR_2</i>	227	420	2169417	2169755	<	documented	
	<i>gatD</i>	228	421	2169855	2170895	<		Galactitol-1-phosphate dehydrogenase
	<i>gatC</i>	229	422	2170943	2172298	<		Galactitol-specific enzyme IIC of PTS
	<i>gatB</i>	230	423	2172302	2172586	<		Galactitol-specific enzyme IIB of PTS

Molecule Number	Gene	Seq ID (Gene)	Seq ID (Protein)	Start	Stop	Orientation	operon prediction	Predicted function
	<i>gatA</i>	231	424	2172617	2173069	<		Galactitol-specific enzyme IIA of phosphotransferase system (PTS)
	<i>gatZ</i>	232	425	2173079	2174341	<		Function unknown
	<i>gatY</i>	233	426	2174370	2175230	<		D-Tagatose-1,6-bisphosphate aldolase
EcXA168	<i>b1720</i>	234	427	1801118	1801591	>	predicted	Unknown
	<i>b1721</i>	235	428	1801602	1803017	>		Unknown
EcXA169							Same operon as EcXA118	Unknown
EcXA170	<i>b0362</i>	236	429	381728	382114	<	predicted	Unknown
	<i>b0363</i>	237	430	381963	383159	<		Unknown
EcXA171	<i>b0876</i>	238	431	915696	917354	>	predicted	Unknown
EcXA172	<i>b2345</i>	239	432	2461032	2462090	>	predicted	Unknown
EcXA173	<i>yhlJ</i>	240	433	3623310	3624437	<	predicted	Unknown
	<i>b3486</i>	241	434	3624434	3627118	<		Unknown
	<i>yhlI</i>	242	435	3627165	3628232	<		Unknown
EcXA174	<i>endA</i>	243	436	3088366	3089073	>	predicted	DNA-specific endonuclease I; extensive DNA breakdown
EcXA175	<i>pykA</i>	244	437	1935673	1937115	>	predicted	Pyruvate kinase A (II); (EC 2.7.1.40)
EcXA176	<i>yjdG</i>	245	438	4346893	4347612	<	predicted	Unknown
	<i>yjdH</i>	246	439	4347609	4349240	<		Unknown
EcXA177	<i>b2378</i>	247	440	2493599	2494585	>	predicted	Unknown
EcXA178	<i>rpsT</i>	248	441	20815	21078	<	predicted	sup20; 30S ribosomal subunit protein S20
EcXA180	<i>yjcF</i>	249	442	4279362	4280654	<	predicted	Unknown
EcXA181	<i>ppc</i>	250	443	4148026	4150677	<	predicted	asp, glu; phosphoenolpyruvate carboxylase (EC 4.1.1.31)
EcXA182	<i>tktA</i>	251	444	3077663	3079654	<	predicted	Transketolase (EC 2.2.1.1)
EcXA183	<i>yabB</i>	252	445	89634	90092	>	predicted	Unknown
	<i>yabC</i>	253	446	90094	91035	>		Unknown

Molecule Number	Gene	Seq ID (Gene)	Seq ID (Protein)	Start	Stop	Orientation	operon prediction	Predicted function
	<i>ftsL</i>	254	447	91032	91397	>		sensitiveCell division and growth; essential gene; cytoplasmic membrane protein
	<i>ftsI</i>	255	448	91413	93179	>		sensitivepbpB, sep; peptidoglycan synthetase; penicillin-binding protein 3
	<i>murE</i>	256	449	93166	94653	>		meso-Diaminopimelate adding enzyme
	<i>murF</i>	257	450	94650	96008	>		mra; D-alanyl:D-alanine adding enzyme
	<i>mraY</i>	258	451	96002	97084	>		UDP-N-acetylmuramoyl-pentapeptide:undecaprenyl-PO4 phosphatase (EC 2.7.8.13)
	<i>murD</i>	259	452	97087	98403	>		UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase (EC 6.3.2.9)
	<i>ftsW</i>	260	453	98403	99647	>		sensitiveCytoplasmic membrane required for PBP 2 expression; homology to rodA
	<i>murG</i>	261	454	99644	100711	>		UDP-NAc-glucosamine: NAc-muramyl-(pentapeptide) pyrophosphoryl-undecaprenolNAc-glucosamine transferase
	<i>murC</i>	262	455	100765	102240	>		L-Alanine adding enzyme
	<i>ddlB</i>	263	456	102233	103153	>		ddl; D-Alanine:D-alanine ligase
EcXA184	<i>cysC</i>	264	457	2871410	2872015	<	documented	Adenylylsulfate kinase (EC 2.7.1.25)
	<i>cysN</i>	265	458	2872015	2873442	<		ATP sulfurylase (ATP:sulfate adenylyltransferase)
EcXA185	<i>rplQ</i>	266	459	3437253	3437636	<	documented	50S ribosomal subunit protein L17
	<i>rpoA</i>	267	460	3437677	3438666	<		phs, sez; phage P2 vir1 resistance; RNA polymerase, -subunit (EC 2.7.7.6).
	<i>rpsD</i>	268	461	3438692	3439312	<		ramA, sud2; 30S ribosomal subunit protein S4
	<i>rpsK</i>	269	462	3439346	3439735	<		30S ribosomal subunit protein S11
	<i>rpsM</i>	270	463	3439752	3440108	<		30S ribosomal subunit protein S13
EcXA186	<i>yagG</i>	271	464	284619	286001	>	predicted	Unknown

Molecule Number	Gene	Seq ID (Gene)	Seq ID (Protein)	Start	Stop	Orientation	operon prediction	Predicted function
	<i>b0271</i>	272	465	286013	287623	>		Unknown
EcXA187	<i>b2271</i>	273	466	2383874	2384851	>	predicted	Unknown
EcXA188	<i>b1113</i>	274	467	1168635	1169597	<	predicted	Unknown
EcXA189a-c	<i>b1828</i>	275	468	1908189	1909673	>	predicted	Unknown
EcXA190a-b	<i>b3052</i>	276	469	3192961	3194394	<	predicted	Unknown
	<i>glnE</i>	277	470	3194442	3197282	<		GS adenylyl transferase (EC 2.7.7.42)
	<i>yglF</i>	278	471	3197305	3198606	<		Unknown
EcXA191a-b	<i>gidB</i>	279	472	3920685	3921308	<	predicted	Glucose effects on cell division, perhaps replication
	<i>gidA</i>	280	473	3921372	3923261	<		Glucose effects on cell division, perhaps replication
	<i>mioC</i>	281	474	3923640	3924083	<		Initiation of replication; transcription of 16-kDa protein proceeds through ori
EcXA192	<i>rbsD</i>	282	475	3930941	3931396	>	documented	rbsP; D-ribose high-affinity transport system
	<i>rbsA</i>	283	476	3931404	3932909	>		rbsP, rbsT; D-ribose high-affinity transport system (may have chemotaxis function)
	<i>rbsC</i>	284	477	3932914	3933879	>		rbsP, rbsT; D-ribose high-affinity transport system
	<i>rbsB</i>	285	478	3933904	3934794	>		prlB, rbsP; D-ribose periplasmic binding protein
	<i>rbsK</i>	286	479	3934920	3935849	>		Ribokinase (EC 2.7.1.15)

Functions for the identified genes were assigned using either Blattner functional class designations, functions referenced in Berlyn, MKB "Linkage Map of *Escherichia coli* K-12, Edition 10: The Traditional Map". (1998) Microbiol. Mol. Biol. Rev. September 62 (3): 814-984, or by comparing identified sequence with known sequences in various databases. A variety of biological functions were noted for the genes to which the clones of the present invention correspond. Biological functions for genes that lie on the same operon as an identified gene have also been made. The functions for the genes of interest appear in Table II.

The genes of interest have a variety of biological functions. For example, genes that are thought to function as transport or binding proteins, that participate in translation or post-translational modification, that are involved in carbon compound catabolism, that are thought to be enzymes, participate in cell processes, energy metabolism and biosynthetic functions appear in Table II. Genes that are involved in cell structure, transcription, RNA processing and degradation also appear in Table II.

Several of the expression vectors contain fragments that correspond to genes of unknown function or if the function is known, it is not known whether the gene is essential. For example, EcXA119, 120, 121, 122a-d, 123, 125, 126, 127a-b, 128, 129, 131, 132, 138, 139a-b, 141, 143, 146, 147, 14, 149a-b, 152, 153, 154, 155, 156, 158, 159, 160, 162, 163, 164, 165, 166, 167, 168, 170, 171, 172, 173, 176, 177, 180, 181, 186, 187, 188, 189a-b, 190a-b, 191a-b, and 192 are all exogenous nucleic acid sequences that correspond to *E. coli* proteins that have no known function or where the function has not been shown to be essential or nonessential.

The present invention reports a number of novel *E. coli* genes and operons that are required for proliferation. From the list of clone sequences identified here, each was identified to be a portion of a gene in an operon required for the proliferation of *E. coli*. Cloned sequences corresponding to genes already known to be required for proliferation in *E. coli* include EcXA118a-d, 124, 130, 133a-c, 136a-b, 142, 145, 150, 157, 169, 178, 182, 183 and 185 are exogenous nucleic acid sequences that correspond to *E. coli* genes that are known to be required for cellular proliferation. The remaining identified sequences correspond to *E. coli* genes previously undesignated as required for proliferation in the art.

An interesting observation of the present invention is that there are also several sequence fragments that correspond to *E. coli* genes that are not thought to be required for *E. coli* proliferation. Nevertheless, under the conditions described above, the antisense expression of these gene fragments causes a reduction in cell growth. This result implies that the genes corresponding to the identified sequences are actually required for proliferation or are in operons required for proliferation. Molecule Nos. corresponding to these genes are EcXA128, 134, 137, 140a-b, 144a-c, 151, 161, 174, 175, and 184.

Following identification of the sequences of interest, these sequences were localized into operons. Since bacterial genes are expressed in a polycistronic manner, the antisense inhibition of a

single gene in an operon might effect the expression of all the other genes on the operon or the genes down stream from the single gene identified. In order to determine which of the gene products in an operon are required for proliferation, each of the genes contained within an operon may be analyzed for their effect on viability as described below.

5

TABLE III
Operon Boundaries

Molecule Number	Start	Stop
EcXA118a-d	3440255	3445786
EcXA119	3022315	3026508
EcXA120	1590689	1596110
EcXA121	4415276	4416031
EcXA122	2183937	2190242
EcXA123	3472315	3474089
EcXA124	3445951	3450907
EcXA125	4090705	4091019
EcXA126	3814303	3815166
EcXA127a-b	2989290	2989781
EcXA128	703167	705113
EcXA129	149715	152854
EcXA130	3913181	3920080
EcXA131	3156944	3159162
EcXA132	1533961	1540614
EcXA133a-c	Same operon as EcXA118	
EcXA134	3373914	3375055
EcXA136a-b	3031677	3037763
EcXA137	259612	261980
EcXA138	3265474	3267243
EcXA139a-b	913181	914128
EcXA140a-b	3848429	3850615
EcXA141	2099917	2106351
EcXA142	Same operon as EcXA118	
EcXA143	2985498	2986190
EcXA144a-c	1686600	1687775
EcXA145	2962383	2964059
EcXA146	3904481	3909153
EcXA147	1167423	1168133
EcXA148	3972208	3976217
EcXA149a-b	3054261	3054809
EcXA150	3819733	3824918
EcXA151	3679791	3681077
EcXA152	2276590	2278503
EcXA153	4248534	4249862
EcXA154	2054880	2055596
EcXA155	2652177	2652962
EcXA156	4059826	4061091
EcXA157	Same operon as	

Molecule Number	Start	Stop
	EcXA124	
EcXA158	2643033	2645345
	2645346	2650307
EcXA159	506510	507304
EcXA160	1823979	1830006
EcXA161	411831	416176
EcXA162	4490155	4491974
EcXA163	3882705	3884351
EcXA164	2350667	2354731
EcXA165	686062	686970
EcXA166	4039996	4041625
EcXA167	2169417	2175230
EcXA168	1801118	1803017
EcXA169	Same operon as EcXA118	
EcXA170	381728	383159
EcXA171	915696	917354
EcXA172	2461032	2462090
EcXA173	3623310	3628232
EcXA174	3088366	3089073
EcXA175	1935673	1937115
EcXA176	4346893	4349240
EcXA177	2493599	2494585
EcXA178	20815	21078
EcXA180	4279362	4280654
EcXA181	4148026	4150677
EcXA182	3077663	3079654
EcXA183	89634	103153
EcXA184	2871410	2873442
EcXA185	3437253	3440108
EcXA186	284619	287623
EcXA187	2383874	2384851
EcXA188	1168635	1169597
EcXA189a-c	1908189	1909673
EcXA190a-b	3192961	3198606
EcXA191a-b	3920685	3924083
EcXA192	3930941	3935849

EXAMPLE 5

5 Identification of Individual Genes within an Operon Required for Proliferation

The following example illustrates a method for determining which gene in an operon is required for proliferation. The clone insert corresponding to Molecule No. EcXA119 possesses nucleic acid sequence homology to the *E. coli* gene *b2883*. This gene is located in an operon containing the *b2882*, *b2883*, *b2884*, and *b2885* genes. To determine which gene or genes in this

10 operon are required for proliferation, each gene is selectively inactivated using homologous recombination. Gene *b2885* is the first gene to be inactivated.

Deletion inactivation of a chromosomal copy of a gene in *E. coli* can be accomplished by integrative gene replacement. The principle of this method (Hamilton, C. M., et al 1989. *J. Bacteriol.* 171: 4617-4622) is to construct a mutant allele of the targeted gene, introduce that allele into the chromosome using a conditional suicide vector, and then force the removal of the native wild type allele and vector sequences. This will replace the native gene with a desired mutation(s) but leave promoters, operators, etc. intact. Essentiality of a gene is determined either by deduction from genetic analysis or by conditional expression of a wild type copy of the targeted gene (trans complementation).

The first step is to generate a mutant *b2885* allele using PCR amplification. Two sets of PCR primers are chosen to produce a copy of *b2885* with a large central deletion to inactivate the gene. In order to eliminate polar effects, it is desirable to construct a mutant allele comprising an in-frame deletion of most or all of the coding region of the *b2885* gene. Each set of PCR primers is chosen such that a region flanking the gene to be amplified is sufficiently long to allow recombination (typically at least 500 nucleotides on each side of the deletion). The targeted deletion or mutation will be contained within this fragment. To facilitate cloning of the PCR product, the PCR primers may also contain restriction endonuclease sites found in the cloning region of a conditional knockout vector such as pKO3 (Link, et al 1997 *J. Bacteriol.* 179 (20): 6228-6237). Suitable sites include *NofI*, *SaII*, *BamHI* and *SmaI*. The *b2885* gene fragments are produced using standard PCR conditions including, but not limited to, those outlined in the manufacturers directions for the Hot Start Taq PCR kit (Qiagen, Inc., Valencia, CA). The PCR reactions will produce two fragments that can be fused together. Alternatively, crossover PCR can be used to generate a desired deletion in one step (Ho, S. N., et al 1989. *Gene* 77: 51-59, Horton, R. M., et al 1989. *Gene* 77: 61-68). The mutant allele thus produced is called a "null" allele because it cannot produce a functional gene product.

The mutant allele obtained from PCR amplification is cloned into the multiple cloning site of pKO3. Directional cloning of the *b2885* null allele is not necessary. The pKO3 vector has a temperature-sensitive origin of replication derived from pSC101. Therefore, clones are propagated at the permissive temperature of 30°C. The vector also contains two selectable marker genes: one that confers resistance to chloramphenicol and another, the *Bacillus subtilis sacB* gene, that allows for counter-selection on sucrose containing growth medium. Clones that contain vector DNA with the null allele inserted are confirmed by restriction endonuclease analysis and DNA sequence analysis of isolated plasmid DNA. The plasmid containing the *b2885* null allele insert is known as a knockout plasmid.

Once the knockout plasmid has been constructed and its sequence verified, it is transformed into a *Rec⁺* *E. coli* host cell. Transformation can be by any standard method such as electroporation. In some fraction of the transformed cells, plasmids will integrate into the *E. coli* chromosome by homologous recombination between the *b2885* null allele in the plasmid and the

b2885 gene in the chromosome. Transformant colonies in which such an event has occurred are readily selected by growth at the non-permissive temperature of 43°C and in the presence of chloramphenicol. At this temperature, the plasmid will not replicate as an episome and will be lost from cells as they grow and divide. These cells are no longer resistant to chloramphenicol and will not grow when it is present. However, cells in which the knockout plasmid has integrated into the *E. coli* chromosome remain resistant to chloramphenicol and propagate.

Cells containing integrated knock-out plasmids are usually the result of a single crossover event that creates a tandem repeat of the mutant and native wild type alleles of *b2885* separated by the vector sequences. A consequence of this is that *b2885* will still be expressed in these cells. In order to determine if the gene is essential for growth, the wild type copy must be removed. This is accomplished by selecting for plasmid excision, a process in which homologous recombination between the two alleles results in looping out of the plasmid sequences. Cells that have undergone such an excision event and have lost plasmid sequences including *sacB* gene are selected for by addition of sucrose to the medium. The *sacB* gene product converts sucrose to a toxic molecule. Thus counter selection with sucrose ensures that plasmid sequences are no longer present in the cell. Loss of plasmid sequences is further confirmed by testing for sensitivity to chloramphenicol (loss of the chloramphenicol resistance gene). The latter test is important because occasionally a mutation in the *sacB* gene can occur resulting in a loss of *sacB* function with no effect on plasmid replication (Link, et. al., 1997 *J. Bacteriol.* 179 (20): 6228-6237). These artifact clones retain plasmid sequences and are therefore still resistant to chloramphenicol.

In the process of plasmid excision, one of the two *b2885* alleles is lost from the chromosome along with the plasmid DNA. In general, it is equally likely that the null allele or the wild type allele will be lost. Therefore, if the *b2885* gene is not essential, half of the clones obtained in this experiment will have the wild type allele on the chromosome and half will have the null allele. However, if the *b2885* gene is essential, cells containing the null allele will not be obtained as a single copy of the null allele would be lethal.

To determine the essentiality of *b2885*, a statistically significant number of the resulting clones, at least 20, are analyzed by PCR amplification of the *b2885* gene. Since the null allele is missing a significant portion of the *b2885* gene, its PCR product is significantly shorter than that of the wild type gene and the two are readily distinguished by gel electrophoretic analysis. The PCR products may also be subjected to sequence determination for further confirmation by methods well known to those in the art.

The above experiment is generally adequate for determining the essentiality of a gene such as *b2885*. However, it may be necessary or desirable to more directly confirm the essentiality of the gene. There are several methods by which this can be accomplished. In general, these involve three steps: 1) construction of an episome containing a wild type allele, 2) isolation of clones containing a single chromosomal copy of the mutant null allele as described above but in the

presence of the episomal wild type allele, and then 3) determining if the cells survive when the expression of the episomal allele is shut off. In this case, the trans copy of wild type *b2885* is made by PCR cloning of the entire coding region of *b2885* and inserting it in the sense orientation downstream of an inducible promoter such as the *E. coli lac* promoter. Transcription of this allele of *b2885* will be induced in the presence of IPTG which inactivates the *lac* repressor. Under IPTG induction *b2885* protein will be expressed as long as the recombinant gene also possesses a ribosomal binding site, also known as a "Shine-Dalgarno Sequence". The trans copy of *b2885* is cloned on a plasmid that is compatible with pSC101. Compatible vectors include p15A, pBR322, and the pUC plasmids, among others. Replication of the compatible plasmid will not be temperature-sensitive. The entire process of integrating the null allele of *b2885* and subsequent plasmid excision is carried out in the presence of IPTG to ensure the expression of functional *b2885* protein is maintained throughout. After the null *b2885* allele is confirmed as integrated on the chromosome in place of the wild type *b2885* allele, then IPTG is withdrawn and expression of functional *b2885* protein shut off. If the *b2885* gene is essential, cells will cease to proliferate under these conditions. However, if the *b2885* gene is not essential, cells will continue to proliferate under these conditions. In this experiment, essentiality is determined by conditional expression of a wild type copy of the gene rather than inability to obtain the intended chromosomal disruption.

An advantage of this method over some other gene disruption techniques is that the targeted gene can be deleted or mutated without the introduction of large segments of foreign DNA. Therefore, polar effects on downstream genes are eliminated or minimized. There are methods described to introduce inducible promoters upstream of potential essential bacterial genes. However in such cases, polarity from multiple transcription start points can be a problem. One way of preventing this is to insert a gene disruption cassette that contains strong transcriptional terminators upstream of the integrated inducible promoter (Zhang, Y, and Cronan, J. E. 1996 *J. Bacteriol.* 178 (12): 3614-3620). The described techniques will all be familiar to one of ordinary skill in the art.

Following the analysis of the *b2885* gene, the other genes of the operon are investigated to determine if they are required for proliferation.

EXAMPLE 6

Expression of the Proteins Encoded by Genes Identified as Required for *E. coli* Proliferation

The following is provided as one exemplary method to express the proliferation-required proteins encoded by the identified sequences described above. First, the initiation and termination codons for the gene are identified. If desired, methods for improving translation or expression of the protein are well known in the art. For example, if the nucleic acid encoding the polypeptide to be expressed lacks a methionine codon to serve as the initiation site, a strong Shine-Dalgarno sequence, or a stop codon, these sequences can be added. Similarly, if the identified nucleic acid sequence lacks a

transcription termination signal, this sequence can be added to the construct by, for example, splicing out such a sequence from an appropriate donor sequence. In addition, the coding sequence may be operably linked to a strong promoter or an inducible promoter if desired. The identified nucleic acid sequence or portion thereof encoding the polypeptide to be expressed is obtained by PCR from the bacterial expression vector or genome using oligonucleotide primers complementary to the identified nucleic acid sequence or portion thereof and containing restriction endonuclease sequences for *NcoI* incorporated into the 5' primer and *BglII* at the 5' end of the corresponding 3'-primer, taking care to ensure that the identified nucleic acid sequence is positioned in frame with the termination signal. The purified fragment obtained from the resulting PCR reaction is digested with *NcoI* and *BglII*, purified and ligated to an expression vector.

The ligated product is transformed into DH5 α or some other *E. coli* strain suitable for the over expression of potential proteins. Transformation protocols are well known in the art. For example, transformation protocols are described in: **Current Protocols in Molecular Biology**, Vol. 1, Unit 1.8, (Ausubel, et al., Eds.) John Wiley & Sons, Inc. (1997). Positive transformants are selected after growing the transformed cells on plates containing 50-100 μ g/ml Ampicillin (Sigma, St. Louis, Missouri). In one embodiment, the expressed protein is held in the cytoplasm of the host organism. In an alternate embodiment, the expressed protein is released into the culture medium. In still another alternative, the expressed protein can be sequestered in the periplasmic space and liberated therefrom using any one of a number of cell lysis techniques known in the art. For example, the osmotic shock cell lysis method described in Chapter 16 of **Current Protocols in Molecular Biology**, Vol. 2, (Ausubel, et al., Eds.) John Wiley & Sons, Inc. (1997). Each of these procedures can be used to express a proliferation-required protein.

Expressed proteins, whether in the culture medium or liberated from the periplasmic space or the cytoplasm, are then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, standard chromatography, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and HPLC. Alternatively, the secreted protein can be in a sufficiently enriched or pure state in the supernatant or growth media of the host to permit it to be used for its intended purpose without further enrichment. The purity of the protein product obtained can be assessed using techniques such as Coomassie or silver staining or using antibodies against the control protein. Coomassie and silver staining techniques are familiar to those skilled in the art.

Antibodies capable of specifically recognizing the protein of interest can be generated using synthetic peptides using methods well known in the art. See, **Antibodies: A Laboratory Manual**, (Harlow and Lane, Eds.) Cold Spring Harbor Laboratory (1988). For example, 15-mer peptides having a sequence encoded by the appropriate identified gene sequence of interest or portion thereof can be chemically synthesized. The synthetic peptides are injected into mice to generate antibodies to the polypeptide encoded by the identified nucleic acid sequence of interest or portion thereof.

Alternatively, samples of the protein expressed from the expression vectors discussed above can be purified and subjected to amino acid sequencing analysis to confirm the identity of the recombinantly expressed protein and subsequently used to raise antibodies. An Example describing in detail the generation of monoclonal and polyclonal antibodies appears in Example 7.

5 The protein encoded by the identified nucleic acid sequence of interest or portion thereof can be purified using standard immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to
10 remove non-specifically bound proteins. The specifically bound secreted protein is then released from the column and recovered using standard techniques. These procedures are well known in the art.

 In an alternative protein purification scheme, the identified nucleic acid sequence of interest or portion thereof can be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies the coding sequence of the identified nucleic acid
15 sequence of interest or portion thereof is inserted in-frame with the gene encoding the other half of the chimera. The other half of the chimera can be maltose binding protein (MBP) or a nickel binding polypeptide encoding sequence. A chromatography matrix having antibody to MBP or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites can be engineered between
20 the MBP gene or the nickel binding polypeptide and the identified expected gene of interest, or portion thereof. Thus, the two polypeptides of the chimera can be separated from one another by protease digestion.

 One useful expression vector for generating maltose binding protein fusion proteins is pMAL (New England Biolabs), which encodes the *malE* gene. In the pMal protein fusion system, the cloned gene is inserted into a pMal vector downstream from the *malE* gene. This results in the expression of
25 an MBP-fusion protein. The fusion protein is purified by affinity chromatography. These techniques as described are well known to those skilled in the art of molecular biology.

EXAMPLE 7

Production of an Antibody to an isolated *E. coli* Protein

Substantially pure protein or polypeptide is isolated from the transformed cells as described in Example
30 6. The concentration of protein in the final preparation is adjusted, for example, by concentration on a 10,000 molecular weight cut off AMICON filter device (Millipore, Bedford, MA), to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can
35 be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495 (1975) or any of the well-known derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom

over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed
5 in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as described by Engvall, E., "Enzyme immunoassay ELISA and EMIT," **Meth. Enzymol.** 70:419 (1980), and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody
10 production are described in Davis, L. et al. **Basic Methods in Molecular Biology** Elsevier, New York. Section 21-2.

Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogeneous epitopes of a single protein or a peptide can be prepared by immunizing suitable animals with the expressed protein or peptides derived
15 therefrom described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than larger molecules and can require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng
20 level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al. **J. Clin. Endocrinol. Metab.** 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar
25 against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. et al., Chap. 19 in: **Handbook of Experimental Immunology** D. Wier (ed) Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μ M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: **Manual of Clinical Immunology**, 2d Ed. (Rose and Friedman,
30 Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980).

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies can also be used in therapeutic compositions for killing bacterial cells
35 expressing the protein.

EXAMPLE 8**Screening Chemical Libraries****A. Protein-Based Assays**

Having isolated and expressed bacterial proteins shown to be required for bacterial proliferation, the present invention further contemplates the use of these expressed proteins in assays to screen libraries of compounds for potential drug candidates. The generation of chemical libraries is well known in the art. For example combinatorial chemistry can be used to generate a library of compounds to be screened in the assays described herein. A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining amino acids in every possible combination to yield peptides of a given length. Millions of chemical compounds theoretically can be synthesized through such combinatorial use of chemical building blocks. For example, one commentator observed that the systematic, combinatorial mixing of 100 interchangeable chemical building blocks results in the theoretical synthesis of 100 million tetrameric compounds or 10 billion pentameric compounds. (Gallop et al., "Applications of Combinatorial Technologies to Drug Discovery, Background and Peptide Combinatorial Libraries," *Journal of Medicinal Chemistry*, Vol. 37, No. 9, 1233-1250 (1994). Other chemical libraries known to those in the art may also be used, including natural product libraries.

Once generated, combinatorial libraries can be screened for compounds that possess desirable biological properties. For example, compounds which may be useful as drugs or to develop drugs would likely have the ability to bind to the target protein identified, expressed and purified as discussed above. Further, if the identified target protein is an enzyme, candidate compounds would likely interfere with the enzymatic properties of the target protein. Any enzyme can be a target protein. For example, the enzymatic function of a target protein can be to serve as a protease, nuclease, phosphatase, dehydrogenase, transporter protein, transcriptional enzyme, and any other type of enzyme known or unknown. Thus, the present invention contemplates using the protein products described above to screen combinatorial and other chemical libraries.

Those in the art will appreciate that a number of techniques exist for characterizing target proteins in order to identify molecules useful for the discovery and development of therapeutics. For example, some techniques involve the generation and use of small peptides to probe and analyze target proteins both biochemically and genetically in order to identify and develop drug leads. Such techniques include the methods described in PCT publications No. WO9935494, WO9819162, WO9954728.

In another example, the target protein is a serine protease and the substrate of the enzyme is known. The present example is directed towards the analysis of libraries of compounds to identify compounds that function as inhibitors of the target enzyme. First, a library of small molecules is

generated using methods of combinatorial library formation well known in the art. U.S. Patent NOs. 5,463,564 and 5,574, 656, to Agrafiotis, et al., entitled "System and Method of Automatically Generating Chemical Compound with Desired Properties," are two such teachings. Then the library compounds are screened to identify library compounds that possess desired structural and functional properties. U.S. Patent No. 5,684,711, also discusses a method for screening libraries.

To illustrate the screening process, the combined target and chemical compounds of the library are exposed to and permitted to interact with the purified enzyme. A labeled substrate is added to the incubation. The label on the substrate is such that a detectable signal is emitted from metabolized substrate molecules. The emission of this signal permits one to measure the effect of the combinatorial library compounds on the enzymatic activity of target enzymes. The characteristics of each library compound is encoded so that compounds demonstrating activity against the enzyme can be analyzed and features common to the various compounds identified can be isolated and combined into future iterations of libraries.

Once a library of compounds is screened, subsequent libraries are generated using those chemical building blocks that possess the features shown in the first round of screen to have activity against the target enzyme. Using this method, subsequent iterations of candidate compounds will possess more and more of those structural and functional features required to inhibit the function of the target enzyme, until a group of enzyme inhibitors with high specificity for the enzyme can be found. These compounds can then be further tested for their safety and efficacy as antibiotics for use in mammals.

It will be readily appreciated that this particular screening methodology is exemplary only. Other methods are well known to those skilled in the art. For example, a wide variety of screening techniques are known for a large number of naturally-occurring targets when the biochemical function of the target protein is known.

25 B. Cell-based Assays

Current cell-based assays used to identify or to characterize compounds for drug discovery and development frequently depend on detecting the ability of a test compound to inhibit the activity of a target molecule located within a cell or located on the surface of a cell. An advantage of cell-based assays is that they allow the effect of a compound on a target molecule's activity to be detected within the physiologically relevant environment of the cell as opposed to an *in vitro* environment. Most often such target molecules are proteins such as enzymes, receptors and the like. However, target molecules may also include other molecules such as DNAs, lipids, carbohydrates and RNAs including messenger RNAs, ribosomal RNAs, tRNAs and the like. A number of highly sensitive cell-based assay methods are available to those of skill in the art to detect binding and interaction of test compounds with specific target molecules. However, these methods are generally not highly effective when the test compound binds to or otherwise interacts with its target molecule with moderate or low affinity. In addition, the target molecule may not be

readily accessible to a test compound in solution, such as when the target molecule is located inside the cell or within a cellular compartment such as the periplasm of a bacterial cell. Thus, current cell-based assay methods are limited in that they are not effective in identifying or characterizing compounds that interact with their targets with moderate to low affinity or compounds that interact with targets that are not readily accessible.

Cell-based assay methods of the present invention have substantial advantages over current cell-based assays practiced in the art. These advantages derive from the use of sensitized cells in which the level or activity of a proliferation-required gene product (the target molecule) has been specifically reduced to the point where the presence or absence of its function becomes a rate-determining step for cellular proliferation. Bacterial, fungal, plant, or animal cells can all be used with the present method. Such sensitized cells become much more sensitive to compounds that are active against the affected target molecule. Thus, cell-based assays of the present invention are capable of detecting compounds exhibiting low or moderate potency against the target molecule of interest because such compounds are substantially more potent on sensitized cells than on non-sensitized cells. The effect may be such that a test compound may be two to several times more potent, at least 10 times more potent, at least 20 times more potent, at least 50 times more potent, at least 100 times more potent, at least 1000 times more potent, or even more than 1000 times more potent when tested on the sensitized cells as compared to the non-sensitized cells.

Due in part to the increased appearance of antibiotic resistance in pathogenic microorganisms and to the significant side-effects associated with some currently used antibiotics, novel antibiotics acting at new targets are highly sought after in the art. Yet, another limitation in the current art related to cell-based assays is the problem of identifying hits against the same kinds of target molecules in the same limited set of biological pathways over and over again. This may occur when compounds acting at such new targets are discarded, ignored or fail to be detected because compounds acting at the "old" targets are encountered more frequently and are more potent than compounds acting at the new targets. As a result, the majority of antibiotics in use currently interact with a relatively small number of target molecules within an even more limited set of biological pathways.

The use of sensitized cells of the current invention provides a solution to the above problem in two ways. First, desired compounds acting at a target of interest, whether a new target or a previously known but poorly exploited target, can now be detected above the "noise" of compounds acting at the "old" targets due to the specific and substantial increase in potency of such desired compounds when tested on the sensitized cells of the current invention. Second, the methods used to sensitize cells to compounds acting at a target of interest may also sensitize these cells to compounds acting at other target molecules within the same biological pathway. For example, expression of an antisense molecule to a gene encoding a ribosomal protein is expected to sensitize the cell to compounds acting at that ribosomal protein and may also sensitize the cells to

compounds acting at any of the ribosomal components (proteins or rRNA) or even to compounds acting at any target which is part of the protein synthesis pathway. Thus an important advantage of the present invention is the ability to reveal new targets and pathways that were previously not readily accessible to drug discovery methods.

5 Sensitized cells of the present invention are prepared by reducing the activity or level of a target molecule. The target molecule may be a gene product, such as an RNA or polypeptide produced from the proliferation-required nucleic acids described herein. Alternatively, the target may be a gene product such as an RNA or polypeptide which is produced from a sequence within the same operon as the proliferation-required nucleic acids described herein. In addition, the target
10 may be an RNA or polypeptide in the same biological pathway as the proliferation-required nucleic acids described herein. Such biological pathways include, but are not limited to, enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such the cell wall.

Current methods employed in the arts of medicinal and combinatorial chemistries are able
15 to make use of structure-activity relationship information derived from testing compounds in various biological assays including direct binding assays and cell-based assays. Occasionally compounds are directly identified in such assays that are sufficiently potent to be developed as drugs. More often, initial hit compounds exhibit moderate or low potency. Once a hit compound is identified with low or moderate potency, directed libraries of compounds are synthesized and tested
20 in order to identify more potent leads. Generally these directed libraries are combinatorial chemical libraries consisting of compounds with structures related to the hit compound but containing systematic variations including additions, subtractions and substitutions of various structural features. When tested for activity against the target molecule, structural features are identified that either alone or in combination with other features enhance or reduce activity. This information is
25 used to design subsequent directed libraries containing compounds with enhanced activity against the target molecule. After one or several iterations of this process, compounds with substantially increased activity against the target molecule are identified and may be further developed as drugs. This process is facilitated by use of the sensitized cells of the present invention since compounds acting at the selected targets exhibit increased potency in such cell-based assays, thus; more
30 compounds can now be characterized providing more useful information than would be obtained otherwise.

Thus, it is now possible using cell-based assays of the present invention to identify or characterize compounds that previously would not have been readily identified or characterized including compounds that act at targets that previously were not readily exploited using cell-based
35 assays. The process of evolving potent drug leads from initial hit compounds is also substantially improved by the cell-based assays of the present invention because, for the same number of test compounds, more structure-function relationship information is likely to be revealed.

The method of sensitizing a cell entails selecting a suitable gene or operon. A suitable gene or operon is one whose expression is required for the proliferation of the cell to be sensitized. The next step is to introduce into the cells to be sensitized, an antisense RNA capable of hybridizing to the suitable gene or operon or to the RNA encoded by the suitable gene or operon. Introduction of the antisense RNA can be in the form of an expression vector in which antisense RNA is produced under the control of an inducible promoter. The amount of antisense RNA produced is limited by varying the inducer concentration to which the cell is exposed and thereby varying the activity of the promoter driving transcription of the antisense RNA. Thus, cells are sensitized by exposing them to an inducer concentration that results in a sub-lethal level of antisense RNA expression.

In one embodiment of the cell-based assays, the identified exogenous *E. coli* nucleotide sequences of the present invention are used to inhibit the production of a proliferation-required protein. Expression vectors producing antisense RNA complementary to identified genes required for proliferation are used to limit the concentration of a proliferation-required protein without severely inhibiting growth. To achieve that goal, a growth inhibition dose curve of inducer is calculated by plotting various doses of inducer against the corresponding growth inhibition caused by the antisense expression. From this curve, various percentages of antisense induced growth inhibition, from 1 to 100% can be determined. If the promoter contained in the expression vector contains a *lac* operator the transcription is regulated by *lac* repressor and expression from the promoter is inducible with IPTG. For example, the highest concentration of the inducer IPTG that does not reduce the growth rate significantly (0% growth inhibition) can be predicted from the curve. Cellular proliferation can be monitored by growth medium turbidity via OD measurements. In another example, the concentration of inducer that reduces growth by 25% can be predicted from the curve. In still another example, a concentration of inducer that reduces growth by 50% can be calculated. Additional parameters such as colony forming units (cfu) can be used to measure cellular viability.

Cells to be assayed are exposed to the above-determined concentrations of inducer. The presence of the inducer at this sub-lethal concentration reduces the amount of the proliferation required gene product to a low amount in the cell that will limit but not prevent growth. Cells grown in the presence of this concentration of inducer are therefore specifically more sensitive to inhibitors of the proliferation-required protein or RNA of interest or to inhibitors of proteins or RNAs in the same biological pathway as the proliferation-required protein or RNA of interest but not to inhibitors of unrelated proteins or RNAs.

Cells pretreated with sub-inhibitory concentrations of inducer and thus containing a reduced amount of proliferation-required target gene product are then used to screen for compounds that reduce cell growth. The sub-lethal concentration of inducer may be any concentration consistent with the intended use of the assay to identify candidate compounds to which the cells are more sensitive. For example, the sub-lethal concentration of the inducer may be such that growth

inhibition is at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60% at least about 75%, 90%, 95% or more. Cells which are pre-sensitized using the preceding method are more sensitive to inhibitors of the target protein because these cells contain less target protein to be inhibited than do wild-type cells.

In another embodiment of the cell-based assays of the present invention, the level or activity of a proliferation required gene product is reduced using a mutation, such as a temperature sensitive mutation, in the proliferation-required sequence and an antisense nucleic acid complementary to the proliferation-required sequence. Growing the cells at an intermediate temperature between the permissive and restrictive temperatures of the temperature sensitive mutant where the mutation is in a proliferation-required gene produces cells with reduced activity of the proliferation-required gene product. The antisense RNA complementary to the proliferation-required sequence further reduces the activity of the proliferation-required gene product. Drugs that may not have been found using either the temperature sensitive mutation or the antisense nucleic acid alone may be identified by determining whether cells in which expression of the antisense nucleic acid has been induced and which are grown at a temperature between the permissive temperature and the restrictive temperature are substantially more sensitive to a test compound than cells in which expression of the antisense nucleic acid has not been induced and which are grown at a permissive temperature. Also drugs found previously from either the antisense nucleic acid alone or the temperature sensitive mutation alone may have a different sensitivity profile when used in cells combining the two approaches, and that sensitivity profile may indicate a more specific action of the drug in inhibiting one or more activities of the gene product.

Temperature sensitive mutations may be located at different sites within the gene and correspond to different domains of the protein. For example, the *dnaB* gene of *Escherichia coli* encodes the replication fork DNA helicase. DnaB has several domains, including domains for oligomerization, ATP hydrolysis, DNA binding, interaction with primase, interaction with DnaC, and interaction with DnaA [(Biswas, E.E. and Biswas, S.B. 1999 Mechanism and DnaB helicase of *Escherichia coli*: structural domains involved in ATP hydrolysis, DNA binding, and oligomerization. *Biochem.* 38:10919-10928; Hiasa, H. and Marians, K.J. 1999 Initiation of bidirectional replication at the chromosomal origin is directed by the interaction between helicase and primase. *J. Biol. Chem.* 274:27244-27248; San Martin, C., Radermacher, M., Wolpensinger, B., Engel, A., Miles, C.S., Dixon, N.E., and Carazo, J.M. 1998 Three-dimensional reconstructions from cryoelectron microscopy images reveal an intimate complex between helicase DnaB and its loading partner DnaC. *Structure* 6:501-9; Sutton, M.D., Carr, K.M., Vicente, M., and Kaguni, J.M. 1998 *Escherichia coli* DnaA protein. The N-terminal domain and loading of DnaB helicase at the *E. coli* chromosomal. *J. Biol. Chem.* 273:34255-62)]. Temperature sensitive mutations in different domains of DnaB confer different phenotypes at the restrictive temperature, which include either an

abrupt stop or slow stop in DNA replication with or without DNA breakdown (Wechsler, J.A. and Gross, J.D. 1971. *Escherichia coli* mutants temperature-sensitive for DNA synthesis. Mol. Gen. Genetics 113:273-284) and termination of growth or cell death. Combining the use of temperature sensitive mutations in the *dnaB* gene that cause cell death at the restrictive temperature with an antisense to the *dnaB* gene could lead to the discovery of very specific and effective inhibitors of one or a subset of activities exhibited by DnaB.

It will be appreciated that the above method may be performed with any mutation which reduces but does not eliminate the activity or level of the gene product which is required for proliferation.

When screening for antimicrobial agents against a gene product required for proliferation, growth inhibition of cells containing a limiting amount of that proliferation-required gene product can be assayed. Growth inhibition can be measured by directly comparing the amount of growth, measured by the optical density of the growth medium, between an experimental sample and a control sample. Alternative methods for assaying cell proliferation include measuring green fluorescent protein (GFP) reporter construct emissions, various enzymatic activity assays, and other methods well known in the art.

It will be appreciated that the above method may be performed in solid phase, liquid phase or a combination of the two. For example, cells grown on nutrient agar containing the inducer of the antisense construct may be exposed to compounds spotted onto the agar surface. A compound's effect may be judged from the diameter of the resulting killing zone, the area around the compound application point in which cells do not grow. Multiple compounds may be transferred to agar plates and simultaneously tested using automated and semi-automated equipment including but not restricted to multi-channel pipettes (for example the Beckman Multimek) and multi-channel spotters (for example the Genomic Solutions Flexys). In this way multiple plates and thousands to millions of compounds may be tested per day.

The compounds may also be tested entirely in liquid phase using microtiter plates as described below. Liquid phase screening may be performed in microtiter plates containing 96, 384, 1536 or more wells per microtiter plate to screen multiple plates and thousands to millions of compounds per day. Automated and semi-automated equipment may be used for addition of reagents (for example cells and compounds) and determination of cell density.

EXAMPLE 9

Cell-based Assay Using Antisense Complementary to Genes Encoding Ribosomal Proteins

The effectiveness of the above cell-based assay was validated using constructs expressing antisense RNA to the proliferation required *E. coli* genes *rplL*, *rplJ*, and *rplW* encoding ribosomal proteins L7/L12, L10 and L23 respectively. These proteins are part of the protein synthesis apparatus of the cell and as such are required for proliferation. These constructs were used to test the effect of antisense expression on cell sensitivity to antibiotics known to bind to the ribosome

and thereby inhibit protein synthesis. Constructs expressing antisense RNA to several other genes (*elaD*, *visC*, *yohH*, and *atpE/B*), the products of which are not involved in protein synthesis were used for comparison.

First, pLEX5BA (Krause et al., J. Mol. Biol. 274: 365 (1997)) expression vectors
5 containing antisense constructs to either *rplW* or to *elaD* were introduced into separate *E. coli* cell populations. Vector introduction is a technique well known to those of ordinary skill in the art. The expression vectors of this example contain IPTG inducible promoters that drive the expression of the antisense RNA in the presence of the inducer. However, those skilled in the art will appreciate that other inducible promoters may also be used. Suitable expression vectors are also
10 well known in the art. The *E. coli* antisense clones to genes encoding ribosomal proteins L7/L12, L10 and L23 were used to test the effect of antisense expression on cell sensitivity to the antibiotics known to bind to these proteins. Expression vectors containing antisense to either the genes encoding L7/L12 and L10 or L23 were introduced into separate *E. coli* cell populations.

The cell populations were exposed to a range of IPTG concentrations in liquid medium to
15 obtain the growth inhibitory dose curve for each clone (Fig. 1). First, seed cultures were grown to a particular turbidity that is measured by the optical density (OD) of the growth solution. The OD of the solution is directly related to the number of bacterial cells contained therein. Subsequently, sixteen 200 ul liquid medium cultures were grown in a 96 well microtiter plate at 37° C with a range of IPTG concentrations in duplicate two-fold serial dilutions from 1600 uM to 12.5 uM (final
20 concentration). Additionally, control cells were grown in duplicate without IPTG. These cultures were started from equal amounts of cells derived from the same initial seed culture of a clone of interest. The cells were grown for up to 15 hours and the extent of growth was determined by measuring the optical density of the cultures at 600 nm. When the control culture reached mid-log phase the percent growth (relative to the control culture) for each of the IPTG containing cultures
25 was plotted against the log concentrations of IPTG to produce a growth inhibitory dose response curve for the IPTG. The concentration of IPTG that inhibits cell growth to 50% (IC₅₀) as compared to the 0 mM IPTG control (0% growth inhibition) was then calculated from the curve. Under these conditions, an amount of antisense RNA was produced that reduced the expression levels of *rplW* and *elaD* to a degree such that growth was inhibited by 50%.

30 Alternative methods of measuring growth are also contemplated. Examples of these methods include measurements of proteins, the expression of which is engineered into the cells being tested and can readily be measured. Examples of such proteins include green fluorescent protein (GFP) and various enzymes.

Cells were pretreated with the selected concentration of IPTG and then used to test the
35 sensitivity of cell populations to tetracycline, erythromycin and other protein synthesis inhibitors. Figure 2 is an IPTG dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing either an antisense clone to the *E. coli rplW* gene (AS-*rplW*) which encodes ribosomal

protein L23 which is required for protein synthesis and essential for cell proliferation, or an antisense clone to the *elaD* (AS-*elaD*) gene which is not known to be involved in protein synthesis and which is also essential for proliferation.

An example of a tetracycline dose response curve is shown in Figures 2A and 2B for the *rplW* and *elaD* genes, respectively. Cells were grown to log phase and then diluted into media alone or media containing IPTG at concentrations which give 20% and 50% growth inhibition as determined by IPTG dose response curves. After 2.5 hours, the cells were diluted to a final OD₆₀₀ of 0.002 into 96 well plates containing (1) +/- IPTG at the same concentrations used for the 2.5 hour pre-incubation; and (2) serial two-fold dilutions of tetracycline such that the final concentrations of tetracycline range from 1 µg/ml to 15.6 ng/ml and 0 µg/ml. The 96 well plates were incubated at 37°C and the OD₆₀₀ was read by a plate reader every 5 minutes for up to 15 hours. For each IPTG concentration and the no IPTG control, tetracycline dose response curves were determined when the control (absence of tetracycline) reached 0.1 OD₆₀₀. To compare tetracycline sensitivity with and without IPTG, tetracycline IC_{50s} were determined from the dose response curves (Figs. 3A-B). Cells with reduced levels of L23 (AS-*rplW*) showed increased sensitivity to tetracycline (Fig. 2A) as compared to cells with reduced levels of the *elaD* gene product (AS-*elaD*) (Fig. 2B). Figure 3 shows a summary bar chart in which the ratios of tetracycline IC_{50s} determined in the presence of IPTG which gives 50% growth inhibition versus tetracycline IC_{50s} determined without IPTG (fold increase in tetracycline sensitivity) were plotted. Cells with reduced levels of either L7/L12 (encoded by genes *rplL*, *rplJ*) or L23 (encoded by the *rplW* gene) showed increased sensitivity to tetracycline (Fig. 3). Cells expressing antisense to genes not known to be involved in protein synthesis (AS-*atpB/E*, AS-*visC*, AS-*elaD*, AS-*yohH*) did not show the same increased sensitivity to tetracycline, validating the specificity of this assay (Fig. 3).

In addition to the above, it has been observed in initial experiments that clones expressing antisense RNA to genes involved in protein synthesis (including genes encoding ribosomal proteins L7/L12 & L10, L7/L12 alone, L22, and L18, as well as genes encoding rRNA and Elongation Factor G) have increased sensitivity to the macrolide, erythromycin, whereas clones expressing antisense to the non-protein synthesis genes *elaD*, *atpB/E* and *visC* do not. Furthermore, the clone expressing antisense to *rplL* and *rplJ* does not show increased sensitivity to nalidixic acid and ofloxacin, antibiotics which do not inhibit protein synthesis.

The results with the ribosomal protein genes *rplL*, *rplJ*, and *rplW* as well as the initial results using various other antisense clones and antibiotics show that limiting the concentration of an antibiotic target makes cells more sensitive to the antimicrobial agents that specifically interact with that protein. The results also show that these cells are sensitized to antimicrobial agents that inhibit the overall function in which the protein target is involved but are not sensitized to antimicrobial agents that inhibit other functions.

The cell-based assay described above may also be used to identify the biological pathway in which a proliferation-required nucleic acid or its gene product lies. In such methods, cells expressing a sub-lethal level of antisense to a target proliferation-required nucleic acid and control cells in which expression of the antisense has not been induced are contacted with a panel of antibiotics known to act in various pathways. If the antibiotic acts in the pathway in which the target proliferation-required nucleic acid or its gene product lies, cells in which expression of the antisense has been induced will be more sensitive to the antibiotic than cells in which expression of the antisense has not been induced.

As a control, the results of the assay may be confirmed by contacting a panel of cells expressing antisense nucleic acids to many different proliferation-required genes including the target proliferation-required gene. If the antibiotic is acting specifically, heightened sensitivity to the antibiotic will be observed only in the cells expressing antisense to a target proliferation-required gene (or cells expressing antisense to other proliferation-required genes in the same pathway as the target proliferation-required gene) but will not be observed generally in all cells expressing antisense to proliferation-required genes.

Similarly, the above method may be used to determine the pathway on which a test compound, such as a test antibiotic acts. A panel of cells, each of which expresses antisense to a proliferation-required nucleic acid in a known pathway, is contacted with a compound for which it is desired to determine the pathway on which it acts. The sensitivity of the panel of cells to the test compound is determined in cells in which expression of the antisense has been induced and in control cells in which expression of the antisense has not been induced. If the test compound acts on the pathway on which an antisense nucleic acid acts, cells in which expression of the antisense has been induced will be more sensitive to the compound than cells in which expression of the antisense has not been induced. In addition, control cells in which expression of antisense to proliferation-required genes in other pathways has been induced will not exhibit heightened sensitivity to the compound. In this way, the pathway on which the test compound acts may be determined.

The Example below provides one method for performing such assays.

EXAMPLE 10

Identification of the Pathway in which a Proliferation-Required Gene Lies or the Pathway on which an Antibiotic Acts

A. Preparation of Bacterial Stocks for Assay

To provide a consistent source of cells to screen, frozen stocks of host bacteria containing the desired antisense construct are prepared using standard microbiological techniques. For example, a single clone of the organism can be isolated by streaking out a sample of the original stock onto an agar plate containing nutrients for cell growth and an antibiotic for which the antisense construct contains a gene which confers resistance. After overnight growth an isolated

colony is picked from the plate with a sterile needle and transferred to an appropriate liquid growth media containing the antibiotic required for maintenance of the plasmid. The cells are incubated at 30°C to 37°C with vigorous shaking for 4 to 6 hours to yield a culture in exponential growth. Sterile glycerol is added to 15% (volume to volume) and 100µL to 500 µL aliquots are distributed into
5 sterile cryotubes, snap frozen in liquid nitrogen, and stored at -80°C for future assays.

B. Growth of Bacteria for Use in the Assay

A day prior to an assay, a stock vial is removed from the freezer, rapidly thawed (37°C water bath) and a loop of culture is streaked out on an agar plate containing nutrients for cell growth and an antibiotic to which the antisense construct confers resistance. After overnight growth at
10 37°C, ten randomly chosen, isolated colonies are transferred from the plate (sterile inoculum loop) to a sterile tube containing 5 mL of LB medium containing the antibiotic to which the antisense vector confers resistance. After vigorous mixing to form a homogeneous cell suspension, the optical density of the suspension is measured at 600 nm (OD_{600}) and if necessary an aliquot of the suspension is diluted into a second tube of 5 mL, sterile, LB medium plus antibiotic to achieve an
15 $OD_{600} \leq 0.02$ absorbance units. The culture is then incubated at 37° C for 1-2 hrs with shaking until the OD_{600} reaches OD 0.2 – 0.3. At this point the cells are ready to be used in the assay.

C. Selection of Media to be Used in Assay

Two fold dilution series of the inducer are generated in culture media containing the appropriate antibiotic for maintenance of the antisense construct. Several media are tested side by
20 side and three to four wells are used to evaluate the effects of the inducer at each concentration in each media. For example, M9 minimal media, LB broth, TBD broth and Muller-Hinton media may be tested with the inducer IPTG at the following concentrations, 50 µM, 100 µM, 200 µM, 400 µM, 600 µM, 800 µM and 1000 µM. Equal volumes of test media-inducer and cells are added to the wells of a 384 well microtiter plate and mixed. The cells are prepared as described above and
25 diluted 1:100 in the appropriate media containing the test antibiotic immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several wells of each media that do not contain inducer, for example 0 µM IPTG. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD_{600} of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of inducer is calculated by comparing
30 the rates of logarithmic growth against that exhibited by cells growing in media without inducer. The medium yielding greatest sensitivity to inducer is selected for use in the assays described below.

D. Measurement of Test Antibiotic Sensitivity in the Absence of Antisense Construct Induction

Two-fold dilution series of antibiotics with a known mechanism of action are generated in
35 the culture media selected for further assay development that has been supplemented with the antibiotic used to maintain the construct. A panel of test antibiotics known to act on different

pathways is tested side by side with three to four wells being used to evaluate the effect of a test antibiotic on cell growth at each concentration. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the media selected for assay development supplemented with the antibiotic required to maintain the antisense construct and are diluted 1:100 in identical media immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several wells that contain the solvent used to dissolve the antibiotics but no antibiotic. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD₆₀₀ of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in media without antibiotic. A plot of percent inhibition against log[antibiotic concentration] allows extrapolation of an IC₅₀ value for each antibiotic.

E. Measurement of Test Antibiotic Sensitivity in the Presence of Antisense Construct Inducer

The culture media selected for use in the assay is supplemented with inducer at concentrations shown to inhibit cell growth by 50% and 80% as described above and the antibiotic used to maintain the construct. Two fold dilution series of the panel of test antibiotics used above are generated in each of these media. Several antibiotics are tested side by side with three to four wells being used to evaluate the effects of an antibiotic on cell growth at each concentration, in each media. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the media selected for use in the assay supplemented with the antibiotic required to maintain the antisense construct. The cells are diluted 1:100 into two 50 mL aliquots of identical media containing concentrations of inducer that have been shown to inhibit cell growth by 50% and 80 % respectively and incubated at 37°C with shaking for 2.5 hours. Immediately prior to addition to the microtiter plate wells, the cultures are adjusted to an appropriate OD₆₀₀ (typically 0.002) by dilution into warm (37°C) sterile media supplemented with identical concentrations of the inducer and antibiotic used to maintain the antisense construct. For a control, cells are also added to several wells that contain solvent used to dissolve test antibiotics but which contain no antibiotic. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD₆₀₀ of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in media without antibiotic. A plot of percent inhibition against log[antibiotic concentration] allows extrapolation of an IC₅₀ value for each antibiotic.

F. Determining the Specificity of the Test Antibiotics

A comparison of the IC₅₀s generated by antibiotics of known mechanism of action under antisense induced and non-induced conditions allows the pathway in which a proliferation-required

nucleic acid lies to be identified. If cells expressing an antisense nucleic acid against a proliferation-required gene are selectively sensitive to an antibiotic acting via a particular pathway, then the gene against which the antisense acts is involved in the pathway in which the antibiotic acts.

5 **G. Identification of Pathway in which a Test Antibiotic Acts**

As discussed above, the cell-based assay may also be used to determine the pathway against which a test antibiotic acts. In such an analysis, the pathways against which each member of a panel of antisense nucleic acids acts are identified as described above. A panel of cells, each containing an inducible nucleic acid complementary to a gene in a known proliferation-required pathway, is contacted with a test antibiotic for which it is desired to determine the pathway on which it acts under inducing and non-inducing conditions. If heightened sensitivity is observed in induced cells expressing antisense complementary to a gene in a particular pathway but not in induced cells expressing antisense complementary to genes in other pathways, then the test antibiotic acts against the pathway for which heightened sensitivity was observed.

15 One skilled in the art will appreciate that further optimization of the assay conditions, such as the concentration of inducer used to induce antisense expression and/or the growth conditions used for the assay (for example incubation temperature and media components) may further increase the selectivity and/or magnitude of the antibiotic sensitization exhibited.

The following example confirms the effectiveness of the methods described above.

20

EXAMPLE 11

Identification of the Pathway in which a Proliferation-Required Gene Lies

Antibiotics of various chemical classes and modes of action were purchased from Sigma Chemicals (St. Louis, MO). Stock solutions were prepared by dissolving each antibiotic in an appropriate aqueous solution based on information provided by the manufacturer. The final working solution of each antibiotic contained no more than 0.2% (w/v) of any organic solvent. To determine their potency against a bacterial strain engineered for expression of an antisense complementary to a proliferation-required gene encoding 50S ribosomal protein, each antibiotic was serially diluted two or three fold in growth medium supplemented with the appropriate antibiotic for maintenance of the anti-sense construct. At least ten dilutions were prepared for each antibiotic. 25 μ L aliquots of each dilution were transferred to discrete wells of a 384-well microplate (the assay plate) using a multi-channel pipette. Quadruplicate wells were used for each dilution of an antibiotic under each treatment condition (plus and minus inducer). Each assay plate contained twenty wells for cell growth controls (growth media replacing antibiotic), ten wells for each treatment (plus and minus inducer, in this example IPTG). Assay plates were usually divided into the two treatments: half the plate containing induced cells and an appropriate concentrations of inducer (in this example IPTG) to maintain the state of induction, the other half containing non-induced cells in the absence of IPTG.

Cells for the assay were prepared as follows. Bacterial cells containing a construct, from which expression of antisense nucleic acid complementary to *rplL* and *rplJ*, which encode proliferation-required 50S ribosomal subunit proteins, is inducible in the presence of IPTG, were grown into exponential growth (OD_{600} 0.2 to 0.3) and then diluted 1:100 into fresh media containing either 400 μ M or 0 μ M inducer (IPTG). These cultures were incubated at 37° C for 2.5 hr. After a 2.5 hr incubation, induced and non-induced cells were respectively diluted into an assay medium at a final OD_{600} value of 0.0004. The medium contained an appropriate concentration of the antibiotic for the maintenance of the anti-sense construct. In addition, the medium used to dilute induced cells was supplemented with 800 μ M IPTG so that addition to the assay plate would result in a final IPTG concentration of 400 μ M. Induced and non-induced cell suspensions were dispensed (25 μ l/well) into the appropriate wells of the assay plate as discussed previously. The plate was then loaded into a plate reader, incubated at constant temperature, and cell growth was monitored in each well by the measurement of light scattering at 595 nm. Growth was monitored every 5 minutes until the cell culture attained a stationary growth phase. For each concentration of antibiotic, a percentage inhibition of growth was calculated at the time point corresponding to mid-exponential growth for the associated control wells (no antibiotic, plus or minus IPTG). For each antibiotic and condition (plus or minus IPTG), a plot of percent inhibition versus log of antibiotic concentration was generated and the IC_{50} determined. A comparison of the IC_{50} for each antibiotic in the presence and absence of IPTG revealed whether induction of the antisense construct sensitized the cell to the mechanism of action exhibited by the antibiotic. Cells which exhibited a significant (standard statistical analysis) numerical decrease in the IC_{50} value in the presence of inducer were considered to have an increased sensitivity to the test antibiotic.

The results are provided in the table below, which lists the classes and names of the antibiotics used in the analysis, the targets of the antibiotics, the IC_{50} in the absence of IPTG, the IC_{50} in the presence of IPTG, the concentration units for the IC_{50} s, the fold increase in IC_{50} in the presence of IPTG, and whether increased sensitivity was observed in the presence of IPTG.

TABLE IV
Effect of Expression of Antisense RNA to rpL and rpJ on Antibiotic Sensitivity

ANTIBIOTIC CLASS /Names	TARGET	IC50 (-IPTG)	IC50 (+IPTG)	Conc. Unit	Fold Increase in Sensitivity	Sensitivity Increased?
PROTEIN SYNTHESIS INHIBITOR						
ANTIBIOTICS						
AMINOGLYCOSIDES						
Gentamicin	30S ribosome function	2715	19.19	ng/ml	141	Yes
Streptomycin	30S ribosome function	11280	161	ng/ml	70	Yes
Spectinomycin	30S ribosome function	18050	<156	ng/ml		Yes
Tobramycin	30S ribosome function	3594	70.58	ng/ml	51	Yes
MACROLIDES						
Erythromycin	50S ribosome function	7467	187	ng/ml	40	Yes
AROMATIC POLYKETIDES						
Tetracycline	30S ribosome function	199.7	1.83	ng/ml	109	Yes
Minocycline	30S ribosome function	668.4	3.897	ng/ml	172	Yes
Doxycycline	30S ribosome function	413.1	27.81	ng/ml	15	Yes
OTHER PROTEIN SYNTHESIS INHIBITORS						
Fusidic acid	Elongation Factor G function	59990	641	ng/ml	94	Yes
Chloramphenicol	30S ribosome function	465.4	1.516	ng/ml	307	Yes
Lincomycin	50S ribosome function	47150	324.2	ng/ml	145	Yes

ANTIBIOTIC CLASS /Names	TARGET	IC50 (-IPTG)	IC50 (+IPTG)	Conc. Unit	Fold Increase in Sensitivity	Sensitivity Increased?
OTHER ANTIBIOTIC MECHANISMS						
B-LACTAMS						
Cefoxitin	Cell wall biosynthesis	2782	2484	ng/ml	1	No
Cefotaxime	Cell wall biosynthesis	24.3	24.16	ng/ml	1	No
DNA SYNTHESIS INHIBITORS						
Nalidixic acid	DNA Gyrase activity	6973	6025	ng/ml	1	No
Ofloxacin	DNA Gyrase activity	49.61	45.89	ng/ml	1	No
OTHER						
Bacitracin	Cell membrane function Dihydrofolate Reductase activity	4077	4677	mg/ml	1	No
Trimethoprim		128.9	181.97	ng/ml	1	No
Vancomycin	Cell wall biosynthesis	145400	72550	ng/ml	2	No

The above results demonstrate that induction of an antisense RNA to genes encoding 50S ribosomal subunit proteins results in a selective and highly significant sensitization of cells to antibiotics that inhibit ribosomal function and protein synthesis. The above results further demonstrate that induction of an antisense construct to an essential gene sensitizes an organism to compounds that interfere with that gene products' biological role. This sensitization is restricted to compounds that interfere with pathways associated with the targeted gene and its product.

Assays utilizing antisense constructs to essential genes can be used to identify compounds that specifically interfere with the activity of multiple targets in a pathway. Such constructs can be used to simultaneously screen a sample against multiple targets in one pathway in one reaction (Combinatorial HTS).

Furthermore, as discussed above, panels of antisense construct containing cells may be used to characterize the point of intervention of any compound affecting an essential biological pathway including antibiotics with no known mechanism of action.

Another embodiment of the present invention is a method for determining the pathway against which a test antibiotic compound is active in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sub-lethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid is a target protein or nucleic acid corresponding to a proliferation-required nucleic acid identified using the methods described above. The method is similar to those described above for determining which pathway a test antibiotic acts against except that rather than reducing the activity or level of a proliferation-required gene product using a sub-lethal level of antisense to a proliferation-required nucleic acid, the activity or level of the proliferation-required gene product is reduced using sub-lethal level of a known antibiotic which acts against the proliferation required gene product.

Interactions between drugs which affect the same biological pathway has been described in the literature. For example, Mecillinam (Amdinocillin) binds to and inactivates the penicillin binding protein 2 (PBP2, product of the *mrdA* in *E. coli*). This antibiotic interacts with other antibiotics that inhibit PBP2 as well as antibiotics that inhibit other penicillin binding proteins such as PBP3 [(Gutmann, L., Vincent, S., Billot-Klein, D., Acar, J.F., Mrena, E., and Williamson, R. (1986) Involvement of penicillin-binding protein 2 with other penicillin-binding proteins in lysis of *Escherichia coli* by some beta-lactam antibiotics alone and in synergistic lytic effect of amdinocillin (mecillinam). Antimicrobial Agents & Chemotherapy, 30:906-912)]. Interactions between drugs could, therefore, involve two drugs that inhibit the same target protein or nucleic acid or inhibit different proteins or nucleic acids in the same pathway [(Fukuoka, T., Domon, H., Kakuta, M., Ishii, C., Hirasawa, A., Utsui, Y., Ohya, S., and Yasuda, H. (1997) Combination effect between panipenem and vancomycin on highly methicillin-resistant *Staphylococcus aureus*. Japan. J. Antibio. 50:411-419; Smith, C.E., Folen, B.E., Barrett, J.F., and Froese, M.B. (1997) Assessment

of the synergistic interactions of levofloxacin and ampicillin against *Enterococcus faecium* by the checkerboard agar dilution and time-kill methods. *Diagnos. Microbiol. Infect. Disease* 27:85-92; den Hollander, J.G., Horrevorts, A.M., van Goor, M.L., Verbrugh, H.A., and Mouton, J.W. (1997) Synergism between tobramycin and ceftazidime against a resistant *Pseudomonas aeruginosa* strain, tested in an in vitro pharmacokinetic model. *Antimicrobial Agents & Chemotherapy*. 41:95-110)].

Two drugs may interact even though they inhibit different targets. For example, the proton pump inhibitor, Omeprazole, and the antibiotic, Amoxycillin, two synergistic compounds acting together, can cure *Helicobacter pylori* infection [(Gabryelewicz, A., Laszewicz, W., Dzieniszewski, J., Ciok, J., Marlicz, K., Bielecki, D., Popiela, T., Legutko, J., Knapik, Z., Poniewierka, E. (1997) Multicenter evaluation of dual-therapy (omeprazol and amoxycillin) for *Helicobacter pylori*-associated duodenal and gastric ulcer (two years of the observation). *J. Physiol. Pharmacol.* 48 Suppl 4:93-105)].

The growth inhibition from the sub-lethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sub-lethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

Cells are contacted with a combination of each member of a panel of known antibiotics at a sub-lethal level and varying concentrations of the test antibiotic. As a control, the cells are contacted with varying concentrations of the test antibiotic alone. The IC_{50} of the test antibiotic in the presence and absence of the known antibiotic is determined. If the IC_{50} s in the presence and absence of the known drug are substantially similar, then the test drug and the known drug act on different pathways. If the IC_{50} s are substantially different, then the test drug and the known drug act on the same pathway.

Another embodiment of the present invention is a method for identifying a candidate compound for use as an antibiotic in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sub-lethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid is a target protein or nucleic acid corresponding to a proliferation-required nucleic acid identified using the methods described above. The method is similar to those described above for identifying candidate compounds for use as antibiotics except that rather than reducing the activity or level of a proliferation-required gene product using a sub-lethal level of antisense to a proliferation-required nucleic acid, the activity or level of the proliferation-required gene product is reduced using a sub-lethal level of a known antibiotic which acts against the proliferation required gene product.

The growth inhibition from the sub-lethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sub-lethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

In order to characterize test compounds of interest, cells are contacted with a panel of known antibiotics at a sub-lethal level and one or more concentrations of the test compound. As a control, the cells are contacted with the same concentrations of the test compound alone. The IC₅₀ of the test compound in the presence and absence of the known antibiotic is determined. If the IC₅₀ of the test compound is substantially different in the presence and absence of the known drug then the test compound is a good candidate for use as an antibiotic. As discussed above, once a candidate compound is identified using the above methods its structure may be optimized using standard techniques such as combinatorial chemistry.

Representative known antibiotics which may be used in each of the above methods are provided in the table below. However, it will be appreciated that other antibiotics may also be used.

ANTIBIOTIC	INHIBITS/TARGET	RESISTANT MUTANTS
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Inhibitors of Transcription

Rifamycin, 1959 Rifampicin Rifabutin Rifaximin	Inhibits initiation of transcription/ β -subunit RNA polymerase, <i>rpoB</i>	<i>rpoB</i> , <i>crp</i> , <i>cyaA</i>
Streptolydigin	Accelerates transcription chain termination/ β -subunit RNA polymerase	<i>rpoB</i>
Streptovaricin	an acyclic ansamycin, inhibits RNA polymerase	<i>rpoB</i>
Actinomycin D+EDTA	Intercalates between 2 successive G-C pairs, <i>rpoB</i> , inhibits RNA synthesis	<i>pldA</i>

Inhibitors of Nucleic Acid Metabolism

Quinolones, 1962 Nalidixic acid Oxolinic acid Fluoroquinolones Ciprofloxacin, 1983 Norfloxacin	α subunit gyrase and/or topoisomerase IV, <i>gyrA</i>	<i>gyrA</i> <i>gyrAorB</i> , <i>icd</i> , <i>sloB</i>
Coumerins Novobiocin	α subunit gyrase, <i>gyrA</i> and/or topoisomerase IV (probable target in Staph)	<i>gyrA</i> <i>norA</i> (efflux in Staph) <i>hipQ</i>
Coumermycin	Inhibits ATPase activity of β -subunit gyrase, <i>gyrB</i>	<i>gyrB</i> , <i>cysB</i> , <i>cysE</i> , <i>nov</i> , <i>ompA</i>
Albicidin Metronidazole	Inhibits ATPase activity of β -subunit gyrase, <i>gyrB</i> DNA synthesis Causes single-strand breaks in DNA	<i>gyrB</i> , <i>hisW</i> <i>tsx</i> (nucleoside channel) <i>nar</i>

Inhibitors of Metabolic Pathways

Sulfonamides, 1932	blocks synthesis of dihydrofolate, dihydro- pteroate synthesis, <i>folP</i>	<i>folP</i> , <i>gpt</i> , <i>pabA</i> , <i>pabB</i> , <i>pabC</i>
Sulfanilamide		
Trimethoprim, 1962	Inhibits dihydrofolate reductase, <i>folA</i>	<i>folA</i> , <i>thyA</i>
Showdomycin	Nucleoside analogue capable of alkylating sulfhydryl groups, inhibitor of thymidylate synthetase	<i>mupC</i> , <i>pnp</i>
Thiolactomycin	type II fatty acid synthase inhibitor	<i>emrB</i> <i>fadB</i> , <i>emrB</i> due to gene dosage
Psicofuranine	Adenosine glycoside antibiotic, target is GMP synthetase	<i>guaA</i> , <i>B</i>
Triclosan	Inhibits fatty acid synthesis	<i>fabI</i> (<i>envM</i>)
Diazaborines	heterocyclic, contains boron, inhibit fatty acid synthesis, enoyl-ACP reductase, <i>fabI</i>	<i>fabI</i> (<i>envM</i>)
Isoniazid		
Ethionamide		

Inhibitors of Translation

Phenylpropanoids		
Chloramphenicol, 1947	Binds to ribosomal peptidyl transfer center preventing peptide translocation/ binds to S6, L3, L6, L14, L16, L25, L26, L27, but preferentially to L16	<i>rrn</i> , <i>cmIA</i> , <i>marA</i> , <i>ompF</i> , <i>ompR</i>
Tetracyclines, 1948, type II polyketides	Binding to 30S ribosomal subunit, "A" site on 30S subunit, blocks peptide elongation, strongest binding to S7	<i>clmA</i> (<i>cmr</i>), <i>mar</i> , <i>ompF</i>
Minocycline		
Doxycycline		
Macrolides (type I polyketides)		
Erythromycin, 1950	Binding to 50 S ribosomal subunit, 23S rRNA, blocks peptide translocation, L15, L4, L12	<i>rrn</i> , <i>rplC</i> , <i>rplD</i> , <i>rplV</i> , <i>mac</i>
Carbomycin		
Spiramycin, etc		
Aminoglycosides		
Streptomycin, 1944	Irreversible binding to 30S ribosomal subunit, prevents translation or causes mistranslation of mRNA/16S rRNA	<i>rpsL</i> , <i>strC</i> , <i>M</i> , <i>ubiF</i> <i>atpA-E</i> , <i>ecfB</i> , <i>hemAC,D,E,G</i> , <i>topA</i> , <i>rpsC,D,E</i> , <i>rrn</i> , <i>spcB</i> <i>atpA-atpE</i> , <i>cpxA</i> , <i>ecfB</i> , <i>hemA,B,L</i> , <i>topA</i> <i>ksgA,B,C,D</i> , <i>rplB,K</i> , <i>rpsL,N,M,R</i> <i>rplF</i> , <i>ubiF</i> <i>cpxA</i> <i>rpsL</i>
Neomycin		
Spectinomycin		
Kanamycin		
Kasugamycin		
Gentamicin, 1963		
Amikacin		
Paromycin		
Lincosamides		
Lincomycin, 1955	Binding to 50 S ribosomal subunit, blocks peptide translocation	<i>linB</i> , <i>rplN</i> , <i>O</i> , <i>rpsG</i>
Clindamycin		
Streptogramins		
Virginiamycin, 1955	2 components, Streptogramins A&B, bind to the 50S ribosomal subunit blocking peptide translocation and peptide bond formation	
Pristinamycin		
Synercid: quinupristin /dalfopristin		
Fusidanes		
Fusidic Acid	Inhibition of elongation factor G (EF-G) prevents peptide translocation	<i>fusA</i>
Kirromycin	Inhibition of elongation factor TU (EF-Tu), prevents peptide bond formation	<i>tufA</i> , <i>B</i>
(Mocimycin)		
Pulvomycin	Binds to and inhibits EF-TU	
Thiopeptin	Sulfur-containing antibiotic, inhibits protein synthesis, EF-G	<i>rplE</i>
Tiamulin	Inhibits protein synthesis	<i>rplC</i> , <i>rplD</i>

Negamycin	Inhibits termination process of protein synthesis	<i>prfB</i>
Oxazolidinones	23S rRNA	
Linezolid		<i>pdx</i>
Isoniazid		<i>rfa</i>
Nitrofurantoin	Inhibits protein synthesis, nitroreductases convert nitrofurantoin to highly reactive electrophilic intermediates which attack bacterial ribosomal proteins non-specifically	<i>rfaA, B</i>
Pseudomonic Acids	Inhibition of isoleucyl tRNA synthetase- used for Staph, topical cream, nasal spray	<i>ileS</i>
Mupirocin (Bactroban)		
Indolmycin	Inhibits tryptophanyl-tRNA synthetase	<i>trpS</i>
Viomycin		<i>rrmA</i> (23S rRNA methyltransferase; mutant has slow growth rate, slow chain elongation rate, and viomycin resistance)
Thiopeptides	Binds to L11-23S RNA complex	
Thiostrepton	Inhibits GTP hydrolysis by EF-G	
Micrococcin	Stimulates GTP hydrolysis by EF-G	

Inhibitors of Cell Walls/Membranes

β-lactams	Inhibition of one or more cell wall transpeptidases, endopeptidases, and glycosidases (PBPs), of the 12 PBPs only 2 are essential: <i>mrdA</i> (PBP2) and <i>fisI</i> (<i>pbpB</i> , PBP3)	<i>ampC, ampD, ampE, envZ, galU, hipA, hipQ, ompC, ompF, ompR, ptsI, rfa, tolD, tolE</i>
Penicillin, 1929		<i>tonB</i>
Ampicillin		
Methicillin, 1960		
Cephalosporins, 1962		
Mecillinam (amdinocillin)	Binds to and inactivates PBP2 (<i>mrdA</i>)	<i>alaS, argS, crp, cyaA, envB, mrdA, B, mreB, C, D</i>
Aztreonam (Furazlocillin)	Inactivates PBP3 (<i>fisI</i>)	
Bacilysin, Tetaine	Dipeptide, inhib glucosamine synthase	<i>dppA</i>
Glycopeptides	Inhib G+ cell wall syn, binds to terminal D-ala-D-ala of pentapeptide,	
Vancomycin, 1955	Prevents dephosphorylation and regeneration of lipid carrier	<i>rfa</i>
Polypeptides	Disrupts multiple aspects of membrane function, including peptidoglycan synthesis, lipoteichoic acid synthesis, and the bacterial membrane potential	
Bacitracin		
Cyclic lipopeptide	Surfactant action disrupts cell membrane lipids, binds lipid A moiety of LPS	<i>pmrA</i>
Daptomycin, 1980	Analogue of P-enolpyruvate, inhibits 1 st step in peptidoglycan synthesis - UDP-N-acetylglucosamine enolpyruvyl transferase, <i>murA</i> . Also acts as Immunosuppressant	<i>murA, crp, cyaA glpT, hipA, ptsI, uhpT</i>
Cyclic polypeptides	Prevents formation of D-ala dimer, inhibits D-ala ligase, <i>ddlA, B</i>	<i>hipA, cycA</i>
Polymixin, 1939		
Fosfomycin, 1969		
Cycloserine		

Alafosfalin	phosphonodipeptide, cell wall synthesis inhibitor, potentiator of β -lactams	<i>pepA</i> , <i>tpp</i>
Inhibitors of Protein Processing/Transport		
Globomycin	Inhibits signal peptidase II (cleaves prolipoproteins subsequent to lipid modification, <i>lspA</i>)	<i>lpp</i> , <i>dnaE</i>

EXAMPLE 12**Transfer of Exogenous Nucleic Acid Sequences to other Bacterial Species Using the *E. coli* Expression**5 **Vectors or Expression Vectors Functional in Bacterial Species other than *E. coli*.**

Molecule No. EcXA190, encoding a portion of the *b3052* gene of *Escherichia coli*, was either transformed directly into *Enterobacter cloacae*, *Salmonella typhimurium* and/or *Klebsiella pneumoniae* or subcloned into an expression vector functional in these species and the subclones transformed into these organisms. Suitable expression vectors are well known in the art. These expression vectors were introduced into *Enterobacter cloacae*, *Salmonella typhimurium* and/or *Klebsiella pneumoniae* cells that were then assayed for growth inhibition according to the method of Example 1. After growth in liquid culture, cells were plated at various serial dilutions and a score determined by calculating the log difference in growth for INDUCED vs. UNINDUCED antisense RNA expression as determined by the maximum 10 fold dilution at which a colony was observed. If there was no effect of antisense RNA expression in one organism, the clone is given a score of zero "0" in that organism. In contrast, a score of "8" means that 10^8 times more cells were required to observe a colony formed on the induced state than in the non-induced state under the conditions used and in that organism.

Expression vectors containing Molecule No. EcXA190 were found to inhibit bacterial growth in all four organisms when expression of the antisense RNA was induced with IPTG. A score of 4 was assigned for *Escherichia coli*, 6 for *Enterobacter cloacae*, and 8 for *Salmonella typhimurium* and 3 for *Klebsiella pneumoniae* (obvious additional growth defect as well). The protein encoded by this sequence may be used as a target sequence to screen candidate compound libraries as described above.

In addition, the above methods were validated using other antisense nucleic acids which inhibit the growth of *E. coli* which were identified using methods similar to those described above. Expression vectors which inhibited growth of *E. coli* upon induction of antisense RNA expression with IPTG were transformed directly into *Enterobacter cloacae*, *Klebsiella pneumonia* or *Salmonella typhimurium*. The transformed cells were then assayed for growth inhibition according to the method of Example 1. After growth in liquid culture, cells were plated at various serial dilutions and a score determined by calculating the log difference in growth for INDUCED vs. UNINDUCED antisense RNA expression as determined by the maximum 10 fold dilution at which

a colony was observed. The results of these experiments are listed in Table V below. If there was no effect of antisense RNA expression in a microorganism, the clone is minus in Table V below. In contrast, a positive in Table V below means that at least 10 fold more cells were required to observe a colony on the induced plate than on the non-induced plate under the conditions used and in that

5 microorganism.

TABLE V

Sensitivity of Other Microorganisms to Antisense Nucleic Acids That Inhibit Proliferation in *E. coli*

Mol. No.	<i>S. typhimurium</i>	<i>E. cloacae</i>	<i>K. pneumoniae</i>
EcXA001	+	+	-
EcXA004	+	-	-
EcXA005	+	+	+
EcXA006	-	-	-
EcXA007	-	+	-
EcXA008	+	-	+
EcXA009	-	-	-
EcXA010	+	+	+
EcXA011	-	+	-
EcXA012	-	+	-
EcXA013	+	+	+
EcXA014	+	+	-
EcXA015	+	+	+
EcXA016	+	+	+
EcXA017	+	+	+
EcXA018	+	+	+
EcXA019	+	+	+
EcXA020	+	+	+
EcXA021	+	+	+
EcXA023	+	+	+
EcXA024	+	-	+
EcXA025	-	-	-
EcXA026	+	+	-
EcXA027	+	+	-
EcXA028	+	-	-
EcXA029	-	-	-
EcXA030	+	+	+
EcXA031	+	-	-
EcXA032	+	+	-
EcXA033	+	+	+
EcXA034	+	+	+
EcXA035	-	-	-
EcXA036	+	-	+
EcXA037	+	+	-
EcXA038	+	+	+
EcXA039	+	-	-
EcXA041	+	+	+
EcXA042	-	+	+

Mol. No.	<i>S. typhimurium</i>	<i>E. cloacae</i>	<i>K. pneumoniae</i>
EcXA043	-	-	-
EcXA044	-	-	-
EcXA045	+	+	+
EcXA046	-	-	-
EcXA047	+	+	-
EcXA048	-	-	-
EcXA049	+	-	-
EcXA050	-	-	-
EcXA051	+	-	-
EcXA052	+	-	-
EcXA053	+	+	+
EcXA054	-	-	+
EcXA055	+	-	-
EcXA056	+	-	+
EcXA057	+	+	-
EcXA058	-	-	-
EcXA059	+	+	+
EcXA060	-	-	-
EcXA061	-	-	-
EcXA062	-	-	-
EcXA063	+	+	-
EcXA064	-	-	-
EcXA065	+	+	-
EcXA066	-	-	-
EcXA067	-	+	-
EcXA068	-	-	-
EcXA069	-	+	-
EcXA070	-	-	-
EcXA071	+	-	-
EcXA072	+	-	+
EcXA073	+	+	+
EcXA074	+	+	+
EcXA075	+	-	-
EcXA076	-	+	-
EcXA077	+	+	-
EcXA079	+	+	+
EcXA080	+	-	-
EcXA082	-	+	-
EcXA083	-	-	-
EcXA084	-	+	-
EcXA086	-	-	-
EcXA087	-	-	-
EcXA088	-	-	-
EcXA089	-	-	-
EcXA090	-	-	-
EcXA091	-	-	-
EcXA092	-	-	-
EcXA093	-	-	-

Mol. No.	<i>S. typhimurium</i>	<i>E. cloacae</i>	<i>K. pneumoniae</i>
EcXA094	+	+	+
EcXA095	+	+	-
EcXA096	-	-	-
EcXA097	+	-	-
EcXA098	+	-	-
EcXA099	-	-	-
EcXA100	-	-	-
EcXA101	-	-	-
EcXA102	-	-	-
EcXA103	-	+	-
EcXA104	+	+	+
EcXA106	+	+	-
EcXA107	-	-	-
EcXA108	-	-	-
EcXA109	-	-	-
EcXA110	+	+	-
EcXA111	-	-	-
EcXA112	-	+	-
EcXA113	+	+	+
EcXA114	-	+	-
EcXA115	-	+	-
EcXA116	+	+	-
EcXA117	+	-	-
EcXA118	-	-	-
EcXA119	+	+	-
EcXA120	-	-	-
EcXA121	-	-	-
EcXA122	+	-	+
EcXA123	+	-	-
EcXA124	-	-	-
EcXA125	-	-	-
EcXA126	-	-	-
EcXA127	+	+	-
EcXA128	-	-	-
EcXA129	-	+	-
EcXA130	+	+	-
EcXA132	-	-	-
EcXA133	-	-	-
EcXA136	-	-	-
EcXA137	-	-	-
EcXA138	+	-	-
EcXA139	-	-	-
EcXA140	+	-	-
EcXA141	+	-	-
EcXA142	-	-	-
EcXA143	-	+	-
EcXA144	+	+	-
EcXA145	-	-	-

Mol. No.	<i>S. typhimurium</i>	<i>E. cloacae</i>	<i>K. pneumoniae</i>
EcXA146	-	-	-
EcXA147	-	-	-
EcXA148	-	-	-
EcXA149	+	+	+
EcXA150	-	-	-
EcXA151	+	-	-
EcXA152	-	-	-
EcXA153	+	+	-
EcXA154	-	-	-
EcXA155	-	-	ND
EcXA156	-	+	-
EcXA157	-	-	-
EcXA158	-	-	-
EcXA159	+	-	-
EcXA160	+	-	-
EcXA162	-	-	-
EcXA163	-	-	-
EcXA164	-	-	-
EcXA165	-	-	-
EcXA166	-	-	-
EcXA167	-	-	-
EcXA168	-	-	-
EcXA169	-	+	-
EcXA171	-	-	-
EcXA172	-	-	-
EcXA173	-	-	-
EcXA174	-	-	-
EcXA175	-	-	-
EcXA176	-	-	-
EcXA178	-	-	-
EcXA179	-	-	-
EcXA180	+	-	-
EcXA181	-	-	-
EcXA182	-	-	-
EcXA183	-	-	-
EcXA184	-	-	-
EcXA185	-	-	-
EcXA186	-	-	-
EcXA187	+	+	+
EcXA189	+	-	-
EcXA190	+	+	+
EcXA191	+	+	-
EcXA192	-	+	-

Thus, the ability of an antisense nucleic acid which inhibits the proliferation of *E. coli* to inhibit the growth of other organisms may be evaluated by either transforming the antisense nucleic acid directly into other *Escherichia* species or inserting the antisense nucleic acid into expression

vectors that are functional in other Gram negative species such as *Enterobacter cloacae*, *Salmonella typhimurium*, and/or *Klebsiella pneumoniae*. Similarly, the antisense nucleic acid can be inserted in expression vectors that are functional in Gram-positive species such as *Staphylococcus aureus*, *Enterococcus faecalis* and *Streptococcus pneumoniae* or other species.

5 Those skilled in the art will appreciate that a negative result in a heterologous microorganism does not mean that that microorganism is missing that gene nor does it mean that the gene is unessential. However, a positive result means that the heterologous microorganism contains a homologous gene which is required for proliferation of that microorganism. The homologous gene may be obtained using the methods described herein. Those cells that are inhibited by antisense may
10 be used in cell-based assays as described herein for the identification and characterization of compounds in order to develop antibiotics effective in these microorganisms. Those skilled in the art will appreciate that an antisense molecule which works in the microorganism from which it was obtained will not always work in a heterologous microorganism.

EXAMPLE 13

15 Use of Identified Exogenous Nucleic Acid Sequences as Probes

The identified sequence of the present invention can be used as probes to obtain the sequence of additional genes of interest from a second organism. For example, probes to genes encoding potential bacterial target proteins may be hybridized to nucleic acids from other organisms including other bacteria and higher organisms, to identify homologous sequences. Such
20 hybridization might indicate that the protein encoded by the gene to which the probe corresponds is found in humans and therefore not necessarily a good drug target. Alternatively, the gene can be conserved only in bacteria and therefore would be a good drug target for a broad spectrum antibiotic or antimicrobial.

Probes derived from the identified nucleic acid sequences of interest or portions thereof can be
25 labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe can be single stranded or double stranded and can be made using techniques known in the art, including *in vitro* transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double
30 stranded, it can be denatured prior to contacting the probe. In some applications, the nucleic acid sample can be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid sample can comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable
35 probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe can be cloned into vectors such as expression vectors, sequencing vectors, or in

vitro transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques can be used to isolate, purify and clone sequences from a genomic library, made from a variety of bacterial species, which are capable of hybridizing to probes made from the sequences identified in Examples 5 and 6.

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EXAMPLE 14

Preparation of PCR Primers and Amplification of DNA

The identified *E. coli* genes corresponding directly to or located within the operon of nucleic acid sequences required for proliferation or portions thereof can be used to prepare PCR primers for a variety of applications, including the identification or isolation of homologous sequences from other species, for example *S. typhimurium*, *E. cloacae*, *E. faecalis*, *S. pneumoniae*, and *K. pneumoniae*, which contain part or all of the homologous genes. Because homologous genes are related but not identical in sequence, those skilled in the art will often employ degenerate sequence PCR primers. Such degenerate sequence primers are designed based on conserved sequence regions, either known or suspected, such as conserved coding regions. The successful production of a PCR product using degenerate probes generated from the sequences identified herein would indicate the presence of a homologous gene sequence in the species being screened. The PCR primers are at least 10 nucleotides, and preferably at least 20 nucleotides in length. More preferably, the PCR primers are at least 20-30 nucleotides in length. In some embodiments, the PCR primers can be more than 30 nucleotides in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White, B.A. Ed. in Methods in Molecular Biology 67: Humana Press, Totowa 1997. When the entire coding sequence of the target gene is known, the 5' and 3' regions of the target gene can be used as the sequence source for PCR probe generation. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

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EXAMPLE 15

Inverse PCR

The technique of inverse polymerase chain reaction can be used to extend the known nucleic acid sequence identified in Examples 5 and 6. The inverse PCR reaction is described generally by Ochman et al., in Ch. 10 of PCR Technology: Principles and Applications for DNA Amplification, (Henry A. Erlich, Ed.) W.H. Freeman and Co. (1992). Traditional PCR requires two primers that are

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used to prime the synthesis of complementary strands of DNA. In inverse PCR, only a core sequence need be known.

Using the sequences identified as relevant from the techniques taught in Examples 5 and 6 and applied to other species of bacteria, a subset of exogenous nucleic sequences are identified that correspond to genes or operons that are required for bacterial proliferation. In species for which a genome sequence is not known, the technique of inverse PCR provides a method for obtaining the gene in order to determine the sequence or to place the probe sequences in full context to the target sequence to which the identified exogenous nucleic acid sequence binds.

To practice this technique, the genome of the target organism is digested with an appropriate restriction enzyme so as to create fragments of nucleic acid that contain the identified sequence as well as unknown sequences that flank the identified sequence. These fragments are then circularized and become the template for the PCR reaction. PCR primers are designed in accordance with the teachings of Example 15 and directed to the ends of the identified sequence. The primers direct nucleic acid synthesis away from the known sequence and toward the unknown sequence contained within the circularized template. After the PCR reaction is complete, the resulting PCR products can be sequenced so as to extend the sequence of the identified gene past the core sequence of the identified exogenous nucleic acid sequence identified. This process can be repeated iteratively if necessary. In this manner, the full sequence of each novel gene can be identified. Additionally the sequences of adjacent coding and noncoding regions can be identified.

EXAMPLE 16

Identification of Genes Required for *Staphylococcus aureus* Proliferation

Genes required for proliferation in *Staphylococcus aureus* are identified according to the methods described above.

EXAMPLE 17

Identification of Genes Required for *Neisseria gonorrhoeae* Proliferation

Genes required for proliferation in *Neisseria gonorrhoeae* are identified according to the methods described above.

EXAMPLE 18

Identification of Genes Required for *Pseudomonas aeruginosa* Proliferation

Genes required for proliferation in *Pseudomonas aeruginosa* are identified according to the methods described above.

EXAMPLE 19

Identification of Genes Required for *Enterococcus faecalis* Proliferation

Genes required for proliferation in *Enterococcus faecalis* are identified according to the methods described above.

EXAMPLE 20**Identification of Genes Required for *Haemophilus influenzae* Proliferation**

Genes required for proliferation in *Haemophilus influenzae* are identified according to the methods described above.

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EXAMPLE 21**Identification of Genes Required for *Salmonella typhimurium* Proliferation**

Genes required for proliferation in *Salmonella typhimurium* are identified according to the methods described above.

EXAMPLE 22

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Identification of Genes Required for *Helicobacter pylori* Proliferation

Genes required for proliferation in *Helicobacter pylori* are identified according to the methods described above.

EXAMPLE 23

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Identification of Genes Required for *Mycoplasma pneumoniae* Proliferation

Genes required for proliferation in *Mycoplasma pneumoniae* are identified according to the methods described above.

EXAMPLE 24**Identification of Genes Required for *Plasmodium ovale* Proliferation**

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Genes required for proliferation in *Plasmodium ovale* are identified according to the methods described above.

EXAMPLE 25**Identification of Genes Required for *Saccharomyces cerevisiae* Proliferation**

Genes required for proliferation in *Saccharomyces cerevisiae* are identified according to the methods described above.

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EXAMPLE 26**Identification of Genes Required for *Entamoeba histolytica* Proliferation**

Genes required for proliferation in *Entamoeba histolytica* are identified according to the methods described above.

EXAMPLE 27

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Identification of Genes Required for *Candida albicans* Proliferation

Genes required for proliferation in *Candida albicans* are identified according to the methods described above.

EXAMPLE 28**Identification of Genes Required for *Klebsiella pneumoniae* Proliferation**

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Genes required for proliferation in *Klebsiella pneumoniae* are identified according to the methods described above.

EXAMPLE 29**Identification of Genes Required for *Salmonella typhi* Proliferation**

Genes required for proliferation in *Salmonella typhi* are identified according to the methods described above.

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EXAMPLE 30**Identification of Genes Required for *Salmonella paratyphi* Proliferation**

Genes required for proliferation in *Salmonella paratyphi* are identified according to the methods described above.

EXAMPLE 31

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Identification of Genes Required for *Salmonella choleraesuis* Proliferation

Genes required for proliferation in *Salmonella choleraesuis* are identified according to the methods described above.

EXAMPLE 32**Identification of Genes Required for *Staphylococcus epidermis* Proliferation**

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Genes required for proliferation in *Staphylococcus epidermis* are identified according to the methods described above.

EXAMPLE 33**Identification of Genes Required for *Mycobacterium tuberculosis* Proliferation**

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Genes required for proliferation in *Mycobacterium tuberculosis* are identified according to the methods described above.

EXAMPLE 34**Identification of Genes Required for *Mycobacterium leprae* Proliferation**

Genes required for proliferation in *Mycobacterium leprae* are identified according to the methods described above.

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EXAMPLE 35**Identification of Genes Required for *Treponema pallidum* Proliferation**

Genes required for proliferation in *Treponema pallidum* are identified according to the methods described above.

EXAMPLE 36

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Identification of Genes Required for *Bacillus anthracis* Proliferation

Genes required for proliferation in *Bacillus anthracis* are identified according to the methods described above.

EXAMPLE 37**Identification of Genes Required for *Yersinia pestis* Proliferation**

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Genes required for proliferation in *Yersinia pestis* are identified according to the methods described above.

EXAMPLE 38**Identification of Genes Required for *Clostridium botulinum* Proliferation**

Genes required for proliferation in *Clostridium botulinum* are identified according to the methods described above.

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EXAMPLE 39**Identification of Genes Required for *Campylobacter jejuni* Proliferation**

Genes required for proliferation in *Campylobacter jejuni* are identified according to the methods described above.

EXAMPLE 40

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Identification of Genes Required for *Chlamydia trachomatis* Proliferation

Genes required for proliferation in *Chlamydia trachomatis* are identified according to the methods described above.

It will be appreciated that genes required for proliferation of any microorganism of interest, including those specifically mentioned herein, may be identified according to the methods described above.

Use of Isolated Exogenous Nucleic Acid Fragments as Antisense Antibiotics

In addition to using the identified sequences to enable screening of molecule libraries to identify compounds useful to identify antibiotics, the sequences themselves can be used as therapeutic agents. Specifically, the identified exogenous sequences in an antisense orientation can be provided to an individual to inhibit the translation of a bacterial target gene.

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Generation of Antisense Therapeutics from Identified Exogenous Sequences

The sequences of the present invention can be used as antisense therapeutics for the treatment of bacterial infections or simply for inhibition of bacterial growth *in vitro* or *in vivo*. The therapy exploits the biological process in cells where genes are transcribed into messenger RNA (mRNA) that is then translated into proteins. Antisense RNA technology contemplates the use of antisense oligonucleotides complementary to a target gene that will bind to its target nucleic acid and decrease or inhibit the expression of the target gene. For example, the antisense nucleic acid may inhibit the translation or transcription of the target nucleic acid. In one embodiment, antisense oligonucleotides can be used to treat and control a bacterial infection of a cell culture containing a population of desired cells contaminated with bacteria. In another embodiment, the antisense oligonucleotides can be used to treat an organism with a bacterial infection.

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Antisense oligonucleotides can be synthesized from any of the sequences of the present invention using methods well known in the art. In a preferred embodiment, antisense oligonucleotides are synthesized using artificial means. Uhlmann & Peymann, Chemical Rev. 90:543-584 (1990) review antisense oligonucleotide technology in detail. Modified or unmodified antisense oligonucleotides can be used as therapeutic agents. Modified antisense oligonucleotides

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are preferred since it is well known that antisense oligonucleotides are extremely unstable. Modification of the phosphate backbones of the antisense oligonucleotides can be achieved by substituting the internucleotide phosphate residues with methylphosphonates, phosphorothioates, phosphoramidates, and phosphate esters. Nonphosphate internucleotide analogs such as siloxane bridges, carbonate bridges, thioester bridges, as well as many others known in the art may also be used. The preparation of certain antisense oligonucleotides with modified internucleotide linkages is described in U.S. Patent No. 5,142,047.

Modifications to the nucleoside units of the antisense oligonucleotides are also contemplated. These modifications can increase the half-life and increase cellular rates of uptake for the oligonucleotides *in vivo*. For example, α -anomeric nucleotide units and modified nucleotides such as 1,2-dideoxy-d-ribofuranose, 1,2-dideoxy-1-phenylribofuranose, and N^4 , N^4 -ethano-5-methyl-cytosine are contemplated for use in the present invention.

An additional form of modified antisense molecules is found in peptide nucleic acids. Peptide nucleic acids (PNA) have been developed to hybridize to single and double stranded nucleic acids. PNA are nucleic acid analogs in which the entire deoxyribose-phosphate backbone has been exchanged with a chemically completely different, but structurally homologous, polyamide (peptide) backbone containing 2-aminoethyl glycine units. Unlike DNA, which is highly negatively charged, the PNA backbone is neutral. Therefore, there is much less repulsive energy between complementary strands in a PNA-DNA hybrid than in the comparable DNA-DNA hybrid, and consequently they are much more stable. PNA can hybridize to DNA in either a Watson/Crick or Hoogsteen fashion (Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* **92**:2637-2641, 1995; Egholm, *Nature* **365**:566-568, 1993; Nielsen et al., *Science* **254**:1497-1500, 1991; Dueholm et al., *New J. Chem.* **21**:19-31, 1997).

Molecules called PNA "clamps" have been synthesized which have two identical PNA sequences joined by a flexible hairpin linker containing three 8-amino-3,6-dioxaoctanoic acid units. When a PNA clamp is mixed with a complementary homopurine or homopyrimidine DNA target sequence, a PNA-DNA-PNA triplex hybrid can form which has been shown to be extremely stable (Bentin et al., *Biochemistry* **35**:8863-8869, 1996; Egholm et al., *Nucleic Acids Res.* **23**:217-222, 1995; Griffith et al., *J. Am. Chem. Soc.* **117**:831-832, 1995).

The sequence-specific and high affinity duplex and triplex binding of PNA have been extensively described (Nielsen et al., *Science* **254**:1497-1500, 1991; Egholm et al., *J. Am. Chem. Soc.* **114**:9677-9678, 1992; Egholm et al., *Nature* **365**:566-568, 1993; Almarsson et al., *Proc. Natl. Acad. Sci. U.S.A.* **90**:9542-9546, 1993; Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* **92**:2637-2641, 1995). They have also been shown to be resistant to nuclease and protease digestion (Demidov et al., *Biochem. Pharm.* **48**:1010-1313, 1994). PNA has been used to inhibit gene expression (Hanvey et al., *Science* **258**:1481-1485, 1992; Nielsen et al., *Nucl. Acids. Res.*, **21**:197-200, 1993; Nielsen et al., *Gene* **149**:139-145, 1994; Good & Nielsen, *Science*, **95**: 2073-2076, 1998), to block restriction enzyme activity (Nielsen et al., *supra*, 1993), to act as an artificial transcription promoter (Mollegaard, *Proc.*

Natl. Acad. Sci. U.S.A. 91:3892-3895, 1994) and as a pseudo restriction endonuclease (Demidov et al., *Nucl. Acids. Res.* 21:2103-2107, 1993). Recently, PNA has also been shown to have antiviral and antitumoral activity mediated through an antisense mechanism (Norton, *Nature Biotechnol.*, 14:615-619, 1996; Hirschman et al., *J. Investig. Med.* 44:347-351, 1996). PNAs have been linked to various peptides in order to promote PNA entry into cells (Basu et al., *Bioconj. Chem.* 8:481-488, 1997; Pardridge et al., *Proc. Natl. Acad. Sci. U.S.A.* 92:5592-5596, 1995).

The antisense oligonucleotides contemplated by the present invention can be administered by direct application of oligonucleotides to a target using standard techniques well known in the art. The antisense oligonucleotides can be generated within the target using a plasmid, or a phage. Alternatively, the antisense nucleic acid may be expressed from a sequence in the chromosome of the target cell. For example, a promoter may be introduced into the chromosome of the target cell near the target gene such that the promoter directs the transcription of the antisense nucleic acid. Alternatively, a nucleic acid containing the antisense sequence operably linked to a promoter may be introduced into the chromosome of the target cell. It is further contemplated that the antisense oligonucleotide contemplated are incorporated in a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi et al., *Pharmacol. Ther.* 50(2):245-254, (1991). The present invention also contemplates using a retron to introduce an antisense oligonucleotide to a cell. Retron technology is exemplified by U.S. Patent No. 5,405,775. Antisense oligonucleotides can also be delivered using liposomes or by electroporation techniques which are well known in the art.

The antisense nucleic acids of the present invention can also be used to design antibiotic compounds comprising nucleic acids which function by intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. The sequences identified as required for proliferation in the present invention, or portions thereof, can be used as templates to inhibit microorganism gene expression in individuals infected with such organisms. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences based on the sequences of the present invention that are required for proliferation are contemplated for use as antibiotic compound templates.

The antisense oligonucleotides of this example employ the identified sequences of the present invention to induce bacterial cell death or at least bacterial stasis by inhibiting target nucleic acid transcription or translation. Antisense oligonucleotides containing from about 8 to 40 nucleotides of the sequences of the present invention have sufficient complementarity to form a duplex with the target sequence under physiological conditions.

To kill bacterial cells or inhibit their growth, the antisense oligonucleotides are applied to the bacteria or to the target cells under conditions that facilitate their uptake. These conditions

include sufficient incubation times of cells and oligonucleotides so that the antisense oligonucleotides are taken up by the cells. In one embodiment, an incubation period of 7-10 days is sufficient to kill bacteria in a sample. An optimum concentration of antisense oligonucleotides is selected for use.

5 The concentration of antisense oligonucleotides to be used can vary depending on the type of bacteria sought to be controlled, the nature of the antisense oligonucleotide to be used, and the relative toxicity of the antisense oligonucleotide to the desired cells in the treated culture. Antisense oligonucleotides can be introduced to cell samples at a number of different concentrations preferably between $1 \times 10^{-10} \text{M}$ to $1 \times 10^{-4} \text{M}$. Once the minimum concentration that can adequately
10 control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of 1×10^{-7} translates into a dose of approximately 0.6 mg/kg body weight. Levels of oligonucleotide approaching 100 mg/kg body weight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the subject are removed, treated with the antisense
15 oligonucleotide, and reintroduced into the subject. This range is merely illustrative and one of skill in the art are able to determine the optimal concentration to be used in a given case.

After the bacterial cells have been killed or controlled in a desired culture, the desired cell population may be used for other purposes.

EXAMPLE 41

20 The following example demonstrates the ability of an *E. coli* antisense oligonucleotide to act as a bactericidal or bacteriostatic agent to treat a contaminated cell culture system. The application of the antisense oligonucleotides of the present invention are thought to inhibit the translation of bacterial gene products required for proliferation.

 The antisense oligonucleotide of this example corresponds to a 30 base phosphorothioate
25 modified oligodeoxynucleotide complementary to a nucleic acid involved in proliferation, such as Molecule Number EcXA118 (SEQ ID NO: 1). A sense oligodeoxynucleotide complementary to the antisense sequence is synthesized and used as a control. The oligonucleotides are synthesized and purified according to the procedures of Matsukura, et al., Gene 72:343 (1988). The test oligonucleotides are dissolved in a small volume of autoclaved water and added to culture medium
30 to make a 100 micromolar stock solution.

Human bone marrow cells are obtained from the peripheral blood of two patients and cultured according standard procedures well known in the art. The culture is contaminated with the K-12 strain of *E. coli* and incubated at 37°C overnight to establish bacterial infection.

35 The control and antisense oligonucleotide containing solutions are added to the contaminated cultures and monitored for bacterial growth. After a 10 hour incubation of culture and oligonucleotides, samples from the control and experimental cultures are drawn and analyzed for the translation of the target bacterial gene using standard microbiological techniques well

known in the art. The target *E. coli* gene is found to be translated in the control culture treated with the control oligonucleotide, however, translation of the target gene in the experimental culture treated with the antisense oligonucleotide of the present invention is not detected or reduced.

One way to determine if a gene is essential for proliferation in a host or virulence in a host is to construct a conditional allele of the gene in an infectious organism. The host is then challenged with the organism under conditions in which the product of the gene is functional or non-functional or has reduced activity or where the gene product is absent or else present but at a reduced level. If the gene is essential for proliferation or virulence the infection of the host will be diminished or abolished under conditions in which the product of the gene is not functional or has reduced activity or where the gene product is absent or else present but at a reduced level.

Since expression of an antisense nucleic acid complementary to a gene required for proliferation also decreases the synthesis of the gene product, antisense nucleic acids may also be used to evaluate whether a gene is essential for the proliferation or virulence of an infectious organism in the host. In such methods, nucleic acids encoding an antisense molecule complementary to the desired target gene are introduced into the infectious organism. For example, plasmids comprising one of SEQ ID NOs: 1-93 or fragments thereof which inhibit proliferation, may be introduced into the infectious organism. In some embodiments, the antisense nucleic acid may be transcribed from the IPTG-inducible promoter in pLEX5BA or from other regulated promoters or vector systems.

E. coli is transformed with the nucleic acid encoding the antisense molecule by electroporation and grown in medium which selects for the presence of the vector from which the antisense nucleic acid is expressed. The essentiality of the target for each antisense nucleic acid is verified in microorganisms grown in culture using the techniques described herein.

The ability of antisense expression to block *E. coli* infection in an animal is tested using the rabbit model of bacterial meningitis. A spinal needle is surgically placed into the cisterna magna of New Zealand White rabbits. The rabbits are inoculated with 10^5 to 10^6 cells of a normally virulent *E. coli* strain expressing an antisense nucleic acid complementary to a gene required for proliferation. Repeated CSF sampling is undertaken to determine multiple parameters of injury and infection such as cytochemical abnormalities, intracranial pressure, cerebral edema, BBB permeability, cerebral perfusion pressure and recovery of viable *E. coli* cells. Control animals are given intravenous injections of saline, which will not induce expression of the antisense nucleic acid, while experimental animals are given IPTG in intravenous injections to induce expression of the antisense nucleic acid. Alternatively, expression of the antisense nucleic acid may be induced by intravenous infusion of IPTG at sub-toxic levels. If other promoters other than IPTG inducible promoters are used, the rabbits may be fed the inducer in their water.

The use of rabbits allows multiple CSF samples per animal (one rabbit can give up to 8 sequential samples without change in CSF pressure). Treated animals receive therapy from 2 hours

post receiving inoculation up to several days. A typical efficacy study consists of 3 control animals and 3 treated animals.

The control animals in which expression of the antisense nucleic acid is not induced are not protected against infection with *E. coli* and there is a logarithmic increase in viable bacteria. In experimental animals, *E. coli* cells recovered from the site of infection are viable until antisense expression is subsequently induced. However, if the antisense nucleic acid is directed against a gene required for proliferation, after treatment with the inducer for antisense expression the *E. coli* cells infecting these rabbits will not multiply and fewer viable cells will be recovered from the site of infection. The *E. coli* cells recovered from the rabbits treated with the inducer are recovered, if still present, and assayed as above to determine if the promoter and gene are still present and functional. Conversely, if the antisense nucleic acid is not complementary to a gene required for proliferation, treatment of the rabbits with inducer will have no effect on *E. coli* viability.

EXAMPLE 42

A subject suffering from an *E. coli* infection is treated with the antisense oligonucleotide preparation of Example 39. The antisense oligonucleotide is provided in a pharmaceutically acceptable carrier at a concentration effective to inhibit the transcription or translation of the target nucleic acid. The present subject is treated with a concentration of antisense oligonucleotide sufficient to achieve a blood concentration of about 100 micromolar. The patient receives daily injections of antisense oligonucleotide to maintain this concentration for a period of 1 week. At the end of the week a blood sample is drawn and analyzed for the presence or absence of the organism using standard techniques well known in the art. There is no detectable evidence of *E. coli* and the treatment is terminated.

EXAMPLE 43

Preparation and use of Triple Helix Probes

The sequences of microorganism genes required for proliferation of the present invention are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches that could be used in triple-helix based strategies for inhibiting gene expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into a population of bacterial cells that normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis, such as GENSET, Paris, France.

The oligonucleotides can be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for a reduction in proliferation using techniques such as monitoring growth levels as compared to untreated cells using optical density measurements. The

oligonucleotides that are effective in inhibiting gene expression in cultured cells can then be introduced *in vivo* using the techniques well known in that art at a dosage level shown to be effective.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin et al. (Science 245:967-971 (1989)).

EXAMPLE 44

Identification of Bacterial Strains from Isolated Specimens by PCR

Classical bacteriological methods for the detection of various bacterial species are time consuming and costly. These methods include growing the bacteria isolated from a subject in specialized media, cultivation on selective agar media, followed by a set of confirmation assays that can take from 8 to 10 days or longer to complete. Use of the identified sequences of the present invention provides a method to dramatically reduce the time necessary to detect and identify specific bacterial species present in a sample.

In one exemplary method, bacteria are grown in enriched media and DNA samples are isolated from specimens of, for example, blood, urine, stool, saliva or central nervous system fluid by conventional methods. A panel of PCR primers based on identified sequences unique to various species of microorganisms are then utilized in accordance with Example 12 to amplify DNA of approximately 100-200 nucleotides in length from the specimen. A separate PCR reaction is set up for each pair of PCR primers and after the PCR reaction is complete, the reaction mixtures are assayed for the presence of PCR product. The presence or absence of bacteria from the species to which the PCR primer pairs belong is determined by the presence or absence of a PCR product in the various test PCR reaction tubes.

Although the PCR reaction is used to assay the isolated sample for the presence of various bacterial species, other assays such as the Southern blot hybridization are also contemplated.

WHAT IS CLAIMED IS:

1. A purified or isolated nucleic acid sequence consisting essentially of one the sequence of nucleotides of SEQ ID NOs: 1-93, wherein expression of said nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism.
- 5 2. The nucleic acid sequence of Claim 1, wherein said nucleic acid sequence is complementary to at least a portion of the nucleotide sequence of the coding strand of a gene whose expression is required for proliferation of a microorganism.
3. The nucleic acid of Claim 1, wherein said nucleic acid sequence has a nucleotide sequence complementary to at least a portion of the nucleotide sequence of an RNA required for
10 proliferation of a microorganism.
4. The nucleic acid of Claim 3, wherein the nucleotide sequence of said RNA encodes more than one gene product.
5. A purified or isolated nucleic acid comprising a fragment of one of the nucleotide sequence of SEQ ID NOs.: 1-93, said fragment selected from the group consisting of fragments
15 comprising at least 10, at least 20, at least 25, at least 30, at least 50 and more than 50 consecutive nucleotides of one of the nucleotide sequences of SEQ ID NOs: 1-93.
6. A vector comprising a promoter operably linked to the nucleic acid sequence of Claims 1,2,3,4, or 5.
7. The vector of Claim 6, wherein said promoter is active in a microorganism selected
20 from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*,
25 *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*,
30 *Yersinia pestis* and any species falling within the genera of any of the above species.
8. A host cell containing the vector of Claim 6.
9. A purified or isolated nucleic acid consisting essentially of the coding sequence of
35 one of SEQ ID NOs: 106-112, 119-122, 134-160, 164-171, 179-265, 271-273, 275, and 279-286.

10. A fragment of the nucleic acid of Claim 8, said fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs: 106-112, 119-122, 134-160, 164-171, 179-265, 271-273, 275, and 279-286.
11. A vector comprising a promoter operably linked to the nucleic acid of Claim 9 or
5 Claim 10.
12. A purified or isolated antisense nucleic acid comprising a nucleic acid sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding region, or 3' noncoding region within an operon comprising a proliferation-required gene whose activity or expression is inhibited
10 by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93.
13. A purified or isolated nucleic acid comprising a nucleic acid having at least 70% identity to a sequence selected from the group consisting of SEQ ID NOs.: 1-93, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 1-93, the sequences complementary to SEQ ID NOs.: 1-93 and the sequences complementary to fragments comprising
15 at least 25 consecutive nucleotides of SEQ ID NOs.: 1-93 as determined using BLASTN version 2.0 with the default parameters.
14. The nucleic acid of Claim 13, wherein said nucleic acid is from an organism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*),
20 *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*,
25 *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*,
30 *Yersinia pestis* and any species falling within the genera of any of the above species.
15. A vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93.
16. A host cell containing the vector of Claim 15.
17. The vector of Claim 15, wherein said polypeptide comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

18. A purified or isolated polypeptide comprising a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93, or a fragment selected from the group consisting of fragments comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the said polypeptides.

19. The polypeptide of Claim 18, wherein said polypeptide comprises a polypeptide comprising one of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479 or a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

20. A purified or isolated polypeptide comprising a polypeptide having at least 25% identity to a polypeptide whose expression is inhibited by a sequence selected from the group consisting of SEQ ID NOs.: 1-93, or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide whose expression is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-93 as determined using FASTA version 3.0t78 with the default parameters.

21. The polypeptide of Claim 20, wherein said polypeptide has at least 25% identity to a polypeptide comprising one of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479 or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising one of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479 as determined using FASTA version 3.0t78 with the default parameters.

22. An antibody capable of specifically binding the polypeptide of one of Claims 18-21.

23. A method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93 into a cell and expressing said polypeptide.

24. The method of Claim 23, further comprising the step of isolating said polypeptide.

25. The method of Claim 23, wherein said polypeptide comprises a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

26. A method of inhibiting proliferation of a microorganism comprising inhibiting the activity or reducing the amount of a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93 or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product.

5 27. The method of Claim 26, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

28. A method for identifying a compound which influences the activity of a gene product required for proliferation, said gene product comprising a gene product whose expression is
10 inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising:

contacting said gene product with a candidate compound; and

determining whether said compound influences the activity of said gene product.

29. The method of Claim 28, wherein said gene product is a polypeptide and said
15 activity is an enzymatic activity.

30. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a carbon compound catabolism activity.

31. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a biosynthetic activity.

20 32. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a transporter activity.

33. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a transcriptional activity.

34. The method of Claim 28, wherein said gene product is a polypeptide and said
25 activity is a DNA replication activity.

35. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a cell division activity.

36. A compound identified using the method of Claim 28.

37. The method of Claim 28, wherein said gene product is a polypeptide comprising a
30 sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

38. A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising:

- 5 (a) providing a target that is a gene or RNA, wherein said target comprises a nucleic acid encoding said gene product;
- (b) contacting said target with a candidate compound or nucleic acid; and
- (c) measuring an activity of said target.

39. The method of Claim 38, wherein said target is a messenger RNA molecule and
10 said activity is translation of said messenger RNA.

40. The method of Claim 38, wherein said target is a messenger RNA molecule and said activity is transcription of a gene encoding said messenger RNA.

41. The method of Claim 38, wherein said target is a gene and said activity is transcription of said gene.

15 42. The method of Claim 38, wherein said target is a nontranslated RNA and said activity is processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex.

43. The method of Claim 38, wherein said target gene or RNA encodes a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-
20 353, 357-364, 372-458, 464-466, 468 and 472-479.

44. A compound or nucleic acid identified using the method of Claim 38.

45. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a microorganism, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a sequence selected from the
25 group consisting of SEQ ID NOs.: 1-93, said method comprising the steps of:

- (a) expressing a sub-lethal level of an antisense nucleic acid complementary to a nucleic acid encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;
- (b) contacting said sensitized cell with a compound; and
- 30 (c) determining whether said compound inhibits the growth of said sensitized cell.

46. The method of Claim 45, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

35 47. The method of Claim 45, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

48. The method of Claim 45, wherein said cell is a Gram negative bacterium.

49. The method of Claim 45, wherein said cell is an *E. coli* cell.

50. The method of Claim 45, wherein said cell is from an organism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*,
5 *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*,
10 *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species
15 falling within the genera of any of the above species.

51. The method of Claim 45, wherein said antisense nucleic acid is transcribed from an inducible promoter.

52. The method of Claim 51, further comprising the step of contacting said cell with a concentration of inducer which induces said antisense nucleic acid to a sub-lethal level.

20 53. The method of Claim 45, wherein growth inhibition is measured by monitoring optical density of a culture growth solution.

54. The method of Claim 45, wherein said gene product is a polypeptide.

55. The method of Claim 54, wherein said polypeptide comprises a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-
25 466, 468 and 472-479.

56. The method of Claim 45, wherein said gene product is an RNA.

57. A compound identified using the method of Claim 45.

58. A method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene whose activity or expression is inhibited by an antisense nucleic acid
30 comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93 or a compound with activity against the product of said gene into a population of cells expressing said gene.

59. The method of Claim 58, wherein said compound is an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, or a proliferation-inhibiting portion thereof.

35 60. The method of Claim 59, wherein said proliferation inhibiting portion of one of SEQ ID NOs.: 1-93 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive nucleotides of one of SEQ ID NOs.: 1-93.

61. The method of Claim 58, wherein said population is a population selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

62. The method of Claim 58, wherein said population is a population of Gram negative bacteria.

5 63. The method of Claim 58, wherein said population is a population of *E. coli* cells.

64. The method of Claim 58, wherein said population is a population selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species.

20 65. The method of Claim 58, wherein said gene encodes a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

66. A preparation comprising an effective concentration of an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable carrier.

25 67. The preparation of Claim 66, wherein said proliferation-inhibiting portion of one of SEQ ID NOs.: 1-93 comprises at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-93.

68. A method for inhibiting the activity or expression of a gene in an operon required for proliferation wherein the activity or expression of at least one gene in said operon is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising contacting a cell in a cell population with an antisense nucleic acid comprising at least a proliferation-inhibiting portion of said operon.

30 69. The method of Claim 68, wherein said antisense nucleic acid comprises a sequence selected from the group consisting of SEQ ID NOs.: 1-93 or a proliferation inhibiting portion thereof.

70. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population.

71. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which expresses said antisense nucleic acid into said cell population.

5 72. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by expressing said antisense nucleic acid from the chromosome of cells in said cell population.

73. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the synthesis of said antisense nucleic acid.

10 74. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.

75. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide.

15 76. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell.

77. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid.

20 78. The method of Claim 68, wherein said antisense nucleic acid is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-93.

79. The method of Claim 68 wherein said antisense nucleic acid is an oligonucleotide.

80. A method for identifying a gene which is required for proliferation of a microorganism comprising:

25 (a) contacting a microorganism other than *E. coli* with a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-93;

(b) determining whether said nucleic acid inhibits proliferation of said microorganism; and

30 (c) identifying the gene in said microorganism which is inhibited by said nucleic acid.

81. The method of Claim 80, wherein said microorganism is a Gram negative bacterium.

82. The method of Claim 80 wherein said microorganism is selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*,

Clostridium botulinum, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*,
5 *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species.

10 83. The method of Claim 80, further comprising introducing said nucleic acid into a vector functional in said microorganism prior to introducing said inhibitory nucleic acid into said microorganism.

84. A method for identifying a compound having the ability to inhibit proliferation of a microorganism comprising:

15 (a) identifying in a first microorganism a homolog of a gene or gene product present in a second microorganism which is different than said first microorganism, wherein the activity or level of said gene or gene product is inhibited by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 1-93 ;

(b) identifying an inhibitory nucleic acid sequence which inhibits the activity
20 of said homolog in said first microorganism;

(c) contacting said first microorganism with a sub-lethal level of said inhibitory nucleic acid, thus sensitizing said first microorganism;

(d) contacting the sensitized microorganism of step (c) with a compound; and

(e) determining whether said compound inhibits proliferation of said sensitized
25 microorganism.

85. The method of Claim 84, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism.

86. The method of Claim 84 wherein step (a) comprises identifying a homologous
30 nucleic acid to a gene or gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-93 or a nucleic acid encoding a homologous polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-93 by using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the
35 default parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database.

87. The method of Claim 84 wherein said step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying nucleic acids which hybridize to said first gene.

88. The method of Claim 84 wherein the step (a) comprises expressing a nucleic acid
5 selected from the group consisting of SEQ ID NOs. 1-93 in said microorganism.

89. The method of Claim 84, wherein said inhibitory nucleic acid is an antisense nucleic acid.

90. The method of Claim 84, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

10 91. The method of Claim 84, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

92. The method of Claim 84, wherein the step of contacting the first microorganism with a sub-lethal level of said inhibitory nucleic acid comprises directly contacting said microorganism with said inhibitory nucleic acid.

15 93. The method of Claim 84, wherein the step of contacting the first microorganism with a sub-lethal level of said inhibitory nucleic acid comprises expressing an antisense nucleic acid to said homolog in said microorganism.

94. The method of Claim 84, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-
20 353, 357-364, 372-458, 464-466, 468 and 472-479.

95. A compound identified using the method of Claim 84.

96. A method of identifying a compound having the ability to inhibit proliferation comprising:

(a) contacting a microorganism other than *E. coli* with a sub-lethal level of a
25 nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 1-93 or a portion thereof which inhibits the proliferation of *E. coli*, thus sensitizing said microorganism;

(b) contacting the sensitized microorganism of step (a) with a compound; and

(c) determining whether said compound inhibits proliferation of said sensitized
30 microorganism.

97. The method of Claim 96, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism.

98. A compound identified using the method of Claim 96.
35

99. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

- 5 (a) sensitizing a cell by expressing a sub-lethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, in said cell to reduce the activity or amount of said gene product;
- (b) contacting the sensitized cell with a compound; and
- 10 (c) determining whether said compound inhibits the growth of said sensitized cell.

100. The method of Claim 99, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

101. The method of Claim 99, wherein said cell is selected from the group consisting of 15 bacterial cells, fungal cells, plant cells, and animal cells.

102. The method of Claim 99, wherein said cell is a Gram negative bacterium.

103. The method of Claim 99, wherein said Gram negative bacterium is *E. coli*.

104. The method of Claim 99, wherein said cell is selected from the group consisting of 20 *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, 25 *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species 30 falling within the genera of any of the above species.

105. The method of Claim 99, wherein said antisense nucleic acid is transcribed from an inducible promoter.

106. The method of Claim 99, further comprising contacting the cell with an agent 35 which induces expression of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is expressed at a sub-lethal level.

107. The method of Claim 99, wherein inhibition of proliferation is measured by monitoring the optical density of a liquid culture.

108. The method of Claim 99, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-
5 353, 357-364, 372-458, 464-466, 468 and 472-479

109. A compound identified using the method of Claim 99.

110. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene
10 product required for proliferation of said cell, wherein said gene product is a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93;

(b) contacting said cell with a compound; and

(c) determining whether said compound reduces proliferation of said contacted
15 cell.

111. The method of Claim 110, wherein said determining step comprises determining whether said compound reduces proliferation of said contacted cell to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

112. The method of Claim 110, wherein said agent which reduces the activity or level of
20 a gene product required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

113. The method of Claim 110, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises a compound known to inhibit growth or proliferation of a microorganism.

25 114. The method of Claim 110, wherein said cell contains a mutation which reduces the activity or level of said gene product required for proliferation of said cell.

115. The method of Claim 114, wherein said mutation is a temperature sensitive mutation.

116. The method of Claim 110, wherein said gene product comprises a polypeptide
30 comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479

117. A compound identified using the method of Claim 110.

118. A method for identifying the biological pathway in which a proliferation-required gene or its gene product lies, wherein said gene or gene product comprises a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising:

- 5 (a) expressing a sub-lethal level of an antisense nucleic acid which inhibits the activity of said proliferation-required gene or gene product in a cell;
- (b) contacting said cell with a compound known to inhibit growth or proliferation of a microorganism, wherein the biological pathway on which said compound acts is known; and
- 10 (c) determining whether said cell is sensitive to said compound.

119. The method of Claim 118, wherein said determining step comprises determining whether said cell has a substantially greater sensitivity to said compound than a cell which does not express said sub-lethal level of said antisense nucleic acid and wherein said gene or gene product lies in the same pathway on which said compound acts if said cell expressing said sub-lethal level of said antisense nucleic acid has a substantially greater sensitivity to said compound than said cell which does not express said sub-lethal level of said antisense nucleic acid.

15

120. The method of Claim 118, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479

20 121. A method for determining the biological pathway on which a test compound acts comprising:

- (a) expressing a sub-lethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a cell, wherein the activity or expression of said proliferation-required nucleic acid is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93 and wherein the biological pathway in which said proliferation-required nucleic acid or a protein encoded by said proliferation-required polypeptide lies is known,
- 25 (b) contacting said cell with said test compound; and
- (c) determining whether said cell is sensitive to said test compound.

30 122. The method of Claim 121, wherein said determining step comprises determining whether said cell has a substantially greater sensitivity to said test compound than a cell which does not express said sub-lethal level of said antisense nucleic acid.

123. The method of Claim 121, further comprising:

(d) expressing a sub-lethal level of a second antisense nucleic acid complementary to a second proliferation-required nucleic acid in a second cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said second cell does not have a substantially greater sensitivity to said test compound than a cell which does not express said sub-lethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological pathway against which the antisense nucleic acid of step (a) acts if said second cell does not have substantially greater sensitivity to said test compound.

124. A purified or isolated nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93.

125. A compound which interacts with a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93 to inhibit proliferation.

126. A compound which interacts with a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93 to inhibit proliferation.

127. A method for manufacturing an antibiotic comprising the steps of:

screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93; and manufacturing the compound so identified.

128. The method of Claim 127, wherein said screening step comprises performing any one of the methods of Claims 28, 38, 45, 96, 99 and 110.

129. A method for inhibiting proliferation of a microorganism in a subject comprising administering a compound that reduces the activity or level of a gene product required for proliferation of said microorganism, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93 to said subject.

130. The method of Claim 129 wherein said subject is selected from the group consisting of vertebrates, mammals, avians, and human beings.

131. The method of Claim 129, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

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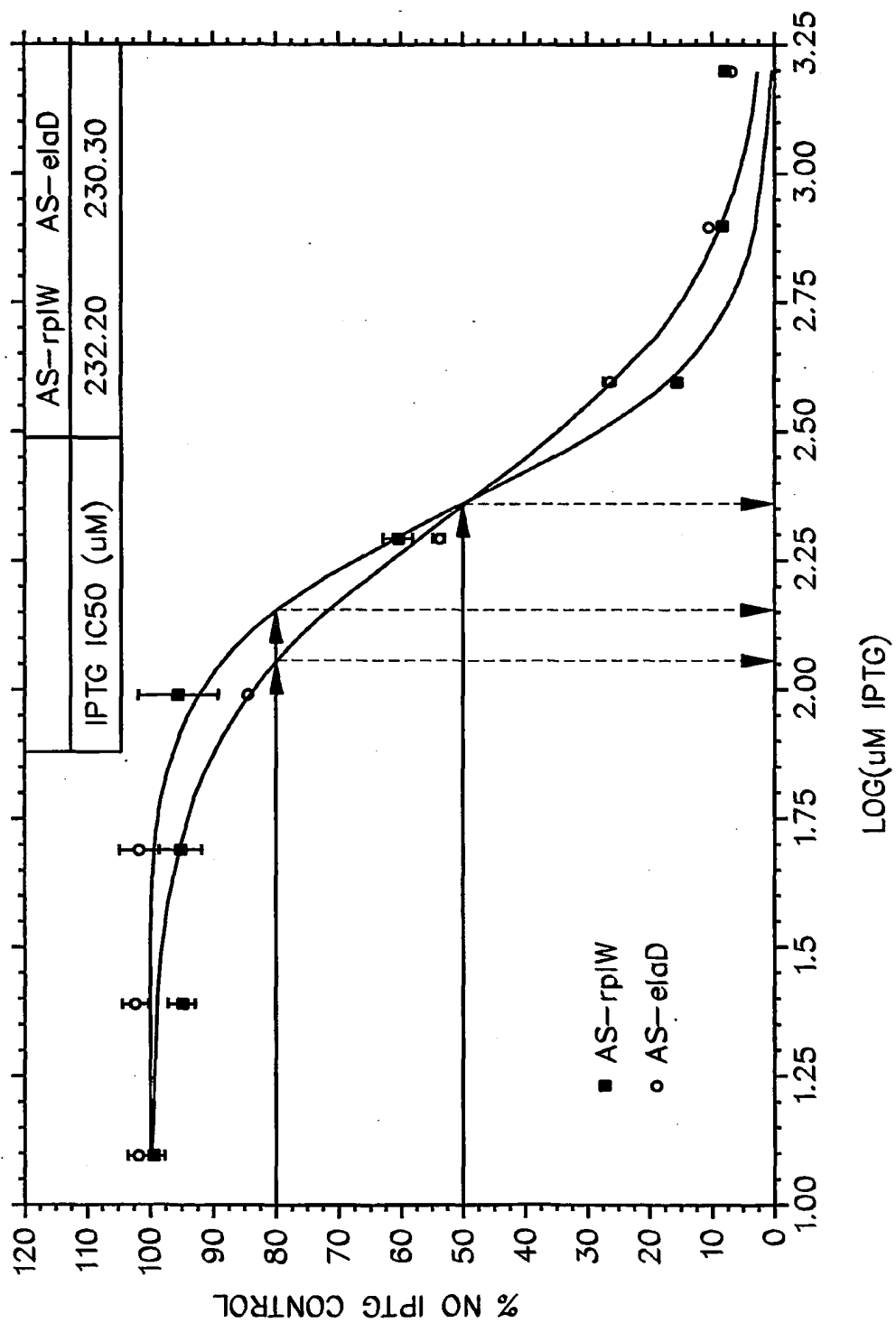
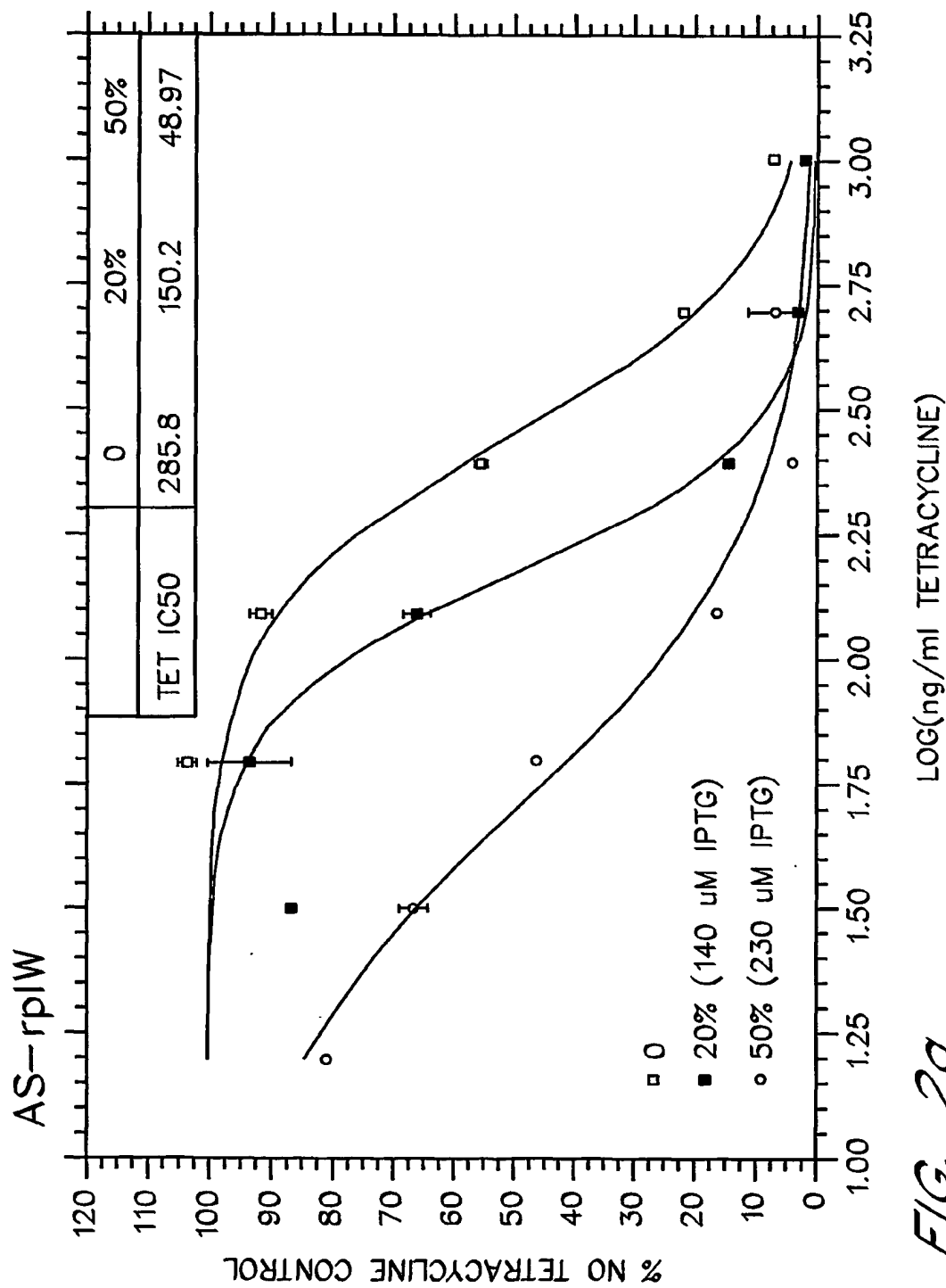


FIG. 1

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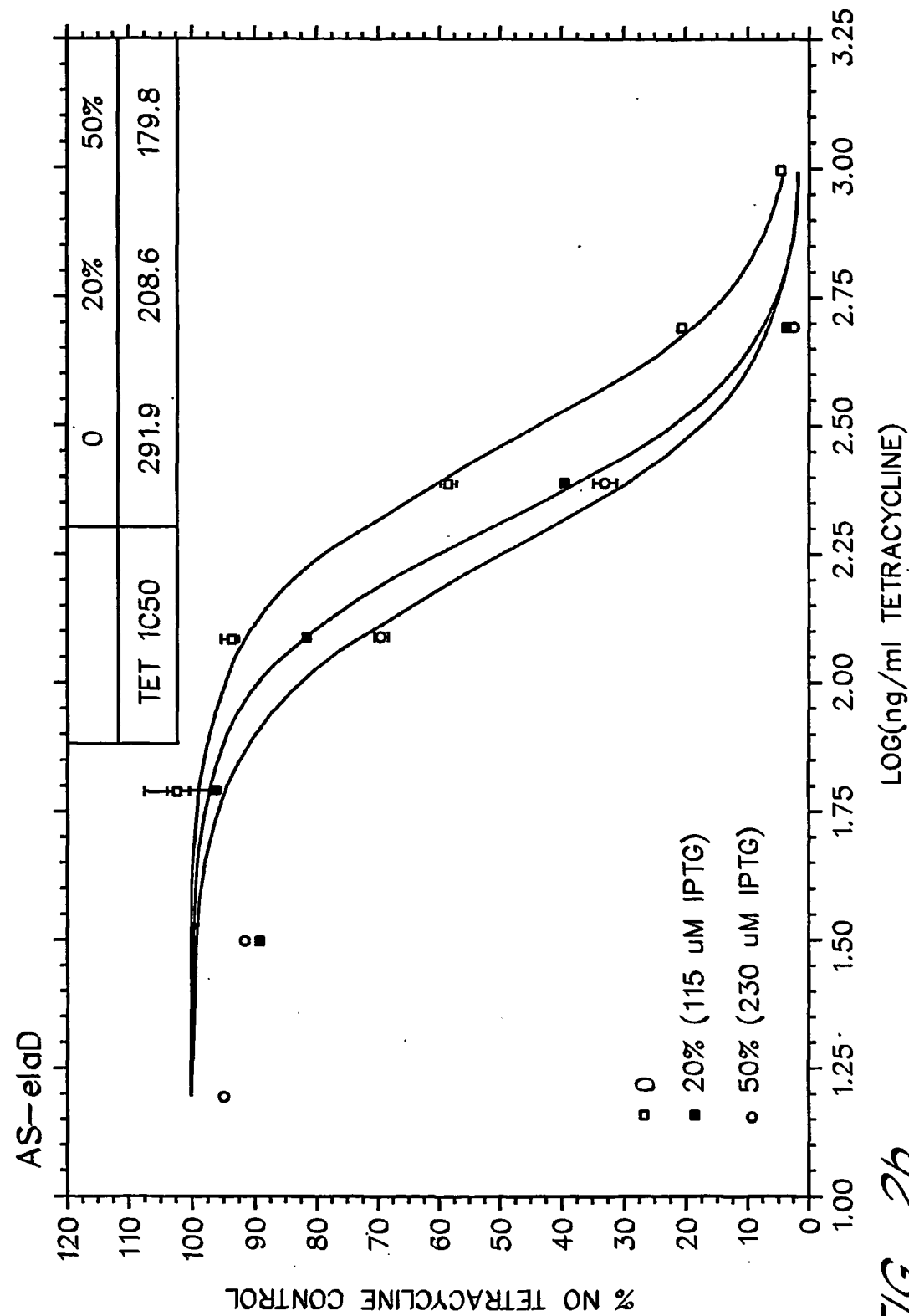


FIG. 2b

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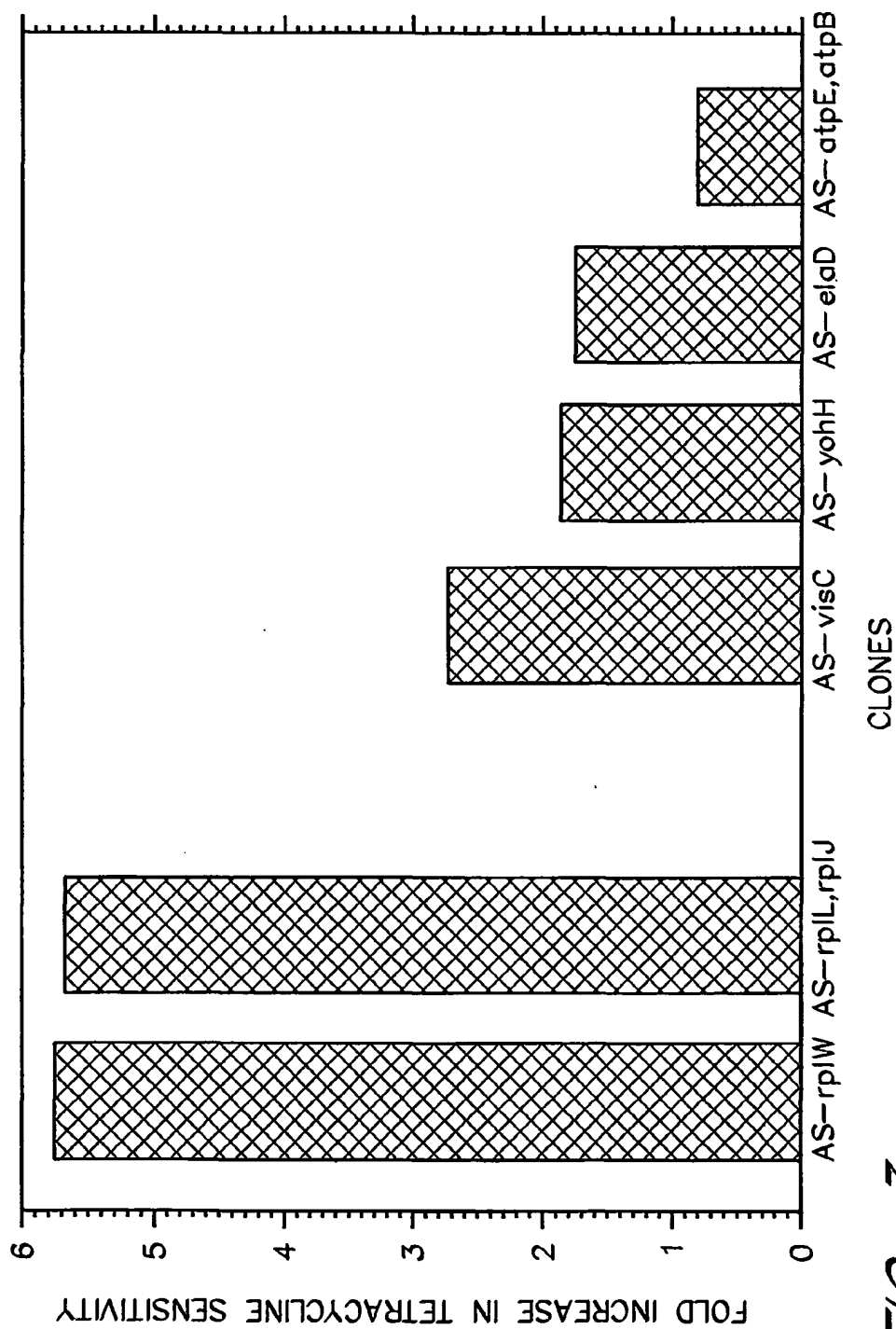


FIG. 3

SEQUENCE LISTING

<110> ELITRA PHARMACEUTICALS, INC.
 FORSYTH, R. Allyn
 OHLSEN, Kari L.
 ZYSKIND, Judith W.

<120> GENES IDENTIFIED AS REQUIRED FOR
 PROLIFERATION OF E. COLI

<130> ELITRA.009VPC

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<151> 1999-12-23

<160> 481

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gcgtgcgaca tcgcgacgca cttgcttcaa cagggtgagac tggtgcagct ggccacttgc 240
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ttactcaciaa tgtatcaggg aaatataact taocgggaga tgtaatatgt ttaatttttc 180
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gtactttctg tgccagagag ataattttca tgaactttct actacgaagc tcacgagtta 180
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<400> 30

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agccattgtc cggagaatct tcgtctttct cgagggtatt atctgaaagt aactcttctg 60
agctagagtc ttctatgttt aaatccatag tataattaat ttgggggacg accagataag 120
cattttcttt ggtattttca taatcttcaa tgattatata cgaatgaatc atatattttt 180
tctgatgaga attctttcat ctctgttaat ttaattctgt tcaagcaatt gatgattttc 240
gatgagcttt tatataatttc ttttgtaat tcattttcta atttatctgt aagagttgcc 300
cttgg 305

```

<210> 31

<211> 425

<212> DNA

<213> *Escherichia coli*

<400> 31

```

aggttactgg cgaggttatc gagaaacgcc agactgatac ccataaaaaa gagaataagg 60
taaaccatcc agcttaatag ctgattaata acttttaacg cagcttggtg gcgaagcgga 120
atgaggtaac ccacaatcag gggaaccaga atgattaaca gccagaaaaa catgaaaacc 180
cagtccttgc aaagatgaag tcgaaatgcg cgatgacaca ctactgaaag cggaaggacg 240
agtaaagttg caattaaaag gaaatgttat gcataaggag cagtagagta ttogttttca 300
tttaaagata ttcttgcgct ttaattacaa actgcaccga tgttggtggc gtcaaaatcg 360
ccgaggcggt ccctgaaggc cggggcagcc cacatggatg tgggctgagg gcgcgtttta 420
caggg 425

```

<210> 32

<211> 381

<212> DNA

<213> *Escherichia coli*

<400> 32

```

aaaagagaat aaggtaaacc atccagctta atagctgatt aataactttt aacgcagctt 60
gttggcgaag cggaatgagg taaccacaa tcagggaac cagaatgatt aacagcccag 120
aaaacatgaa aaccagctcc ttgcaaagat gaagtcgaaa tgcgcgatga cactactctg 180
aaagcggaag gacgagtaaa gttgcaatta aaaggaaatg ttatgcataa ggagcagtag 240
agtattcggt ttcatttaaa gatattcttg cgctttaatt acaaactgca ccgatgttgg 300
tggcgtaaaa atcgccgagg cgttccttga aggcgggggc agcccacatg gatgtgggct 360
gagggcgcgt ttacaggga t 381

```

<210> 33

<211> 329
 <212> DNA
 <213> *Escherichia coli*

<220>
 <221> misc_feature
 <222> (1)...(329)
 <223> n = A,T,C or G

<400> 33
 gtogatgttg tgcccgaact tgccatgctc cagtcctttt cttctggggc gactttccgg 60
 gaggtgctta aacgaaaaac cccgcccggt ttgcgcgggc ggggttttgg aatcgtgtgt 120
 tgttccagtc cctacggcgc attgccgacg accaccacca cacgcacgac gaccactgcg 180
 gcggatgggc gcagttggta gtagttttgc gttgagcatg gaagtagtca ttggggacct 240
 tgttgggttt gtgtttaaca atatttatac aagcacagct ttacagggga gacaatggaa 300
 aatttttcag caagggaaaa ttgaggggn 329

<210> 34
 <211> 442
 <212> DNA
 <213> *Escherichia coli*

<400> 34
 gatgttgtgc ccgaacttgc catgctccag tccttttctt ctgggcccgc tttccgggag 60
 gtgcttaaac gaaaaacccc gcccggtttg cgcggcgagg gttttggaat cgtgtgttgt 120
 tccagtccct acggcgcatt gccgacgacc accaccacac gcacgacgac cactgcggcg 180
 gatggcgag ttggtagtag ttttgcgttg agcatggaag tagtcattgg ggaccttgtt 240
 gggttttgtt ttaacaatat ttatacaagc acagctttac aggggagaca atggaaaatt 300
 tttcagcaag ggaaaattga ggggttgatc acgttttgta ctgaattgca gataacaaaa 360
 aacccgcgcg gagcgagggt tcgtcagtcg cctgcggctg gtaaccgcaa agcacactgt 420
 attatgtcaa cactgaaagt at 442

<210> 35
 <211> 272
 <212> DNA
 <213> *Escherichia coli*

<400> 35
 cgattatagg gctgaccaa tacatggata gataatatgc catccccca ggcagtccac 60
 gtaaaaagag catatacaag gagaatagaa cacctacagc tgtaataaga taaacataat 120
 gttttactct attaacacct acgatgaatg cataagagat gataaccata aagacaattt 180
 gcttaccagt attcagtata attgcaaaga tgaatacaat aaaaacaagt aaagttaatg 240
 ttttacttac ctttgtatta gttaaatttt ta 272

<210> 36
 <211> 255
 <212> DNA
 <213> *Escherichia coli*

<400> 36
 tgcgattacg gcattgcttat gatcaggaat gttaatgcct gctatacggg ccactatgca 60
 ctctactat ttaatatgta cggtccatgc tgaaaagccc gttttcagga tactcaaattg 120
 gaaacgcaca gacatacaaa agattggctg gctaattctag ccagctcaac ccaactttgc 180
 aagaaaaata tgcgaaaaaa tcagccttgg cgctgtttat gcttcggctc ggcactgcaa 240
 atcacacgga tgaca 255

<210> 37
 <211> 389
 <212> DNA
 <213> *Escherichia coli*

<400> 37

```

aacgtaaaac tttacgtaaa ttaacatggt taacatttat gccactattg tttgtaaatt 60
catatttcgt aatgcttctg aatttttcgt gtgatgggtt taaatactat ggtgtttact 120
cttgagggga cggcctatct ataaaatacg gacatttcaa taaatgcccg tataaacaga 180
gtatgattct ggctggctgt tgagtatcaa tgttggaacg aatgtgaacg aataaataat 240
tcgtttatct taccacccat tctcttttcg attcgttgct tgtacgcgta gatgctacgg 300
atatccatat ccagaacttc agcaatctga tatggattat aaccagaaac catatacccc 360
attatggtga attccatctg agttaatgt 389

```

<210> 38

<211> 178

<212> DNA

<213> *Escherichia coli*

<400> 38

```

gtggtttagga tctttatagt tacgctcggc ggcattccatc gggatacctg cggcattttc 60
tttggcaaaa ccgatttcag aattgtgttt gtttgatga acctgaatgg agagtggctg 120
tgctgcgcac aatactttga acaggaaagg cagttcgcca aagcgtttgg caacggcc 178

```

<210> 39

<211> 191

<212> DNA

<213> *Escherichia coli*

<400> 39

```

tcgcaaggaa aggcgtcagc gcaaaaacca gctccggctt gtggtttagga tctttatagt 60
tacgctcggc ggcattccatc gggatacctg cggcattttc tttggcaaaa ccgatttcag 120
aattgtgttt gtttgatga acctgaatgg agagtggctg tgctgcgcac aatactttga 180
acaggaaagg c 191

```

<210> 40

<211> 158

<212> DNA

<213> *Escherichia coli*

<400> 40

```

ccggcttggt gtttaggatc ttatagttac gctcggcggc atccatcggg atacctgcgg 60
cattttcttt ggcaaaaccg atttcagaat tgtgtttgtt tggatgaacc tgaatggaga 120
gtggctgtgc tgcgcataat actttgaaca gaaaaggc 158

```

<210> 41

<211> 184

<212> DNA

<213> *Escherichia coli*

<400> 41

```

tcgaagaatt taacggaggg taaaaaaacc gacgcacact ggcgtcggct ctggcaggat 60
gtttcgtaat tagatagcca ccggcgcttt aatgcccgga tgcggatcgt agccttcaat 120
ctcaaagtct tcgaaacggt agtcgaagat ggattcgggt ttacgtttga taatcaactt 180
cggc 184

```

<210> 42

<211> 122

<212> DNA

<213> *Escherichia coli*

<400> 42

```

gtagaagttc aaattacgaa cctgaatttt actcggggca gtttcaacca tactcattgc 60
aatcttttcc tcatcgtgcc tgatgcactt cgtaatcag gcttaccgta ggccggatca 120
gg 122

```

<210> 43
<211> 163
<212> DNA
<213> Escherichia coli

<400> 43
taaattccgc gtatagcgtg ggcgctttgg ctccggtcgc ttcgacgagg tccgcaagag 60
aagtcgcttc ataaccgtgt tgccagaaca atttcatggc cttatcaagc gcggcatccc 120
tgtcgaacac ttttggggcg ccacggcttt tttttacaca ttg 163

<210> 44
<211> 161
<212> DNA
<213> Escherichia coli

<400> 44
gcaaattgttt tcgtaattca ggagaaatgg caaataaagc attaaaaatt tgaatgcttt 60
gtgtaataaa aaagcagaca ggcgacggag tgaccactcc gtcgctttac aaagagagga 120
aatcatagg ttgcccgtgt agtgccagcg taaataacgc a 161

<210> 45
<211> 251
<212> DNA
<213> Escherichia coli

<400> 45
ggctgtaacg gtaaagccct caccgaagcg agggcttgaa ggagaagggg tatgatgcga 60
cttgtcatca tactgattgt actgttactc ataagtttca gcgcttatta acagtcagtc 120
tcaggggagg agcaatcctc ccttaccctt actcactaaa ttaggtcaaa gaatcaacga 180
tgtcaatcag ggcgatgcgg ttgtatcgcc cttaccactc ccagactttc gacggtgtaa 240
ccaccgcagg a 251

<210> 46
<211> 286
<212> DNA
<213> Escherichia coli

<400> 46
caccgaagcg agggcttgaa ggagaagggg tatgatgcga cttgtcatca tactgattgt 60
actgttactc ataagtttca gcgcttatta acagtcagtc tcaggggagg agcaatcctc 120
ccttaccctt actcactaaa ttaggtcaaa gaatcaacga tgtcaatcag ggcgatgcgg 180
gtgtatcgcc cttaccactc ccagactttc gacggtgtaa ccaccgcagg aagagggata 240
tcccactctt caacggggag tttttccacc aactgacaat catgcg 286

<210> 47
<211> 180
<212> DNA
<213> Escherichia coli

<400> 47
ccggggctga cgtgggcgat aatcgggtcg ccaggaatag ggcggcagca tttcgcaaag 60
gtgatcagca cgccatcggc acctttaatg ggcagatgtc cgtggctttg ggttgccggg 120
ggaatggagg cgtcccatg ttgcagattt ttcgcgacca ccacgctcat tgcgttacca 180

<210> 48
<211> 254
<212> DNA
<213> Escherichia coli

<400> 48

```

tgtcgagcat acgcggcagc gccgactcgg aagatgaagt cccaggtaca atcagcagtt 60
cttcacggat gtagcggata aatttgaaga tactgaaacc agtcgcttta gcgattgaac 120
ccaataccag caccacaaac aggatacagg taatgtagaa acagataatc agctgcccc 180
gttgaccag tgtgcggacg ccgtatttac cgatggtaaa cgccattgcc ccgaacgcac 240
caatagggtgc caga 254

```

```

<210> 49
<211> 300
<212> DNA
<213> Escherichia coli

```

```

<220>
<221> misc_feature
<222> (1) ... (300)
<223> n = A,T,C or G

```

```

<400> 49
agctgatcga tgggtgtttgc caacgcacac gccaccgcgg cggcggcaaa caccancgta 60
ccgcogagca ccaccggctt acgcccgaag ctgtctgccca tcggcccgtta gattaactgc 120
cccaacgcaa agcccagaat ataagtactg aggggtcatct gcgtactgcc cgnccggtacg 180
ccaaactcgc ctgaaattac cggtagcgcg ggcagataca tatcaatcga cagcggcatc 240
aacatggcca gcaggccaag gataaaaaca atagcaaacg acgaatgctg tcgggtggtc 300

```

```

<210> 50
<211> 207
<212> DNA
<213> Escherichia coli

```

```

<400> 50
caacatctca tgtctggatt tgtagatata cgtggaattc caattgggtat cttttgtagg 60
attcaacata tcatgtaagc gctgggagct taccaccata actggcccat catcgactga 120
ggagaacagg ataaagatat tatcgtttcg tgtaattca ttcgtgtaa aggttcttaa 180
attatcttca gtttctataa atatagg 207

```

```

<210> 51
<211> 213
<212> DNA
<213> Escherichia coli

```

```

<400> 51
ttctgtaatc agaaaaagaa gaactggaat tttaataaat attatttctc tgggaacggg 60
ggggtataat caatatgacg agttgaatat tatatttttt ataagaatta tatgagatta 120
aagaaatctg ccgtaaagac agatttcttt aaaagataat tagagatttg cgacgttatg 180
ataaactttt tgtacatcgt cgtcatcttc aag 213

```

```

<210> 52
<211> 381
<212> DNA
<213> Escherichia coli

```

```

<400> 52
tctgttagtg tattatccac tggggccctt tccgcgtct cgcaaacggg cgctggcttt 60
aggaaaggat gttccgtggc cgtaaagca ggtgtttcac agcgcttgct atcgcgga 120
tatcgccagt ggtgctgtcg tgatgcggtc ttgcgatgga ccgcacaatg aagatacgg 180
gcttttgat cgtacttatt gtttctgggt cgctgttaac cgaggtaaat aataaccgga 240
gtctctccgg cgacaattta ctgggtggtta acaaccttca gagcagcaag taagcccgaa 300
tgccgccctt tgggcgccat attttagatt atccgattct gtttaaagtc acgcaaaaaa 360
ccacccagc gacgttcata g 381

```

```

<210> 53

```

<211> 154
<212> DNA
<213> *Escherichia coli*

<400> 53
aaatagaccg gcatactttc gtgcggcagc ataatcaaca gtacgagcgc agcgggtacta 60
atgataaagg tgtagcatag atattttactt ggcgatttca ggatcttata tgaaatcatg 120
ccaccaatcg gtccaccaat catttttcaga cagt 154

<210> 54
<211> 191
<212> DNA
<213> *Escherichia coli*

<400> 54
tccttagtca ggtactgacg tacttttaaaa tcgctgtcca ggttgtcagc gaattctttg 60
gtgttcgcaa accaggtaga gttccatggt tttacaatac ccaggcgaat accattagga 120
tgtactttct gacccattgc tagtctccag agtctcagcg atcggacaca accacagtga 180
tgtggctggt g 191

<210> 55
<211> 190
<212> DNA
<213> *Escherichia coli*

<400> 55
gctggtgccc gttttccatg ccagtggggc gacgcggggc aaggcactat ccggcaaggg 60
ttgcgcttca tcagccataa tccggcgaat gatccaogcc gccccgacg acattaaagg 120
ccgttcaagc agcggatcgt caggctgtaa gcgcaatttg cctgccttgc cgtggcgagc 180
aaacgcggtg 190

<210> 56
<211> 402
<212> DNA
<213> *Escherichia coli*

<400> 56
aaaaaatgaa attcctcttt gacggggccaa tagcgatatt ggccattttt ttagcgcaac 60
atgtgcggca aattcccttc tccatacagg tgtagtgcac cgaccgcgac cacatatcgc 120
cccggcgcca tggcgcgtaa tttatcccgc caggcgagat ttcgctgatg catcagcaca 180
tcgtacagcg actgactgaa cgtattgggc agcgttatat cattattttg cggcgggtgca 240
ttcagccacc agctcatcat ttgttgacgc aaccgtgcgt tggtagcca gtgggtcagc 300
gtatcgacca gcagcgccag tcctttgtca gggagctgga gcaacatggc aatctggttt 360
tcagcccctt ccagttcaat cacgggttta tgttggtgct tc 402

<210> 57
<211> 595
<212> DNA
<213> *Escherichia coli*

<220>
<221> misc_feature
<222> (1)...(595)
<223> n = A,T,C or G

<400> 57
aattaatcag agcaacggta aaacaatgaa agtgtaaaaa acactttttgc gccatttatg 60
gagaaaaaaa gaaaatttga tggagagtga tgagagaata ttacaacacg atgatttttg 120
agagattatg aagaactata cgggatgact ggtgataaat aaagcaaata accaggatta 180
atctgtatta atttataaga aagcaactta ataccgcag aatgatttct gcgggtaagt 240
attagcttat tttttcgagc attaatcccg cgcgtaatcc caacgctacc aacggattag 300

```

ggaataacac atactctaca tcatgggtta cggtaaaacg ttctctctcg tctgcgcca 360
gcaatgttcc tttctcaaac ggcataaaat tcagcgtgtc acttgccata tgcatttcga 420
aggacggcga gtggcgagta atttgcgaaa ccacccgata acggagcggc ggtgttctca 480
cgataccgac actctcacca gatagcagcg cagcaattgc gctggcagtt actgcaaact 540
ggcgaagatc gttttgcccc aagggcaacg ctttgccaag ttncagccgt acang      595

```

<210> 58
 <211> 250
 <212> DNA
 <213> Escherichia coli

```

<400> 58
gaaactcagt ggaatggggg agccgcaata gcgaacatgt tccatgccgc caataatctg 60
tgcgcggtga atatgcccga gcgcgatgta gtcggctggt ggaaagtttt gtgccggaaa 120
cgctccagc gtgccaatat aaatgtcacg cacggcgctca cttttactgg cccccacggt 180
cgttaaatgt cccgtggcga tgatgggcag aggctgatcg ccgcgcagtt tgcaggcatc 240
ggcatagtgt                                     250

```

<210> 59
 <211> 236
 <212> DNA
 <213> Escherichia coli

```

<400> 59
aaaggttcgg caaaagccat aaccttttcg tcagctttgg ccggataagg gacacattgc 60
gacgtttcga ccattttata acgggtaaaa ccaccatcaa catgagggaa atacatggca 120
ctgccaaaaa aacgcataatc tgtacactga ttctcgttat gttcaatgca gtatttgcag 180
tgaccgcacg gtttagacgg attaatggct accgtttgcc cttcatgtaa ttctga    236

```

<210> 60
 <211> 92
 <212> DNA
 <213> Escherichia coli

```

<400> 60
gaagagatgt tcaggttttc gttatcgcca atggtatcga acttgtaatt ctcatacttc 60
tcgtcaggcg tggagtacgc cgcgccacgg aa                                     92

```

<210> 61
 <211> 62
 <212> DNA
 <213> Escherichia coli

```

<400> 61
tgtcgacatt cagcacttcc gggatttcgt cgcgcagggc aaatgtacag gttgaggagg 60
tg                                              62

```

<210> 62
 <211> 72
 <212> DNA
 <213> Escherichia coli

```

<400> 62
acttatcaaa ccatttttcc gtttcaccgg aggtctgcac ctgagcgatg gtgtcatcca 60
tcagcttttt ga                                     72

```

<210> 63
 <211> 66
 <212> DNA
 <213> Escherichia coli

```

<400> 63
aaacgcgatgg cgcgtaaagg ttcaatcagt ccgatttcag cgggtgctgaa ctgcgctaaat 60
tcttca 66

<210> 64
<211> 143
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(143)
<223> n = A,T,C or G

<400> 64
tataggggnc tatttcatta acccgacact ggattaattc aacaggaata ttatgattct 60
gacacaactc ttttaatttct tccgccgcca tcgtagaggt cgcaaccgcg cctccgcaag 120
cgacaataat cttgcgtttc ata 143

<210> 65
<211> 210
<212> DNA
<213> Escherichia coli

<400> 65
gaggaaccgt gtgacacaca aagggtgatt attttccatt ggggcgtata atcctggctc 60
accatcatgt attttcatgg ctaaaatact catcaccagt tttttgttta aaagctcttg 120
tgctattgga gtgggttaatg cattcagaaa gatatcgatt atttcatcga atccatacaa 180
catggagata taaagtccag gtgtttcgtt 210

<210> 66
<211> 118
<212> DNA
<213> Escherichia coli

<400> 66
agagctgtga aggagaaaaat acgaccaact ttaacggttt tagatacgcg gtttaccgcg 60
atcagctttt cctgcagttc gccagcttgt ttttcgatgt gagccatctt acacctct 118

<210> 67
<211> 531
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(531)
<223> n = A,T,C or G

<400> 67
cctttcaacg cagtagaggg gaatgncncc tacggcatcg gcaccgcgct caatttctgc 60
cagcatatag cccattccgt cttgatcggg cggaacatag gtgtcggcat cacttaaaaa 120
aacctggtcg caggtggcgt aattgaggcc attcatcagc gcaccacctt taccggtatt 180
tttttgctg acggcaacaa agcggtcgcc ccatttgcgt ttgacttccg ccatgaccgc 240
ttcgggtattg tccgtggagc cgtcgttaac gcaaattacc cggcaaaaat aanggggttcg 300
cagtaantta tccagtgact ggcgcagac acgggccttt tttntnecga gntttaatgg 360
cgtcnaatac agcctttttt tttantgggt ttacntnta necgtnttta aaaaccata 420
gcaaccattg ttttngacct tcanaatnaa aaattcnggg ttttaaaagc gcgttttccg 480
gcaacttgnt ggacagggca aaaaattcct gcctgggtcg ccgnatctgn g 531

<210> 68

```


<211> 102
 <212> DNA
 <213> Escherichia coli

<400> 68
 agcgccggtta acgcccgtta aatgtttctcg ttccggcttcc cgatcggttat tcaacaggct 60
 gcgtaccgta gcggcatatt tcttccctgc ttcacgcga tc 102

<210> 69
 <211> 167
 <212> DNA
 <213> Escherichia coli

<400> 69
 aaaactcacc ttttttgttg ttatccctca attaccacaa gtaaaaggag ataaaccgac 60
 aatgacctag acgtaattat gtaaaaatac tgatgttcgt cactgactat ttccgatatt 120
 cagctgttga aaaatcaaaa aactggaaaa ataattttta atatcat 167

<210> 70
 <211> 83
 <212> DNA
 <213> Escherichia coli

<400> 70
 gccacgcca gcataaacag cgggatcgag ctttcaatcg gtacgcccag tacacctttc 60
 accatcagca ccagcgataa tcc 83

<210> 71
 <211> 103
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(103)
 <223> n = A,T,C or G

<400> 71
 gccnggcggg aaccgacatg ttcccactct acgcccgtcg gcgcggtttt cattttttgcg 60
 cacctgatag ccgcacgatt gcagatcaac aacgcctttt ttg 103

<210> 72
 <211> 121
 <212> DNA
 <213> Escherichia coli

<400> 72
 tagctttcttc cacattgtcg aactgaacgt ccagacggtg tttagaaacg ttgatgctcg 60
 ggattttttc cgcaccacag caaacgcgcg ccatggctgc aacggtttct gacggatact 120
 g 121

<210> 73
 <211> 163
 <212> DNA
 <213> Escherichia coli

<400> 73
 tagttattgg ctgttttgag aatgtaactt tccaactgct tataactctt cagatgcaat 60
 aatccgagaa tcacatgcaa tttattcata aattcgtggg atcgttcacg aagtgcgtca 120
 gcatagttga ccagaccgtc gagtcgctgc atcagtttac gta 163

<210> 74
 <211> 106
 <212> DNA
 <213> Escherichia coli

<400> 74
 aaaaccatga gggtattatg gccgatttga ggagggaaaag agtaagagca gtttggttaa 60
 tgtacaacga cgattctccc accgggcgcg ttttaaagcg acggtg 106

<210> 75
 <211> 319
 <212> DNA
 <213> Escherichia coli

<400> 75
 ctggagattg agtagatatt cttgttcaga atgtatcagc ccgatgggtc tacgattctt 60
 aagccacgaa gagttcagat agtacaacgg catgtctctt ttgactatct ggcaaccggg 120
 cagtgtgttc tctcacgcat caaaaagca gcaggcataa aaaaaccggc ttgcgcggct 180
 ttttcacaaa gcttcagcaa attggcgatt aagccagttt gttgatctgt gcagtcaggt 240
 tagccttatg acgtgcagct ttgtttttgt ggatcaaacc tttagcagcc tgacgggtcca 300
 cgatcggttg catttcggt 319

<210> 76
 <211> 237
 <212> DNA
 <213> Escherichia coli

<400> 76
 cgaaccaacg acccccacca tgtcaagggtg gtgctctaac caactgagct atgaacgcaa 60
 cgttgtagggt gacaacgggg acgaatatta gcggcagagt gggaagggtg caagaggcaa 120
 aacgtaattt tctgcgctat ttcgaccgtt tgcagagctt ttaagcaaat tggctatatt 180
 ttgttgattt gcaaggggtga tttttattca ggatcgcatt tacatctgat acaacc 237

<210> 77
 <211> 241
 <212> DNA
 <213> Escherichia coli

<400> 77
 tgtgacagag tggttatcgt taatcaggca aagagggaaa aacatattat ttaaaccatt 60
 atagcgcata aaatatcctt ataattaaca agaaagaaaa ggcattattct ctgcattatc 120
 attttctacg actgtcaaaa atcgtcatt ttttaatgag tttatttgtt taatattatg 180
 ggaaaagggt atgcatttgg gagaggaaga gtattccccg gtcagacgac cggggaaggg 240
 g 241

<210> 78
 <211> 89
 <212> DNA
 <213> Escherichia coli

<400> 78
 cccggctggg ttttttcaag tttacgcagg ggtgcgggcg atcacttccg ggttgctggc 60
 agcttcgcct ttcggcgaaa tgctgtgg 89

<210> 79
 <211> 140
 <212> DNA
 <213> Escherichia coli

<400> 79
 tcgcgaacac cgtagtggat gtagttaccc gcagcatctt cgttgattgc tttagaacca 60

gaccacaggg tcaggttaga cggcgccagg tcagcagaac cgccgaggaa ttccggcaac 120
agcggaccga acgcttcgat 140

<210> 80
<211> 189
<212> DNA
<213> Escherichia coli

<400> 80
gttagtaaaag ccgatgaggt gagcagtcac ttccgccggac ggatagtaac ggcgagactc 60
ttcacgcaga tgaatccccg gcagtttcag ttttttgatg tagtccgcca tgtcagggtt 120
cacctgacgc gccagataaa taaagcgccc ttccgggttg gcgttaatgc gggctgaaag 180
ctgatccag 189

<210> 81
<211> 347
<212> DNA
<213> Escherichia coli

<400> 81
gcagttcacc ggcacgcgct ttcttatata agcctttggg atcgcgggct tcgcaaactc 60
ccagcggcgt atcgacaaac acttcgataa agcgcccttc tcctacgcgt tcgcgaacca 120
tctggcgctt ggcgcggtgt ggcgagataa atcgcggtcag caccaccagt ccggcttcaa 180
ccatcaaatt cgccacttca ccgacgcgac ggatattctc tttacgatcg gcatcgctaa 240
aaccgagatc gctgcataat ccgtggcgaa cattgtcgcc atccagcaga tacgtactga 300
cgccgagttt atgtaacgcc tcctccagcg ccccgcgac cgttgat 347

<210> 82
<211> 67
<212> DNA
<213> Escherichia coli

<400> 82
ccctgacgat cagtgatagt cacgatggtg ttggtgaaag aagcatggat atgagccacg 60
ccgtcag 67

<210> 83
<211> 176
<212> DNA
<213> Escherichia coli

<400> 83
agcaaacgga gccgaacatg gtggcgaggc tgccgtaaaag taaaaactgg gtcgccaact 60
ccgggtgatc catcacgtat ttcacgaagt agagcgctgc cccgcgcgc accacgttg 120
agcagtgctc catcatcttg aacgcgcaca tgatgcgcga ctggctgttg ccagc 176

<210> 84
<211> 632
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(632)
<223> n = A,T,C or G

<400> 84
tnncannnnn nnnnnnnnnn nnnnnnnn ntncctagan tntcnangtc tncnncnncn 60
tnncnnnncc cttcnnnnncc nnnnnanangn ncnnncnccc cnnnccnnnt tttgttttgg 120
aaantccgtt tcaggaanag cttctgaatc ccgancgntt gataactggn ggccagagtc 180
ataatgcgca ccaataataa tcagcggncn atcggcagga ccataatcag caacaatggn 240

```

nnggtagggg ccacccgtaa tggggaccgt cctgcgaggt aactctggca ccgctactga 300
caaagacctc ttttatatat tctgcgggac ctattcagat tatcaatatt gtcnggcact 360
acgtggatgc acaagtttgt gtaagataac gaactgnntt ttctaattgc tcaggacttt 420
gcgtgtcggg gccgttgacg gtaatgcatt gaccagggtt tggtaaaaaa taatcatagg 480
gagtaaaaac acaaataata taataaaagc caagattatt tttttcataat gcaaaaattat 540
taatgggggt gcgtttgggt aatcattatn ttgctatggg tttcgatatt gngattttta 600
ttaaagatta agcangggat tataccaaaa ga 632

```

<210> 85

<211> 161

<212> DNA

<213> *Escherichia coli*

<400> 85

```

gcgctattca gcgtaattgg cagcagctgc ggatcgctcat caatcttctc tgacagcggc 60
tgatgtactt caaccagacg cgcaccgttt ggttcggcag agacttttat cggagtgttg 120
atgatattca ctttggtgcc tggggtgacc tggctaaaga g 161

```

<210> 86

<211> 188

<212> DNA

<213> *Escherichia coli*

<400> 86

```

caaggggtgag catttgcagc gaatcagaaa gggcgcagaa cagtgaagac aacagaaaaa 60
cgaccagacc gcatttataa atacgtcgat agccaaacat atcgcccaga aacgaaaacg 120
agagcagggg gatgacaatg gcgatttgat aggcgttcac taccagatg gaactggctg 180
gcgtggca 188

```

<210> 87

<211> 175

<212> DNA

<213> *Escherichia coli*

<400> 87

```

tgagcatttg cagcgaatca gaaagggcgc agaacagtga agacaacaga aaaacgacca 60
gaccgcattt ataaatacgt cgatagccaa acatatcgcc cagaaacgaa aacgagagca 120
gggagatgac aatggcgatt tgataggcgt tcactaccca gatggaactg gctgg 175

```

<210> 88

<211> 194

<212> DNA

<213> *Escherichia coli*

<400> 88

```

cgcaaggggt agcatttgca gcgaatcaga aagggcgcag aacagtgaag acaacagaaa 60
aacgaccaga ccgcatttat aaatacgtcg atagccaaac atatcgccca gaaacgaaaa 120
cgagagcagg gagatgacaa tggcgatttg ataggcgttc actaccaga tgggaactggc 180
tggcgtggca tgaa 194

```

<210> 89

<211> 272

<212> DNA

<213> *Escherichia coli*

<400> 89

```

ccttgatataa ggaaaggggt atgatgaagc tgcgtcatcat actggttggt ttgttactgt 60
taagtttccc gacttactaa caactcatca gaggggggag aaatcctccc ttacccttgt 120
tcctttactc taggttgaaa aaacaacagc gtcaataggc ctgccatgta cgaagcgaga 180
tcgtggaacc gctttccggg tagcctttt tatcctgttg gatcttcttg atgatgttgg 240
tcgtcgagca accgtcttca aagttgagca cc 272

```

<210> 90
 <211> 245
 <212> DNA
 <213> Escherichia coli

<400> 90
 ccttggtataa ggaaagggtt atgatgaagc tcgtcatcat actggttggtg ttgttactgt 60
 taagtttccc gacttactaa caactcatca gaggggggag aaatcctccc ttacccttgt 120
 tcctttactc taggttgaaa aaacaacagc gtcaataggc ctgccatgta cgaagcgaga 180
 tctgtgaacc gctttccggt tagccttttt tatcctgttg gatccttctg atgatggttg 240
 tcgtc 245

<210> 91
 <211> 203
 <212> DNA
 <213> Escherichia coli

<400> 91
 taccaaaaaa agccacgtta tcttggtgat gcaaaagagt gaacgtggcg ttaaattgtaa 60
 ccagttatat cagtagaaaa cctggttggt gttaacagtc taaccggtca attttttatg 120
 atttttttga taaaaattaa attttatttg ctttaatcac caccagatga cgttcgccat 180
 ccagggtctg aacctgaagt tta 203

<210> 92
 <211> 189
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1) ... (189)
 <223> n = A,T,C or G

<400> 92
 ctaatgactt attttctgct taccaaaaaa agccacgtta tcttggtgat gcnaaagagt 60
 gaacgtggcg ttaaattgtac cagttatata agtagaaaac ctggttgntg ntaacagtct 120
 aaccggcaat tttttatgat ttttttgata aaaattaaat tttatttgct ttaatcacca 180
 ccagatgac 189

<210> 93
 <211> 221
 <212> DNA
 <213> Escherichia coli

<400> 93
 agcgcaacag cggaaccag ggtagccagt tttttcatgt tcatattcaa gatgtcctgt 60
 agtcggtatt actgcttttt gttgtctacc agcaccgcca gcaaaatcac caccgctttg 120
 acgatcatct ggtaatagga ggaaacacct aacaaattca atccattatt aaggaagcca 180
 agaattaatg cgccgatcaa cgtccaaca atgcgacctt t 221

<210> 94
 <211> 117
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1) ... (117)

<400> 94

```

atg aaa gtt cgt gct tcc gtc aag aaa tta tgc cgt aac tgc aaa atc 48
Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
  1           5           10          15

gtt aag cgt gat ggt gtc atc cgt gtg att tgc agt gcc gag ccg aag 96
Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
          20          25          30

cat aaa cag cgc caa ggc tga 117
His Lys Gln Arg Gln Gly *
      35

<210> 95
<211> 1332
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1332)

<400> 95
atg gct aaa caa ccg gga tta gat ttt caa agt gcc aaa ggt ggc tta 48
Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
  1           5           10          15

ggc gag ctg aaa cgc aga ctg ctg ttt gtt atc ggt gcg ctg att gtg 96
Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
          20          25          30

ttc cgt att ggc tct ttt att ccg atc cct ggt att gat gcc gct gta 144
Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
          35          40          45

ctt gcc aaa ctg ctt gag caa cag cga ggc acc atc att gag atg ttt 192
Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe
          50          55          60

aac atg ttc tct ggt ggt gct ctc agc cgt gct tct atc ttt gct ctg 240
Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu
          65          70          75          80

ggg atc atg ccg tat att tcg gcg tcg atc att atc cag ctg ctg acg 288
Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Ile Gln Leu Leu Thr
          85          90          95

gtg gtt cac cca acg ttg gca gaa att aag aaa gaa ggg gag tct ggt 336
Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly
          100          105          110

cgt cgt aag atc agc cag tac acc cgc tac ggt act ctg gtg ctg gca 384
Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala
          115          120          125

ata ttc cag tcg atc ggt att gct acc ggt ctg ccg aat atg cct ggt 432
Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly
          130          135          140

atg caa ggc ctg gtg att aac ccg ggc ttt gca ttc tac ttc acc gct 480
Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala

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145	150	155	160	
gtt gta agt ctg gtc	aca gga acc atg ttc ctg atg tgg ttg ggc gaa	528		
Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu				
165	170	175		
cag att act gaa cga ggt atc ggc aac ggt att tca atc att atc ttc	576			
Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Ile Phe				
180	185	190		
gcc ggt att gtc gcg gga ctc ccg cca gcc att gcc cat act atc gag	624			
Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu				
195	200	205		
caa gcg cgt caa ggc gac ctg cac ttc ctc gtg ttg ctg ttg gtt gca	672			
Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Leu Val Ala				
210	215	220		
gta tta gta ttt gca gtg acg ttc ttt gtt gta ttt gtt gag cgt ggt	720			
Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly				
225	230	235	240	
caa cgc cgc att gtg gta aac tac gcg aaa cgt cag caa ggt cgt cgt	768			
Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg				
245	250	255		
gtc tat gct gca cag agc aca cat tta ccg ctg aaa gtg aat atg gcg	816			
Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala				
260	265	270		
ggg gta atc ccg gca atc ttc gct tcc agt att att ctg ttc ccg gcg	864			
Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala				
275	280	285		
acc atc gcg tca tgg ttc ggg ggc ggt act ggt tgg aac tgg ctg aca	912			
Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr				
290	295	300		
aca att tcg ctg tat ttg cag cct ggg caa ccg ctt tat gtg tta ctc	960			
Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu				
305	310	315	320	
tat gcg tct gca atc atc ttc ttc tgt ttc ttc tac acg gcg ttg gtt	1008			
Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val				
325	330	335		
ttc aac ccg cgt gaa aca gca gat aac ctg aag aag tcc ggt gca ttt	1056			
Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe				
340	345	350		
gta cca gga att cgt ccg gga gag caa acg gcg aag tat atc gat aaa	1104			
Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys				
355	360	365		
gta atg acc cgc ctg acc ctg gtt ggt gcg ctg tat att acc ttt atc	1152			
Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile				
370	375	380		
tgc ctg atc ccg gag ttc atg cgt gat gca atg aaa gta ccg ttc tac	1200			
Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr				
385	390	395	400	

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ttc ggt ggg acc tca ctg ctt atc gtt gtt gtc gtg att atg gac ttt 1248
Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe
      405      410      415

atg gct caa gtg caa act ctg atg atg tcc agt cag tat gag tct gca 1296
Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala
      420      425      430

ttg aag aag gcg aac ctg aaa ggc tac ggc cga taa 1332
Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg *
      435      440

<210> 96
<211> 435
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(435)

<400> 96
atg cgt tta aat act ctg tct ccg gcc gaa ggc tcc aaa aag gcg ggt 48
Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly
  1          5          10          15

aaa cgc ctg ggt cgt ggt atc ggt tct ggc ctc ggt aaa acc ggt ggt 96
Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly
      20      25      30

cgt ggt cac aaa ggt cag aag tct cgt tct ggc ggt ggc gta cgt cgc 144
Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Gly Val Arg Arg
      35      40      45

ggt ttc gag ggt ggt cag atg cct ctg tac cgt cgt ctg ccg aaa ttc 192
Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe
      50      55      60

ggc ttc act tct cgt aaa gca gcg att aca gcc gaa att cgt ctg tct 240
Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser
      65      70      75      80

gac ctg gct aaa gta gaa ggc ggt gta gta gac ctg aac acg ctg aaa 288
Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys
      85      90      95

gcg gct aac att atc ggt atc cag atc gag ttc gcg aaa gtg atc ctg 336
Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu
      100      105      110

gct ggc gaa gta acg act ccg gta act gtt cgt ggc ctg cgt gtt act 384
Ala Gly Glu Val Thr Thr Pro Val Thr Val Arg Gly Leu Arg Val Thr
      115      120      125

aaa ggc gct cgt gct gct atc gaa gct gct ggc ggt aaa atc gag gaa 432
Lys Gly Ala Arg Ala Ala Ile Glu Ala Ala Gly Gly Lys Ile Glu Glu
      130      135      140

taa 435

```


*

<210> 97
 <211> 180
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(180)

<400> 97
 atg gca aag act att aaa att act caa acc cgc agt gca atc ggt cgt 48
 Met Ala Lys Thr Ile Lys Ile Thr Gln Thr Arg Ser Ala Ile Gly Arg
 1 5 10 15
 ctg ccg aaa cac aag gca acg ctg ctt ggc ctg ggt ctg cgt cgt att 96
 Leu Pro Lys His Lys Ala Thr Leu Leu Gly Leu Gly Leu Arg Arg Ile
 20 25 30
 ggt cac acc gta gag cgc gag gat act cct gct att cgc ggt atg atc 144
 Gly His Thr Val Glu Arg Glu Asp Thr Pro Ala Ile Arg Gly Met Ile
 35 40 45
 aac gcg gtt tcc ttc atg gtt aaa gtt gag gag taa 180
 Asn Ala Val Ser Phe Met Val Lys Val Glu Glu *
 50 55

<210> 98
 <211> 504
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(504)

<400> 98
 atg gct cac atc gaa aaa caa gct ggc gaa ctg cag gaa aag ctg atc 48
 Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile
 1 5 10 15
 gcg gta aac cgc gta tct aaa acc gtt aaa ggt ggt cgt att ttc tcc 96
 Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser
 20 25 30
 ttc aca gct ctg act gta gtt ggc gat ggt aac ggt cgc gtt ggt ttt 144
 Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe
 35 40 45
 ggt tac ggt aaa gcg cgt gaa gtt cca gca gcg atc cag aaa gcg atg 192
 Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met
 50 55 60
 gaa aaa gcc cgt cgc aat atg att aac gtc gcg ctg aat aac ggc act 240
 Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr
 65 70 75 80

```

ctg caa cac cct gtt aaa ggt gtt cac acg ggt tct cgc gta ttc atg 288
Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met
      85                      90                      95

cag ccg gct tcc gaa ggt acc ggt atc atc gcc ggt ggt gca atg cgc 336
Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg
      100                      105                      110

gcc gtt ctg gaa gtc gct ggg gtt cat aac gtt ctg gct aaa gcc tat 384
Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr
      115                      120                      125

ggt tcc acc aac ccg atc aac gtg gtt cgt gca act att gat ggc ctg 432
Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
      130                      135                      140

gaa aat atg aat tct cca gaa atg gtc gct gcc aag cgt ggt aaa tcc 480
Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser
      145                      150                      155                      160

ggt gaa gaa att ctg ggg aaa taa 504
Val Glu Glu Ile Leu Gly Lys *
      165

```

<210> 99
 <211> 354
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1) ... (354)

```

<400> 99
atg gat aag aaa tct gct cgt atc cgt cgt gcg acc cgc gca cgc cgc 48
Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
  1              5              10              15

aag ctc cag gag ctg ggc gca act cgc ctg gtg gta cat cgt acc ccg 96
Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
      20              25              30

cgt cac att tac gca cag gta att gca ccg aac ggt tct gaa gtt ctg 144
Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu
      35              40              45

gta gct gct tct act gta gaa aaa gct atc gct gaa caa ctg aag tac 192
Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr
      50              55              60

acc ggt aac aaa gac gcg gct gca gct gtg ggt aaa gct gtc gct gaa 240
Thr Gly Asn Lys Asp Ala Ala Ala Ala Val Gly Lys Ala Val Ala Glu
      65              70              75              80

cgc gct ctg gaa aaa ggc atc aaa gat gta tcc ttt gac cgt tcc ggg 288
Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly
      85              90              95

ttc caa tat cat ggt cgt gtc cag gca ctg gca gat gct gcc cgt gaa 336
Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu

```

100	105	110	
gct ggc ctt cag ttc taa			354
Ala Gly Leu Gln Phe *			
115			
<210> 100			
<211> 534			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(534)			
<400> 100			
atg tct cgt gtt gct aaa gca ccg gtc gtt gtt cct gcc ggc gtt gac			48
Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp			
1 5 10 15			
gta aaa atc aac ggt cag gtt att acg atc aaa ggt aaa aac ggc gag			96
Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu			
20 25 30			
ctg act cgt act ctc aac gat gct gtt gaa gtt aaa cat gca gat aat			144
Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn			
35 40 45			
acc ctg acc ttc ggt ccg cgt gat ggt tac gca gac ggt tgg gca cag			192
Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln			
50 55 60			
gct ggt acc gcg cgt gcc ctg ctg aac tca atg gtt atc ggt gtt acc			240
Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr			
65 70 75 80			
gaa ggc ttc act aag aag ctg cag ctg gtt ggt gta ggt tac cgt gca			288
Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala			
85 90 95			
gcg gtt aaa ggc aat gtg att aac ctg tct ctg ggt ttc tct cat cct			336
Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro			
100 105 110			
gtt gac cat cag ctg cct gcg ggt atc act gct gaa tgt ccg act cag			384
Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln			
115 120 125			
act gaa atc gtg ctg aaa ggc gct gat aag cag gtg atc ggc cag gtt			432
Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val			
130 135 140			
gca gcg gat ctg cgc gcc tac cgt cgt cct gag cct tat aaa ggc aag			480
Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys			
145 150 155 160			
ggg gtt cgt tac gcc gac gaa gtc gtg cgt acc aaa gag gct aag aag			528
Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys			
165 170 175			

aag taa

534

Lys *

<210> 101

<211> 393

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(393)

<400> 101

atg agc atg caa gat ccg atc gcg gat atg ctg acc cgt atc cgt aac 48

Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn

1

5

10

15

ggc cag gcc gcg aac aaa gct gcg gtc acc atg cct tcc tcc aag ctg 96

Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu

20

25

30

aaa gtg gca atc gcc aac gtg ctg aag gaa gaa ggt ttt att gaa gat 144

Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp

35

40

45

ttt aaa gtt gaa ggc gac acc aag cct gaa ctg gaa ctt act ctg aag 192

Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys

50

55

60

tat ttc cag ggc aaa gct gtt gta gaa agc att cag cgt gtc agc cgc 240

Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg

65

70

75

80

cca ggt ctg cgc atc tat aaa cgt aaa gat gag ctg ccg aaa gtt atg 288

Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met

85

90

95

gcg ggt ctg ggt atc gca gtt gtt tct acc tct aaa ggt gtt atg act 336

Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr

100

105

110

gat cgt gca gcg cgc cag gct ggt ctt ggt ggc gaa att atc tgc tac 384

Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr

115

120

125

gta gcc taa

393

Val Ala *

130

<210> 102

<211> 306

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(306)

<400> 102

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atg gct aag caa tca atg aaa gca cgc gaa gta aaa cgc gta gct tta 48
Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu
1 5 10 15

gct gat aaa tac ttc gcg aaa cgc gct gaa ctg aaa gcg atc atc tct 96
Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser
20 25 30

gat gtg aac gct tcc gac gaa gat cgt tgg aac gct gtt ctc aag ctg 144
Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu
35 40 45

cag act ctg ccg cgt gat tcc agc ccg tct cgt cag cgt aac cgc tgc 192
Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys
50 55 60

cgt caa aca ggt cgt ccg cat ggt ttc ctg cgg aag ttc ggg ttg agc 240
Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser
65 70 75 80

cgt att aag gtc cgt gaa gcc gct atg cgc ggt gaa atc ccg ggt ctg 288
Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu
85 90 95

aaa aag gct agc tgg taa 306
Lys Lys Ala Ser Trp *
100

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<210> 103

<211> 540

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(540)

<400> 103

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atg gcg aaa ctg cat gat tac tac aaa gac gaa gta gtt aaa aaa ctc 48
Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu
1 5 10 15

atg act gag ttt aac tac aat tct gtc atg caa gtc cct cgg gtc gag 96
Met Thr Glu Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu
20 25 30

aag atc acc ctg aac atg ggt gtt ggt gaa gcg atc gct gac aaa aaa 144
Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys
35 40 45

ctg ctg gat aac gca gca gca gac ctg gca gca atc tcc ggt caa aaa 192
Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys
50 55 60

ccg ctg atc acc aaa gca cgc aaa tct gtt gca ggc ttc aaa atc cgt 240
Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg
65 70 75 80

cag ggc tat ccg atc ggc tgt aaa gta act ctg cgt ggc gaa cgc atg 288

```

Gln	Gly	Tyr	Pro	Ile	Gly	Cys	Lys	Val	Thr	Leu	Arg	Gly	Glu	Arg	Met	
				85					90					95		
tgg	gag	ttc	ttt	gag	cgc	ctg	atc	act	att	gct	gta	cct	cgt	atc	cgt	336
Trp	Glu	Phe	Phe	Glu	Arg	Leu	Ile	Thr	Ile	Ala	Val	Pro	Arg	Ile	Arg	
			100				105						110			
gac	ttc	cgt	ggc	ctg	tcc	gct	aag	tct	ttc	gac	ggg	cgt	ggg	aac	tac	384
Asp	Phe	Arg	Gly	Leu	Ser	Ala	Lys	Ser	Phe	Asp	Gly	Arg	Gly	Asn	Tyr	
		115					120					125				
agc	atg	ggg	gtc	cgt	gag	cag	atc	atc	ttc	cca	gaa	atc	gac	tac	gat	432
Ser	Met	Gly	Val	Arg	Glu	Gln	Ile	Ile	Phe	Pro	Glu	Ile	Asp	Tyr	Asp	
	130					135					140					
aaa	gtc	gac	cgc	gtt	cgt	ggg	ttg	gat	att	acc	att	acc	act	act	gcg	480
Lys	Val	Asp	Arg	Val	Arg	Gly	Leu	Asp	Ile	Thr	Ile	Thr	Thr	Thr	Ala	
	145				150					155					160	
aaa	tct	gac	gaa	gaa	ggc	cgc	gct	ctg	ctg	gct	gcc	ttt	gac	ttc	ccg	528
Lys	Ser	Asp	Glu	Glu	Gly	Arg	Ala	Leu	Leu	Ala	Ala	Phe	Asp	Phe	Pro	
			165					170						175		
ttc	cgc	aag	taa													540
Phe	Arg	Lys	*													

<210> 104

<211> 315

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(315)

<400> 104

atg	gca	gcg	aaa	atc	cgt	cgt	gat	gac	gaa	gtt	atc	gtg	tta	acc	ggg	48
Met	Ala	Ala	Lys	Ile	Arg	Arg	Asp	Asp	Glu	Val	Ile	Val	Leu	Thr	Gly	
1				5					10				15			
aaa	gat	aaa	ggg	aaa	cgc	ggg	aaa	gtt	aag	aat	gtc	ctg	tct	tcc	ggc	96
Lys	Asp	Lys	Gly	Lys	Arg	Gly	Lys	Val	Lys	Asn	Val	Leu	Ser	Ser	Gly	
			20					25					30			
aag	gtc	att	gtt	gaa	ggg	atc	aac	ctg	gtt	aag	aaa	cat	cag	aag	ccg	144
Lys	Val	Ile	Val	Glu	Gly	Ile	Asn	Leu	Val	Lys	Lys	His	Gln	Lys	Pro	
		35				40						45				
gtt	ccg	gcc	ctg	aac	caa	ccg	ggg	ggc	atc	gtt	gaa	aaa	gaa	gcc	gct	192
Val	Pro	Ala	Leu	Asn	Gln	Pro	Gly	Gly	Ile	Val	Glu	Lys	Glu	Ala	Ala	
	50					55					60					
att	cag	gtt	tcc	aac	gta	gca	atc	ttc	aat	gcg	gca	acc	ggc	aag	gct	240
Ile	Gln	Val	Ser	Asn	Val	Ala	Ile	Phe	Asn	Ala	Ala	Thr	Gly	Lys	Ala	
	65				70				75						80	
gac	cgt	gta	ggc	ttt	aga	ttc	gaa	gac	ggg	aaa	aaa	gtc	cgt	ttc	ttc	288
Asp	Arg	Val	Gly	Phe	Arg	Phe	Glu	Asp	Gly	Lys	Lys	Val	Arg	Phe	Phe	
				85					90						95	

aag tct aac agc gaa act atc aag taa
 Lys Ser Asn Ser Glu Thr Ile Lys *
 100

315

<210> 105
 <211> 372
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(372)

<400> 105
 atg atc caa gaa cag act atg ctg aac gtc gcc gac aac tcc ggt gca 48
 Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala
 1 5 10 15
 cgt cgc gta atg tgt atc aag gtt ctg ggt ggc tgc cac cgt cgc tac 96
 Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr
 20 25 30
 gca ggc gta ggc gac atc atc aag atc acc atc aaa gaa gca att ccg 144
 Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro
 35 40 45
 cgt ggt aag gtc aaa aaa ggt gat gtg ctg aag gcg gta gtg gtg cgc 192
 Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg
 50 55 60
 acc aag aag ggt gtt cgt cgc ccg gac ggt tct gtc att cgc ttc gat 240
 Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp
 65 70 75 80
 ggt aat gct tgt gtt ctt ctg aac aac aac agc gag cag cct atc ggt 288
 Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly
 85 90 95
 acg cgt att ttt ggg ccg gta act cgt gag ctt cgt agt gag aag ttc 336
 Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe
 100 105 110
 atg aaa att atc tct ctg gca cca gaa gta ctc taa 372
 Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu *
 115 120

<210> 106
 <211> 1458
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1458)

<400> 106
 gtg gga att tat ttt act aat tca gat gat caa att tac ttt aaa agg 48
 Met Gly Ile Tyr Phe Thr Asn Ser Asp Asp Gln Ile Tyr Phe Lys Arg

1	5	10	15	
agt gaa ggg atg tct gat ata aac cat gca ggt tct gac ctt ata ttt				96
Ser Glu Gly Met Ser Asp Ile Asn His Ala Gly Ser Asp Leu Ile Phe	20	25	30	
gaa ctg gag gat cgc cct ccc ttt cat cag gct ctc gtt ggt gcc att				144
Glu Leu Glu Asp Arg Pro Pro Phe His Gln Ala Leu Val Gly Ala Ile	35	40	45	
acc cat ctg ttg gca att ttc gtt ccg atg gta acc ccc gcg tta atc				192
Thr His Leu Leu Ala Ile Phe Val Pro Met Val Thr Pro Ala Leu Ile	50	55	60	
gtg ggt gcg gcc tta cag ctt tcc gct gaa aca act gcc tat ctt gtt				240
Val Gly Ala Ala Leu Gln Leu Ser Ala Glu Thr Thr Ala Tyr Leu Val	65	70	75	80
tct atg gcg atg atc gcc tct ggt att ggt acc tgg tta caa gta aac				288
Ser Met Ala Met Ile Ala Ser Gly Ile Gly Thr Trp Leu Gln Val Asn	85	90	95	
cgc tac ggc atc gtc ggt tct ggc cta ctc tca att cag tca gtc aat				336
Arg Tyr Gly Ile Val Gly Ser Gly Leu Leu Ser Ile Gln Ser Val Asn	100	105	110	
ttt tca ttt gtt acg gtc atg att gcg ctg ggc agc agc atg aaa agc				384
Phe Ser Phe Val Thr Val Met Ile Ala Leu Gly Ser Ser Met Lys Ser	115	120	125	
gac ggt ttt cac gaa gag tta atc atg tgc tgc ctt ctc ggc gtc tcc				432
Asp Gly Phe His Glu Glu Leu Ile Met Ser Ser Leu Leu Gly Val Ser	130	135	140	
ttc gtt ggc gca ttt ctg gtt gtc gga tct tca ttt atc ttg ccc tat				480
Phe Val Gly Ala Phe Leu Val Val Gly Ser Ser Phe Ile Leu Pro Tyr	145	150	155	160
tta cgt cgg gtt att acg cct acc gtc agc ggt att gtg gta ctg atg				528
Leu Arg Arg Val Ile Thr Pro Thr Val Ser Gly Ile Val Val Leu Met	165	170	175	
atc ggc tta agc ctg att aaa gtc ggc att atc gat ttt ggt gga gga				576
Ile Gly Leu Ser Leu Ile Lys Val Gly Ile Ile Asp Phe Gly Gly Gly	180	185	190	
ttt gca gcc aaa agc agc ggt acg ttc ggc aat tac gaa cat ctc ggc				624
Phe Ala Ala Lys Ser Ser Gly Thr Phe Gly Asn Tyr Glu His Leu Gly	195	200	205	
gtt ggt tta ttg gtt tta att gtg gtg atc ggc ttt aac tgc tgt cgc				672
Val Gly Leu Leu Val Leu Ile Val Val Ile Gly Phe Asn Cys Cys Arg	210	215	220	
agt ccg ttg cta cgc atg gga ggg atc gcc att ggg cta tgt gtc ggc				720
Ser Pro Leu Leu Arg Met Gly Gly Ile Ala Ile Gly Leu Cys Val Gly	225	230	235	240
tat atc gca tgc tta tgc ctg ggc atg gtg gat ttc agc agt atg cgc				768
Tyr Ile Ala Ser Leu Cys Leu Gly Met Val Asp Phe Ser Ser Met Arg	245	250	255	

aat ttg ccg tta atc acc atc ccg cat ccg ttc aaa tac ggc ttt agt	816
Asn Leu Pro Leu Ile Thr Ile Pro His Pro Phe Lys Tyr Gly Phe Ser	
260 265 270	
ttt agc ttc cat cag ttc ctg gtg gtt ggc acg att tat ctg ctt agc	864
Phe Ser Phe His Gln Phe Leu Val Val Gly Thr Ile Tyr Leu Leu Ser	
275 280 285	
gtg ctg gaa gca gtc ggc gat atc acc gcc acg gca atg gtt tcc cgc	912
Val Leu Glu Ala Val Gly Asp Ile Thr Ala Thr Ala Met Val Ser Arg	
290 295 300	
cgc ccc att cag ggg gaa gag tat cag tcc cgg ctg aaa ggc ggc gtg	960
Arg Pro Ile Gln Gly Glu Glu Tyr Gln Ser Arg Leu Lys Gly Gly Val	
305 310 315 320	
ctg gca gat ggt ctg gtt tct gtt atc gcc tcc gct gtc ggt tca tta	1008
Leu Ala Asp Gly Leu Val Ser Val Ile Ala Ser Ala Val Gly Ser Leu	
325 330 335	
cca tta acc acg ttt gcg caa aat aat ggg gtt att cag atg act ggc	1056
Pro Leu Thr Thr Phe Ala Gln Asn Asn Gly Val Ile Gln Met Thr Gly	
340 345 350	
gtc gct tca cgt tat gtc ggg cga acc atc gcg gta atg ctg gtt atc	1104
Val Ala Ser Arg Tyr Val Gly Arg Thr Ile Ala Val Met Leu Val Ile	
355 360 365	
ctc ggc tta ttt ccg atg att ggc ggc ttc ttc acg acc att ccc tcg	1152
Leu Gly Leu Phe Pro Met Ile Gly Gly Phe Phe Thr Thr Ile Pro Ser	
370 375 380	
gca gtt ctg gga ggc gca atg acg ttg atg ttt tcc atg att gcc atc	1200
Ala Val Leu Gly Gly Ala Met Thr Leu Met Phe Ser Met Ile Ala Ile	
385 390 395 400	
gca ggg att cgc atc atc atc acc aac ggt tta aag cgc cgt gaa aca	1248
Ala Gly Ile Arg Ile Ile Ile Thr Asn Gly Leu Lys Arg Arg Glu Thr	
405 410 415	
ctt att gtc gcc act tct tta ggt tta ggg ctt ggc gtc tcc tac gat	1296
Leu Ile Val Ala Thr Ser Leu Gly Leu Gly Leu Gly Val Ser Tyr Asp	
420 425 430	
ccc gaa att ttt aaa ata ttg cca gcc tct att tat gta tta gtt gaa	1344
Pro Glu Ile Phe Lys Ile Leu Pro Ala Ser Ile Tyr Val Leu Val Glu	
435 440 445	
aac cct att tgt gct ggc ggg tta act gcg att tta tta aat att atc	1392
Asn Pro Ile Cys Ala Gly Gly Leu Thr Ala Ile Leu Leu Asn Ile Ile	
450 455 460	
ctc cct ggt ggc tac cga cag gaa aac gtt ctg cct ggt att acc tca	1440
Leu Pro Gly Gly Tyr Arg Gln Glu Asn Val Leu Pro Gly Ile Thr Ser	
465 470 475 480	
gcg gaa gag atg gat taa	1458
Ala Glu Glu Met Asp *	
485	

<210> 107

<211> 1320

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1320)

<400> 107

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atg atg tca gga gaa cac acg tta aaa gcg gta cga ggc agt ttt att 48
Met Met Ser Gly Glu His Thr Leu Lys Ala Val Arg Gly Ser Phe Ile
  1           5           10           15

gat gtc acc cgt acg atc gat aac ccg gaa gag att gcc tct gcg ctg 96
Asp Val Thr Arg Thr Ile Asp Asn Pro Glu Glu Ile Ala Ser Ala Leu
          20           25           30

cgg ttt att gag gat ggt tta tta ctc att aaa cag gga aaa gtg gaa 144
Arg Phe Ile Glu Asp Gly Leu Leu Leu Ile Lys Gln Gly Lys Val Glu
          35           40           45

tgg ttt ggc gaa tgg gaa aac gga aag cat caa att cct gac acc att 192
Trp Phe Gly Glu Trp Glu Asn Gly Lys His Gln Ile Pro Asp Thr Ile
          50           55           60

cgc gtg cgc gac tat cgc ggc aaa ctg ata gta ccg ggc ttt gtc gat 240
Arg Val Arg Asp Tyr Arg Gly Lys Leu Ile Val Pro Gly Phe Val Asp
          65           70           75           80

aca cat atc cat tat ccg caa agt gaa atg gtg ggg gcc tat ggt gag 288
Thr His Ile His Tyr Pro Gln Ser Glu Met Val Gly Ala Tyr Gly Glu
          85           90           95

caa ttg ctg gag tgg ttg aat aaa cac acc ttc cct act gaa cgt cgt 336
Gln Leu Leu Glu Trp Leu Asn Lys His Thr Phe Pro Thr Glu Arg Arg
          100           105           110

tat gag gat tta gag tac gcc cgc gaa atg tcg gcg ttc ttc atc aag 384
Tyr Glu Asp Leu Glu Tyr Ala Arg Glu Met Ser Ala Phe Phe Ile Lys
          115           120           125

cag ctt tta cgt aac gga acc acc acg gcg ctg gtg ttt ggc act gtt 432
Gln Leu Leu Arg Asn Gly Thr Thr Thr Ala Leu Val Phe Gly Thr Val
          130           135           140

cat ccg caa tct gtt gat gcg ctg ttt gaa gcc gcc agt cat atc aat 480
His Pro Gln Ser Val Asp Ala Leu Phe Glu Ala Ala Ser His Ile Asn
          145           150           155           160

atg cgt atg att gcc ggt aag gtg atg atg gac cgc aac gca ccg gat 528
Met Arg Met Ile Ala Gly Lys Val Met Met Asp Arg Asn Ala Pro Asp
          165           170           175

tat ctg ctc gac act gcc gaa agc agc tat cac caa agc aaa gaa ctg 576
Tyr Leu Leu Asp Thr Ala Glu Ser Ser Tyr His Gln Ser Lys Glu Leu
          180           185           190

atc gaa cgc tgg cac aaa aat ggt cgt ctg cta tat gcg att acg cca 624
Ile Glu Arg Trp His Lys Asn Gly Arg Leu Leu Tyr Ala Ile Thr Pro

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195	200	205	
cgc ttc gcc ccg acc tca tct cct gaa cag atg gcg atg gcg caa cgc			672
Arg Phe Ala Pro Thr Ser Ser Pro Glu Gln Met Ala Met Ala Gln Arg			
210	215	220	
ctg aaa gaa gaa tat ccg gat acg tgg gta cat acc cat ctc tgt gaa			720
Leu Lys Glu Glu Tyr Pro Asp Thr Trp Val His Thr His Leu Cys Glu			
225	230	235	240
aac aaa gat gaa att gcc tgg gtg aaa tcg ctt tat cct gac cat gat			768
Asn Lys Asp Glu Ile Ala Trp Val Lys Ser Leu Tyr Pro Asp His Asp			
	245	250	255
ggc tat ctg gat gtt tac cat cag tac ggc ctg acc ggt aaa aac tgt			816
Gly Tyr Leu Asp Val Tyr His Gln Tyr Gly Leu Thr Gly Lys Asn Cys			
	260	265	270
gtc ttt gct cac tgc gtc cat ctc gaa gaa aaa gag tgg gat cgt ctc			864
Val Phe Ala His Cys Val His Leu Glu Glu Lys Glu Trp Asp Arg Leu			
	275	280	285
agc gaa acc aaa tcc agc att gct ttc tgt ccg acc tcc aac ctt tac			912
Ser Glu Thr Lys Ser Ser Ile Ala Phe Cys Pro Thr Ser Asn Leu Tyr			
	290	295	300
ctc ggc agc ggc tta ttc aac ttg aaa aaa gca tgg cag aag aaa gtt			960
Leu Gly Ser Gly Leu Phe Asn Leu Lys Lys Ala Trp Gln Lys Lys Val			
305	310	315	320
aaa gtg ggc atg gga acg gat atc ggt gcc gga acc act ttc aac atg			1008
Lys Val Gly Met Gly Thr Asp Ile Gly Ala Gly Thr Thr Phe Asn Met			
	325	330	335
ctg caa acg ctg aac gaa gcc tac aaa gta ttg caa tta caa ggc tat			1056
Leu Gln Thr Leu Asn Glu Ala Tyr Lys Val Leu Gln Leu Gln Gly Tyr			
	340	345	350
cgc ctc tcg gca tat gaa gcg ttt tac ctg gcc acg ctc ggc gga gcg			1104
Arg Leu Ser Ala Tyr Glu Ala Phe Tyr Leu Ala Thr Leu Gly Gly Ala			
	355	360	365
aaa tct ctg ggc ctt gac gat ttg att ggc aac ttt tta cct ggc aaa			1152
Lys Ser Leu Gly Leu Asp Asp Leu Ile Gly Asn Phe Leu Pro Gly Lys			
	370	375	380
gag gct gat ttc gtg gtg atg gaa ccc acc gcc act ccg cta cag cag			1200
Glu Ala Asp Phe Val Val Met Glu Pro Thr Ala Thr Pro Leu Gln Gln			
385	390	395	400
ctg cgc tat gac aac tct gtt tct tta gtc gac aaa ttg ttc gtg atg			1248
Leu Arg Tyr Asp Asn Ser Val Ser Leu Val Asp Lys Leu Phe Val Met			
	405	410	415
atg acg ttg ggc gat gac cgt tcg atc tac cgc acc tac gtt gat ggt			1296
Met Thr Leu Gly Asp Asp Arg Ser Ile Tyr Arg Thr Tyr Val Asp Gly			
	420	425	430
cgt ctg gtg tac gaa cgc aac taa			1320
Arg Leu Val Tyr Glu Arg Asn *			
435			

<210> 108
 <211> 570
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1) ... (570)

<400> 108
 atg tct gga gac atc cta caa aca ccg gac gca cca aag cca cag ggc 48
 Met Ser Gly Asp Ile Leu Gln Thr Pro Asp Ala Pro Lys Pro Gln Gly
 1 5 10 15

gcg ctg gat aat tat ttt aaa att acc gct cgt ggc agt acc gtt cgt 96
 Ala Leu Asp Asn Tyr Phe Lys Ile Thr Ala Arg Gly Ser Thr Val Arg
 20 25 30

cag gaa gta ctg gct ggc tta acg acc ttt ctg gcc atg gtt tat tcc 144
 Gln Glu Val Leu Ala Gly Leu Thr Thr Phe Leu Ala Met Val Tyr Ser
 35 40 45

gtt atc gtc gtt ccg gga atg ctg ggc aaa gca ggt ttt cct ccc gca 192
 Val Ile Val Val Pro Gly Met Leu Gly Lys Ala Gly Phe Pro Pro Ala
 50 55 60

gct gtg ttt gtt gcc acc tgt ctg gtc gcg ggc ttc ggc tcg ttg ctg 240
 Ala Val Phe Val Ala Thr Cys Leu Val Ala Gly Phe Gly Ser Leu Leu
 65 70 75 80

atg gga tta tgg gct aat ttg cca atg gcg att ggt tgc gcg att tcc 288
 Met Gly Leu Trp Ala Asn Leu Pro Met Ala Ile Gly Cys Ala Ile Ser
 85 90 95

ttg acg gcg ttt acc gca ttc agt ctg gta ctc ggg caa caa att agc 336
 Leu Thr Ala Phe Thr Ala Phe Ser Leu Val Leu Gly Gln Gln Ile Ser
 100 105 110

gtt cct gtc gca ctg ggc gcg gta ttt ctg atg ggc gtc atc ttc acc 384
 Val Pro Val Ala Leu Gly Ala Val Phe Leu Met Gly Val Ile Phe Thr
 115 120 125

gcc att tcc gta acc ggt gtg cgt acc tgg atc tta cgt aat ttg ccg 432
 Ala Ile Ser Val Thr Gly Val Arg Thr Trp Ile Leu Arg Asn Leu Pro
 130 135 140

atg ggt atc gct cac ggt aca ggt atc ggt atc ggg ctg ttt ctg ctg 480
 Met Gly Ile Ala His Gly Thr Gly Ile Gly Ile Gly Leu Phe Leu Leu
 145 150 155 160

ctg att gct gct aac ggt gtg ggt atg gtt atc aaa aac ccg att gaa 528
 Leu Ile Ala Ala Asn Gly Val Gly Met Val Ile Lys Asn Pro Ile Glu
 165 170 175

ggc ttg cag tgg cgc tcg gtg cgt tta cct cct tcc cgg tga 570
 Gly Leu Gln Trp Arg Ser Val Arg Leu Pro Pro Ser Arg *
 180 185

<210> 109

<211> 831

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(831)

<400> 109

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gtg gcg ctc ggt gcg ttt acc tcc ttc ccg gtg atg atg agc ttg ctg 48
Met Ala Leu Gly Ala Phe Thr Ser Phe Pro Val Met Met Ser Leu Leu
  1             5             10             15

ggg ctg gcg gtc atc ttc ggc ctg gag aag tgt cgc gta ccc ggc ggg 96
Gly Leu Ala Val Ile Phe Gly Leu Glu Lys Cys Arg Val Pro Gly Gly
          20             25             30

atc ttg ttg gtg att att gca att tcg atc atc ggc tta atc ttt gac 144
Ile Leu Leu Val Ile Ile Ala Ile Ser Ile Ile Gly Leu Ile Phe Asp
          35             40             45

cca gcg gtg aaa tac cac ggt ctg gtg gcg atg cca agc ctg act ggc 192
Pro Ala Val Lys Tyr His Gly Leu Val Ala Met Pro Ser Leu Thr Gly
          50             55             60

gaa gat ggt aag tct ctg att ttc agc ctc gat att atg ggt gca ctc 240
Glu Asp Gly Lys Ser Leu Ile Phe Ser Leu Asp Ile Met Gly Ala Leu
          65             70             75             80

cag cca act gta ctt ccg agt gta ctg gca ttg gtg atg acc gca gtg 288
Gln Pro Thr Val Leu Pro Ser Val Leu Ala Leu Val Met Thr Ala Val
          85             90             95

ttc gac gct act ggc acc atc cgt gcc gtc gcc ggt cag gcg aat ttg 336
Phe Asp Ala Thr Gly Thr Ile Arg Ala Val Ala Gly Gln Ala Asn Leu
          100             105             110

ttg gat aaa gac aac cag atc atc aac ggc ggc aaa gcc ctg acc agt 384
Leu Asp Lys Asp Asn Gln Ile Ile Asn Gly Gly Lys Ala Leu Thr Ser
          115             120             125

gac tca gta agt tca ata ttc tcc ggc ctg gtg ggc gca gcg ccc gca 432
Asp Ser Val Ser Ser Ile Phe Ser Gly Leu Val Gly Ala Ala Pro Ala
          130             135             140

gcg gtt tat atc gaa tca gcg gca gga acc gcc gcc ggg ggt aaa aca 480
Ala Val Tyr Ile Glu Ser Ala Ala Gly Thr Ala Ala Gly Gly Lys Thr
          145             150             155             160

ggg tta acc gca acc gta gtg ggg gcg tta ttc ctg tta att ctg ttt 528
Gly Leu Thr Ala Thr Val Val Gly Ala Leu Phe Leu Leu Ile Leu Phe
          165             170             175

tta tca ccg ctg tca ttt ttg atc cct ggt tac gcc act gca ccc gct 576
Leu Ser Pro Leu Ser Phe Leu Ile Pro Gly Tyr Ala Thr Ala Pro Ala
          180             185             190

ctg atg tac gta ggt ttg ctg atg tta agt aac gtc tcg aag ctg gat 624
Leu Met Tyr Val Gly Leu Leu Met Leu Ser Asn Val Ser Lys Leu Asp

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195	200	205	
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Phe Asn Asp Phe Ile Asp Ala Met Ala Gly Leu Val Cys Ala Val Phe			
210	215	220	
atc gtt ctg act tgt aat atc gtt acc ggt att atg ctg ggc ttt gtg			720
Ile Val Leu Thr Cys Asn Ile Val Thr Gly Ile Met Leu Gly Phe Val			
225	230	235	240
aca ctg gtc gta ggc cgc gtc ttt gca cgc gaa tgg caa aag ctg aat			768
Thr Leu Val Val Gly Arg Val Phe Ala Arg Glu Trp Gln Lys Leu Asn			
245	250	255	
att ggt acg gtg atc att act gcc gca ctg gtc gca ttt tac gcg ggt			816
Ile Gly Thr Val Ile Ile Thr Ala Ala Leu Val Ala Phe Tyr Ala Gly			
260	265	270	
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Gly Trp Ala Ile *			
275			

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aac tat acc gga aac aat ggc ctg atg acg ttc aac gcg acg ctg ggc	96
Asn Tyr Thr Gly Asn Asn Gly Leu Met Thr Phe Asn Ala Thr Leu Gly	
20 25 30	
ggc gat aat tcg ccc acc gat aag atg aac gtg aaa ggc gat acc caa	144
Gly Asp Asn Ser Pro Thr Asp Lys Met Asn Val Lys Gly Asp Thr Gln	
35 40 45	
ggg aac act cgc gtt cgg gtt gat aac att ggc ggc gtc ggt gca caa	192
Gly Asn Thr Arg Val Arg Val Asp Asn Ile Gly Gly Val Gly Ala Gln	
50 55 60	
acg gtc aac ggt att gaa ctc att gag gtt ggc ggt aat tct gca ggt	240
Thr Val Asn Gly Ile Glu Leu Ile Glu Val Gly Gly Asn Ser Ala Gly	
65 70 75 80	
aac ttc gcg ctg acc acc gga act gtc gaa gct ggg gct tac gtc tac	288
Asn Phe Ala Leu Thr Thr Gly Thr Val Glu Ala Gly Ala Tyr Val Tyr	
85 90 95	
acg ctg gct aaa ggg aag ggg aat gac gag aaa aac tgg tat ctg acc	336
Thr Leu Ala Lys Gly Lys Gly Asn Asp Glu Lys Asn Trp Tyr Leu Thr	
100 105 110	

agt aaa tgg gac ggc gta acg cca gcg gat aca ccc gat ccc atc aat	384
Ser Lys Trp Asp Gly Val Thr Pro Ala Asp Thr Pro Asp Pro Ile Asn	
115 120 125	
aat ccc cct gtt gtg gat ccg gaa ggc cca tca gtt tat cgc ccg gag	432
Asn Pro Pro Val Val Asp Pro Glu Gly Pro Ser Val Tyr Arg Pro Glu	
130 135 140	
gcc gga agc tat atc agc aac att gcc gca gcc aac tcg ctg ttt agc	480
Ala Gly Ser Tyr Ile Ser Asn Ile Ala Ala Asn Ser Leu Phe Ser	
145 150 155 160	
cat cgt tta cac gac cgt ctg ggt gag ccg cag tat aca gat tca ctg	528
His Arg Leu His Asp Arg Leu Gly Glu Pro Gln Tyr Thr Asp Ser Leu	
165 170 175	
cat tct cag ggg tcg gca agc agt atg tgg atg cgt cat gtc gga ggg	576
His Ser Gln Gly Ser Ala Ser Ser Met Trp Met Arg His Val Gly Gly	
180 185 190	
cac gaa cgt tca agg gcc ggt gac ggt cag cta aat act cag gct aac	624
His Glu Arg Ser Arg Ala Gly Asp Gly Gln Leu Asn Thr Gln Ala Asn	
195 200 205	
cgc tat gta ttg cag cta ggc ggc gat ttg gcg cag tgg agt agc aac	672
Arg Tyr Val Leu Gln Leu Gly Gly Asp Leu Ala Gln Trp Ser Ser Asn	
210 215 220	
gcg cag gat cgc tgg cat ctt ggc gtg atg gca ggc tac gcc aat cag	720
Ala Gln Asp Arg Trp His Leu Gly Val Met Ala Gly Tyr Ala Asn Gln	
225 230 235 240	
cac agt aat act cag agt aat cgt gtg ggt tat aaa tcg gat ggg cgc	768
His Ser Asn Thr Gln Ser Asn Arg Val Gly Tyr Lys Ser Asp Gly Arg	
245 250 255	
atc agc ggt tac agc gct ggg ctg tac gcg acc tgg tat cag aac gat	816
Ile Ser Gly Tyr Ser Ala Gly Leu Tyr Ala Thr Trp Tyr Gln Asn Asp	
260 265 270	
gcg aat aag acc ggc gct tat gtt gac agc tgg gcg ctg tat aac tgg	864
Ala Asn Lys Thr Gly Ala Tyr Val Asp Ser Trp Ala Leu Tyr Asn Trp	
275 280 285	
ttt gat aac agc gtc agt tcc gat aac cgt tct gct gac gac tat gat	912
Phe Asp Asn Ser Val Ser Ser Asp Asn Arg Ser Ala Asp Asp Tyr Asp	
290 295 300	
tct cgc ggt gtg acg gcc tct gtt gag ggt ggg tat acc ttt gaa gcg	960
Ser Arg Gly Val Thr Ala Ser Val Glu Gly Gly Tyr Thr Phe Glu Ala	
305 310 315 320	
gga aca ttt agc ggc agc gaa ggg acg ctg aat acc tgg tac gtc cag	1008
Gly Thr Phe Ser Gly Ser Glu Gly Thr Leu Asn Thr Trp Tyr Val Gln	
325 330 335	
cca cag gcg caa atc acc tgg atg ggt gtg aaa gat tcc gac cat acc	1056
Pro Gln Ala Gln Ile Thr Trp Met Gly Val Lys Asp Ser Asp His Thr	
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Arg Lys Asp Gly Thr Arg Ile Glu Thr Glu Gly Asp Gly Asn Val Gln
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acg cga ctt ggg gtg aaa acc tac ctg aac agc cat cac cag cgt gac 1152
Thr Arg Leu Gly Val Lys Thr Tyr Leu Asn Ser His His Gln Arg Asp
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gat ggt aaa cag cgt gag ttc cag cct tac att gaa gcg aac tgg atc 1200
Asp Gly Lys Gln Arg Glu Phe Gln Pro Tyr Ile Glu Ala Asn Trp Ile
    385                                390                                395                                400

aac aat agc aaa gtc tac gcc gtg aag atg aat ggt caa acc gta ggc 1248
Asn Asn Ser Lys Val Tyr Ala Val Lys Met Asn Gly Gln Thr Val Gly
    405                                410                                415

cgt gaa ggt gcg cgt aat ctc ggt gaa gta cgt acc ggg gtt gag gcg 1296
Arg Glu Gly Ala Arg Asn Leu Gly Glu Val Arg Thr Gly Val Glu Ala
    420                                425                                430

aaa gta aat aac aac ctt agc ctg tgg ggg aat gtc ggt gtg caa cta 1344
Lys Val Asn Asn Asn Leu Ser Leu Trp Gly Asn Val Gly Val Gln Leu
    435                                440                                445

ggg gat aaa ggc tat agc gat act cag ggc atg ctg gga gtg aaa tat 1392
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Ser Trp *
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cag gcc tgc tog gaa tta act cgc agg gca ggt aaa aca tog acg gtt 96
Gln Ala Cys Ser Glu Leu Thr Arg Arg Ala Gly Lys Thr Ser Thr Val
    20                                25                                30

aat ttg cgt aaa tcc tct gga ctg aca acg aaa ttc agt aga ttg acg 144
Asn Leu Arg Lys Ser Ser Gly Leu Thr Thr Lys Phe Ser Arg Leu Thr
    35                                40                                45

ctg ggt gtt ttg ctg gca cta agc ggt tca gcg tct ggt gca agt ctg 192
Leu Gly Val Leu Leu Ala Leu Ser Gly Ser Ala Ser Gly Ala Ser Leu
    50                                55                                60

gaa gtt gat aat gat cag att acc aat att gat act gat gtt gct tat 240
Glu Val Asp Asn Asp Gln Ile Thr Asn Ile Asp Thr Asp Val Ala Tyr
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gat gcc tac ctg gtt ggc tgg tat ggc act gga gtg ctt aat att ttg	288
Asp Ala Tyr Leu Val Gly Trp Tyr Gly Thr Gly Val Leu Asn Ile Leu	
85 90 95	
gct ggc ggt aat gcc tcc tta acc act att act acc agc gtc att ggc	336
Ala Gly Gly Asn Ala Ser Leu Thr Thr Ile Thr Thr Ser Val Ile Gly	
100 105 110	
gct aat gag gac tca gag ggc acc gtt aat gtt ttg ggt ggc acc tgg	384
Ala Asn Glu Asp Ser Glu Gly Thr Val Asn Val Leu Gly Gly Thr Trp	
115 120 125	
cga ttg tat gat agc gga aat aat gca agg cct tta aat gtg ggt caa	432
Arg Leu Tyr Asp Ser Gly Asn Asn Ala Arg Pro Leu Asn Val Gly Gln	
130 135 140	
tcc gga acg ggg acg ctg aat att aaa cag aag ggt cac gtc gat gga	480
Ser Gly Thr Gly Thr Leu Asn Ile Lys Gln Lys Gly His Val Asp Gly	
145 150 155 160	
ggc tat tta aga tta ggt tct tcg aca gga ggc gtc ggg acg gtc aat	528
Gly Tyr Leu Arg Leu Gly Ser Ser Thr Gly Gly Val Gly Thr Val Asn	
165 170 175	
gtt gag gga gag gac tct gtt ctg acg acc gaa tta ttc gaa ata ggt	576
Val Glu Gly Glu Asp Ser Val Leu Thr Thr Glu Leu Phe Glu Ile Gly	
180 185 190	
agc tat ggc aca ggt tca tta aat att acg gat aag ggt tac gtc acg	624
Ser Tyr Gly Thr Gly Ser Leu Asn Ile Thr Asp Lys Gly Tyr Val Thr	
195 200 205	
agt tca atc gtc gcc att tta ggc tat cag gcg ggc agt aat ggc cag	672
Ser Ser Ile Val Ala Ile Leu Gly Tyr Gln Ala Gly Ser Asn Gly Gln	
210 215 220	
gtt gtc gtt gaa aag ggt ggc gag tgg cta ata aaa aat aat gat tcc	720
Val Val Val Glu Lys Gly Gly Glu Trp Leu Ile Lys Asn Asn Asp Ser	
225 230 235 240	
tca att gaa ttt caa att ggt aat caa gga act ggg gag gcg act att	768
Ser Ile Glu Phe Gln Ile Gly Asn Gln Gly Thr Gly Glu Ala Thr Ile	
245 250 255	
cgc gag ggg ggg ttg gtt acg gct gaa aat acg att atc ggt ggc aat	816
Arg Glu Gly Gly Leu Val Thr Ala Glu Asn Thr Ile Ile Gly Gly Asn	
260 265 270	
gcc acc ggt atc gga acc ctg aat gtg cag gat caa gac tct gtc atc	864
Ala Thr Gly Ile Gly Thr Leu Asn Val Gln Asp Gln Asp Ser Val Ile	
275 280 285	
acg gta cgc aga ctc tat aat gga tat ttc ggt aat ggc aca gtc aat	912
Thr Val Arg Arg Leu Tyr Asn Gly Tyr Phe Gly Asn Gly Thr Val Asn	
290 295 300	
att tcc aat aat gga ctg att aat aac aaa gaa tat tca ttg gtg ggc	960
Ile Ser Asn Asn Gly Leu Ile Asn Asn Lys Glu Tyr Ser Leu Val Gly	
305 310 315 320	

gtt cag gac ggt tcc cac ggt gtc gtc aac gtg acc gat aaa ggg cat	1008
Val Gln Asp Gly Ser His Gly Val Val Asn Val Thr Asp Lys Gly His	
325 330 335	
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Trp Asn Phe Leu Gly Thr Gly Glu Ala Phe Arg Tyr Ile Tyr Ile Gly	
340 345 350	
gat gct ggc gac ggt gaa ctt aat gtc tcg agt gaa ggc aaa gta gat	1104
Asp Ala Gly Asp Gly Glu Leu Asn Val Ser Ser Glu Gly Lys Val Asp	
355 360 365	
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Ser Gly Ile Ile Thr Ala Gly Met Lys Glu Thr Gly Thr Gly Asn Ile	
370 375 380	
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Thr Val Lys Asp Lys Asn Ser Val Ile Thr Asn Leu Gly Thr Asn Leu	
385 390 395 400	
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Gly Tyr Asp Gly His Gly Glu Met Asn Ile Ser Asn Gln Gly Leu Val	
405 410 415	
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Val Ser Asn Gly Gly Ser Ser Leu Gly Tyr Gly Glu Thr Gly Val Gly	
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435 440 445	
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Tyr Thr Thr Ile Gly Val Ala Gly Val Gly Asn Leu Asn Ile Ser Asp	
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465 470 475 480	
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Ser Gly Ile Gly Thr Leu Asn Leu Met Asp Ala Thr Ser Ser Phe Asp	
485 490 495	
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Thr Val Gly Ile Asn Val Gly Asn Phe Gly Ser Gly Ile Val Asn Val	
500 505 510	
agt aat ggt gcc acc ctt aat tca acg ggc tat gga ttt atc gga gga	1584
Ser Asn Gly Ala Thr Leu Asn Ser Thr Gly Tyr Gly Phe Ile Gly Gly	
515 520 525	
aat gcc tcc ggt aag ggg ata gtt aat att tca acg gac agt ctc tgg	1632
Asn Ala Ser Gly Lys Gly Ile Val Asn Ile Ser Thr Asp Ser Leu Trp	
530 535 540	
aat tta aag aca tca tct act aac gca caa ttg cta cag gtc ggt gta	1680
Asn Leu Lys Thr Ser Ser Thr Asn Ala Gln Leu Leu Gln Val Gly Val	
545 550 555 560	
tta ggc acg ggt gaa ctg aat att acc acc gga ggt ata gtt aaa gcg	1728

Leu Gly Thr Gly Glu Leu Asn Ile Thr Thr Gly Gly Ile Val Lys Ala	
565 570 575	
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Arg Asp Thr Gln Ile Ala Leu Asn Asp Lys Ser Lys Gly Asp Val Arg	
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Val Asp Gly Gln Asn Ser Leu Leu Glu Thr Phe Asn Met Tyr Val Gly	
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Val Glu Gly Gly Glu Val Tyr Leu Gly Val Phe Glu Pro Ala Val Gly	
625 630 635 640	
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Phe Ile Thr Asn Ala Thr Lys Val Glu Phe Gly Leu Gly Glu Gly Val	
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Met Leu Ile Thr Gly Asp Asp Lys Asp Gly Lys Val Ile His Asp Ala	
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Gly His Thr Val Phe Asn Ala Gly Asn Thr Tyr Ser Gly Lys Thr Leu	
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725 730 735	
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Thr Gly Met Gly Ser Ser Glu Val Thr Ile Ala Asn Pro Gly Thr Leu	
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Asp Ile Leu Ala Ser Thr Asn Ser Ala Gly Asp Tyr Thr Leu Thr Asn	
755 760 765	
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Ala Leu Lys Gly Asp Gly Leu Met Arg Val Gln Leu Ser Ser Ser Asp	
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Lys Met Phe Gly Phe Thr His Ala Thr Gly Thr Glu Phe Ala Gly Val	
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Ala Gln Leu Lys Asp Ser Thr Phe Thr Leu Glu Arg Asp Asn Thr Ala	

805										810										815									
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			835					840					845																
acc	atc	att	ttc	gat	acg	gat	att	cct	gct	gcg	acg	ctc	gcg	gag	gga														
Thr	Ile	Ile	Phe	Asp	Thr	Asp	Ile	Pro	Ala	Ala	Thr	Leu	Ala	Glu	Gly														
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tat	atc	agc	gtc	gat	acg	ctg	gtt	gtc	ggc	gcg	ggg	gac	tac	acc	tgg														
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Val	Pro	Lys	Pro	Trp	Asn	Asp	Pro	Met	Ala	Asn	Asn	Pro	Leu	Thr	Thr														
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Asn	Gly	Thr	Val	Val	Ala	Glu	Gly	Asp	Tyr	Gly	Phe	Arg	Leu	Thr	Thr														
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gca	cca	ggg	aat	ggg	ttg	tac	gtt	aac	tat	ggg	ctg	aaa	gcg	ctg	aac														
Ala	Pro	Gly	Asn	Gly	Leu	Tyr	Val	Asn	Tyr	Gly	Leu	Lys	Ala	Leu	Asn														
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atc	cat	ggg	ggg	caa	aag	ctg	acg	tta	gcc	gaa	cat	ggc	gga	gcc	tat														
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Tyr	Gln	Gly	Ala	Thr	Tyr	Val	Gln	Met	Gly	Thr	Leu	Arg	Thr	Asp	Ala														
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Asp Gly Ala Leu Gly Asn Thr Arg Glu Leu Asn Ile Ser Asn Ala Ala	
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Ile Val Asp Leu Asn Gly Ser Thr Gln Thr Val Glu Thr Phe Thr Gly	
1075 1080 1085	
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Gln Met Gly Ser Thr Val Leu Phe Lys Glu Gly Ala Leu Thr Val Asn	
1090 1095 1100	
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Lys Gly Gly Ile Ser Gln Gly Glu Leu Thr Gly Gly Gly Asn Leu Asn	
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Gln Gly Leu Gly Arg Gly Asn Ile Ala Asn Asp Gly Leu Leu Thr Leu	
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aaa aac gtg act ggc gaa ctg cgt aat agc ata agc ggg aag ggt atc	3552
Lys Asn Val Thr Gly Glu Leu Arg Asn Ser Ile Ser Gly Lys Gly Ile	
1170 1175 1180	
gtg agc gca acc gcc agg aca gat gta gag ttg gat ggc gat aat agc	3600
Val Ser Ala Thr Ala Arg Thr Asp Val Glu Leu Asp Gly Asp Asn Ser	
1185 1190 1195 1200	
cgc ttt gtg ggg caa ttc aac att gat aca ggc agc gcg ctc agc gtc	3648
Arg Phe Val Gly Gln Phe Asn Ile Asp Thr Gly Ser Ala Leu Ser Val	
1205 1210 1215	
aac gag cag aaa aac ctg ggt gat gct tcc gtt atc aat aat ggc ctg	3696
Asn Glu Gln Lys Asn Leu Gly Asp Ala Ser Val Ile Asn Asn Gly Leu	
1220 1225 1230	
ctc acc atc tcc act gag cgt agc tgg gcg atg acg cac agt atc agc	3744
Leu Thr Ile Ser Thr Glu Arg Ser Trp Ala Met Thr His Ser Ile Ser	
1235 1240 1245	
ggt agc ggt gat gtg aca aaa ctg ggt acc ggg atc ctg act ctt aac	3792
Gly Ser Gly Asp Val Thr Lys Leu Gly Thr Gly Ile Leu Thr Leu Asn	
1250 1255 1260	
aac gat tcc gcg gcg tat cag ggt acg acg gat atc gtg ggg ggg gaa	3840
Asn Asp Ser Ala Ala Tyr Gln Gly Thr Thr Asp Ile Val Gly Gly Glu	
1265 1270 1275 1280	
att gct ttc ggt tcc gac tct gcc att aat atg gca agt caa cac att	3888
Ile Ala Phe Gly Ser Asp Ser Ala Ile Asn Met Ala Ser Gln His Ile	
1285 1290 1295	

aat atc cat aac agc ggt gtg atg tcg gga aat gtc acc act gca ggt 3936
 Asn Ile His Asn Ser Gly Val Met Ser Gly Asn Val Thr Thr Ala Gly
 1300 1305 1310

gat atg aac gtt atg cct ggg ggg ggc act gcg tgt cgc taa 3978
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<211> 756

<212> DNA

<213> Escherichia coli

<220>

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<222> (1)...(756)

<400> 112

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 1 5 10 15

ttg ggc ttt gtg acc gtt gag aaa gtc gtt gag cgt ctg gga att tcg 96
 Leu Gly Phe Val Thr Val Glu Lys Val Val Glu Arg Leu Gly Ile Ser
 20 25 30

cct gcc act gcg cga cgc gat atc aat aaa ctt gac gaa agc ggc aaa 144
 Pro Ala Thr Ala Arg Arg Asp Ile Asn Lys Leu Asp Glu Ser Gly Lys
 35 40 45

ctg aaa aaa gtg cgc aat ggc gca gaa gct att acc caa cag cgc ccg 192
 Leu Lys Lys Val Arg Asn Gly Ala Glu Ala Ile Thr Gln Gln Arg Pro
 50 55 60

cgc tgg acg ccg atg aat ctg cat cag gcg cag aat cac gat gaa aaa 240
 Arg Trp Thr Pro Met Asn Leu His Gln Ala Gln Asn His Asp Glu Lys
 65 70 75 80

gta cgt atc gct aaa gcg gcc tcg cag ctg gtt aat ccg ggc gaa agc 288
 Val Arg Ile Ala Lys Ala Ala Ser Gln Leu Val Asn Pro Gly Glu Ser
 85 90 95

gta gtc atc aac tgc ggc tcc acc gcg ttt ctg ctt ggg cgg gaa atg 336
 Val Val Ile Asn Cys Gly Ser Thr Ala Phe Leu Leu Gly Arg Glu Met
 100 105 110

tgt ggc aag cca gtg caa atc atc act aat tat cta ccg ctg gca aat 384
 Cys Gly Lys Pro Val Gln Ile Ile Thr Asn Tyr Leu Pro Leu Ala Asn
 115 120 125

tac ctg atc gat caa gaa cat gac agc gtg atc att atg ggc gga cag 432
 Tyr Leu Ile Asp Gln Glu His Asp Ser Val Ile Ile Met Gly Gly Gln
 130 135 140

tac aac aaa agt cag tcc atc act tta agc ccg cag ggc agc gaa aac 480
 Tyr Asn Lys Ser Gln Ser Ile Thr Leu Ser Pro Gln Gly Ser Glu Asn
 145 150 155 160

agt ctc tat gcc ggg cac tgg atg ttt acc agc gga aaa ggg ctg acc 528

Ser Leu Tyr Ala Gly His Trp Met Phe Thr Ser Gly Lys Gly Leu Thr
 165 170 175
 gca gaa ggg ttg tat aaa acc gat atg ctg aca gca atg gca gag cag 576
 Ala Glu Gly Leu Tyr Lys Thr Asp Met Leu Thr Ala Met Ala Glu Gln
 180 185 190
 aag atg ctg agc gtg gta ggg aaa ctg gtg gta ctg gtt gat agc agt 624
 Lys Met Leu Ser Val Val Gly Lys Leu Val Val Leu Val Asp Ser Ser
 195 200 205
 aag att ggc gaa cgc gcg gga atg ctt ttt agc cgt gcc gat caa atc 672
 Lys Ile Gly Glu Arg Ala Gly Met Leu Phe Ser Arg Ala Asp Gln Ile
 210 215 220
 gat atg ctt atc acc ggc aaa aat gct aac ccg gaa atc ctg caa caa 720
 Asp Met Leu Ile Thr Gly Lys Asn Ala Asn Pro Glu Ile Leu Gln Gln
 225 230 235 240
 ctg gaa gcg caa ggg gtc agc att ctg cgt gtt taa 756
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 atc ccc agc gcc atc tta ctt ggt gcg ctt cat ggc ctg gaa cca ggg 96
 Ile Pro Ser Ala Ile Leu Leu Gly Ala Leu His Gly Leu Glu Pro Gly
 20 25 30
 cac tca aaa acg atg atg gcg gcg ttt atc atc gcc atc aaa ggc acc 144
 His Ser Lys Thr Met Met Ala Ala Phe Ile Ile Ala Ile Lys Gly Thr
 35 40 45
 att aaa caa gcg gtg atg ctc gga ctg gca gca act att tcg cat acc 192
 Ile Lys Gln Ala Val Met Leu Gly Leu Ala Ala Thr Ile Ser His Thr
 50 55 60
 gca gtg gtc tgg tta att gcc ttt ggc ggg atg gtg atc agc aag cgc 240
 Ala Val Val Trp Leu Ile Ala Phe Gly Gly Met Val Ile Ser Lys Arg
 65 70 75 80
 ttt act gct caa tca gca gaa ccg tgg ctc cag ctg att tcc gca gtg 288
 Phe Thr Ala Gln Ser Ala Glu Pro Trp Leu Gln Leu Ile Ser Ala Val
 85 90 95
 atc att att agc acc gcg ttc tgg atg ttc tgg cgt acc tgg cgc ggc 336
 Ile Ile Ile Ser Thr Ala Phe Trp Met Phe Trp Arg Thr Trp Arg Gly
 100 105 110

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gaa cgc aac tgg ctg gag aat atg cac ggg cat gat tat gag cat cat 384
Glu Arg Asn Trp Leu Glu Asn Met His Gly His Asp Tyr Glu His His
      115                      120                      125

cat cac gat cac gaa cat cac cac gac cat gga cat cat cac cat cac 432
His His Asp His Glu His His His Asp His Gly His His His His His
      130                      135                      140

gaa cat ggc gag tat cag gat gcc cat gca cga gcc cat gcc aat gac 480
Glu His Gly Glu Tyr Gln Asp Ala His Ala Arg Ala His Ala Asn Asp
145                      150                      155                      160

att aaa cga cgc ttt gat ggt aga gag gtc acc aac tgg caa att ttg 528
Ile Lys Arg Arg Phe Asp Gly Arg Glu Val Thr Asn Trp Gln Ile Leu
      165                      170                      175

tta ttt ggc tta acc ggt ggc ctt atc ccc tgc ccg gca gca att acc 576
Leu Phe Gly Leu Thr Gly Gly Leu Ile Pro Cys Pro Ala Ala Ile Thr
      180                      185                      190

gtg ctg ttg ata tgc att cag ttg aaa gcc ctg aca ctg ggc gca aca 624
Val Leu Leu Ile Cys Ile Gln Leu Lys Ala Leu Thr Leu Gly Ala Thr
      195                      200                      205

ctg gtc gtc agt ttc agc att ggc ctg gcg tta acg ctt gtc acc gta 672
Leu Val Val Ser Phe Ser Ile Gly Leu Ala Leu Thr Leu Val Thr Val
      210                      215                      220

ggc gtt ggc gca gca atc agc gtt cag cag gtc gca aaa cgc tgg agc 720
Gly Val Gly Ala Ala Ile Ser Val Gln Gln Val Ala Lys Arg Trp Ser
225                      230                      235                      240

gga ttt aac act ctc gct aaa cgc gcc ccc tat ttt tcc agt ctg ttg 768
Gly Phe Asn Thr Leu Ala Lys Arg Ala Pro Tyr Phe Ser Ser Leu Leu
      245                      250                      255

att ggc tta gtc ggt gtg tat atg ggc gta cat ggc ttc atg ggc ata 816
Ile Gly Leu Val Gly Val Tyr Met Gly Val His Gly Phe Met Gly Ile
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atg cga taa
Met Arg * 825

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<210> 114
<211> 519
<212> DNA
<213> Escherichia coli

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<220>
<221> CDS
<222> (1)...(519)

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<400> 114
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Met Ile Leu Lys Ser Ala Ile Ser Ala Asp Ser Leu Leu Ala Lys Asp
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gct ttt agg gca tcc ttt cat tta cac ttt tta cga aat cat ggg atc 96

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Ala	Phe	Arg	Ala	Ser	Phe	His	Leu	His	Phe	Leu	Arg	Asn	His	Gly	Ile	
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act	aac	aaa	ata	tcg	ctt	gtc	agt	tat	att	gta	tgg	cag	gaa	aga	tat	144
Thr	Asn	Lys	Ile	Ser	Leu	Val	Ser	Tyr	Ile	Val	Trp	Gln	Glu	Arg	Tyr	
		35					40					45				
gcg	act	gat	att	aca	gat	ccc	caa	agt	gga	gag	ttt	atg	acc	att	aaa	192
Ala	Thr	Asp	Ile	Thr	Asp	Pro	Gln	Ser	Gly	Glu	Phe	Met	Thr	Ile	Lys	
	50					55					60					
aat	aag	atg	ttg	ctg	ggg	gcg	ctt	ttg	ctg	gtt	acc	agt	gcc	gcc	tgg	240
Asn	Lys	Met	Leu	Leu	Gly	Ala	Leu	Leu	Leu	Val	Thr	Ser	Ala	Ala	Trp	
	65				70					75					80	
gcc	gca	cca	gcc	acc	gcg	ggg	tcg	acc	aat	acc	tcg	gga	att	tct	aag	288
Ala	Ala	Pro	Ala	Thr	Ala	Gly	Ser	Thr	Asn	Thr	Ser	Gly	Ile	Ser	Lys	
				85					90					95		
tat	gag	tta	agt	agt	ttc	att	gct	gac	ttt	aag	cat	ttc	aaa	cca	ggg	336
Tyr	Glu	Leu	Ser	Ser	Phe	Ile	Ala	Asp	Phe	Lys	His	Phe	Lys	Pro	Gly	
			100					105					110			
gac	acc	gta	cca	gaa	atg	tac	cgt	acc	gat	gag	tac	aac	att	aag	cag	384
Asp	Thr	Val	Pro	Glu	Met	Tyr	Arg	Thr	Asp	Glu	Tyr	Asn	Ile	Lys	Gln	
		115					120					125				
tgg	cag	ttg	cgt	aac	ctg	ccc	gcg	cct	gat	gcc	ggg	acg	cac	tgg	acc	432
Trp	Gln	Leu	Arg	Asn	Leu	Pro	Ala	Pro	Asp	Ala	Gly	Thr	His	Trp	Thr	
	130					135					140					
tat	atg	ggg	ggc	gcg	tac	gtg	ttg	atc	agc	gac	acc	gac	ggg	aaa	atc	480
Tyr	Met	Gly	Gly	Ala	Tyr	Val	Leu	Ile	Ser	Asp	Thr	Asp	Gly	Lys	Ile	
	145				150					155					160	
att	aaa	gcc	tac	gac	ggg	gag	att	ttt	tat	cat	cgc	taa				519
Ile	Lys	Ala	Tyr	Asp	Gly	Glu	Ile	Phe	Tyr	His	Arg	*				
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<210> 115

<211> 1035

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1035)

<400> 115

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Met	Glu	Ile	Arg	Ile	Met	Leu	Phe	Ile	Leu	Met	Met	Met	Val	Met	Pro	
1				5					10					15		
gtg	agc	tat	gcg	gca	tgt	tat	agt	gag	tta	tct	gtt	cag	cac	aac	ttg	96
Val	Ser	Tyr	Ala	Ala	Cys	Tyr	Ser	Glu	Leu	Ser	Val	Gln	His	Asn	Leu	
			20					25					30			
gtt	gtt	cag	ggg	gat	ttt	gca	ctt	act	caa	aca	caa	atg	gcg	aca	tat	144
Val	Val	Gln	Gly	Asp	Phe	Ala	Leu	Thr	Gln	Thr	Gln	Met	Ala	Thr	Tyr	
		35					40					45				

gag cat aat ttt aat gat tcg tca tgc gta agt aca aat act atc acc	192
Glu His Asn Phe Asn Asp Ser Ser Cys Val Ser Thr Asn Thr Ile Thr	
50 55 60	
cct atg agc ccg tcg gat att att gtt gga ctt tat aac gat acc ata	240
Pro Met Ser Pro Ser Asp Ile Ile Val Gly Leu Tyr Asn Asp Thr Ile	
65 70 75 80	
aaa tta aat tta cat ttt gaa tgg acc aat aaa aac aac atc acg ttg	288
Lys Leu Asn Leu His Phe Glu Trp Thr Asn Lys Asn Asn Ile Thr Leu	
85 90 95	
tca aat aat cag acc agt ttc acc agt ggt tat tca gtt acg gtg aca	336
Ser Asn Asn Gln Thr Ser Phe Thr Ser Gly Tyr Ser Val Thr Val Thr	
100 105 110	
cct gcg gcc agt aat gca aaa gtg aat gtt tct gcg ggg ggc ggc ggt	384
Pro Ala Ala Ser Asn Ala Lys Val Asn Val Ser Ala Gly Gly Gly Gly	
115 120 125	
tca gtg atg att aat ggt gtt gcg aca tta tcc agt gct tca tca tcg	432
Ser Val Met Ile Asn Gly Val Ala Thr Leu Ser Ser Ala Ser Ser Ser	
130 135 140	
aca cgc ggg agt gcc gca gta caa ttt cta ctg tgt tta tta ggt ggc	480
Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly	
145 150 155 160	
aag tca tgg gat gca tgt gta aat agc tac aga aat gca ttg gca caa	528
Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln	
165 170 175	
aat gca ggt gtc tat tcc ttt aat ctg aca ttg tca tac aac ccg ata	576
Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile	
180 185 190	
acc aca acc tgc aaa ccg gac gat tta tta att act tta gac agt att	624
Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile	
195 200 205	
ccc gtt tca caa tta cca gcc aca ggt aac aaa gca aca ata aat agt	672
Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser	
210 215 220	
aaa caa ggg gat att att ctg cgt tgt aaa aat tta tta ggt caa caa	720
Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln	
225 230 235 240	
aat caa aca tca cgg aaa atg cag gtg tat tta tca agt tct gac ttg	768
Asn Gln Thr Ser Arg Lys Met Gln Val Tyr Leu Ser Ser Ser Asp Leu	
245 250 255	
tta acc aac agc aac aca ata ctg aaa ggt gcg gaa gat aat ggc gta	816
Leu Thr Asn Ser Asn Thr Ile Leu Lys Gly Ala Glu Asp Asn Gly Val	
260 265 270	
gga ttt att ctt gaa agt aat ggt tcg cca gtc aca ctt tta aat atc	864
Gly Phe Ile Leu Glu Ser Asn Gly Ser Pro Val Thr Leu Leu Asn Ile	
275 280 285	

act aac agc agt aaa gga tat aca aat tta aag gaa gtt gcg gcg aag 912
 Thr Asn Ser Ser Lys Gly Tyr Thr Asn Leu Lys Glu Val Ala Ala Lys
 290 295 300

tca aaa ctt aca gat aca acg gtt tca att ccg ata aca gcc agt tac 960
 Ser Lys Leu Thr Asp Thr Thr Val Ser Ile Pro Ile Thr Ala Ser Tyr
 305 310 315 320

tac gtc tac gat aca aac aaa gtt aaa tct ggc gca ctg gag gca acc 1008
 Tyr Val Tyr Asp Thr Asn Lys Val Lys Ser Gly Ala Leu Glu Ala Thr
 325 330 335

gca tta atc aac gtg aaa tac gac taa 1035
 Ala Leu Ile Asn Val Lys Tyr Asp *
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<210> 116

<211> 2481

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (2481)

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ggc att gaa gct tat gca gct gaa gaa acc ttt gat acc cat ttt atg 96
 Gly Ile Glu Ala Tyr Ala Ala Glu Glu Thr Phe Asp Thr His Phe Met
 20 25 30

ata ggt gga atg aaa gac cag cag gtt gca aat att cgt ctt gat gat 144
 Ile Gly Gly Met Lys Asp Gln Gln Val Ala Asn Ile Arg Leu Asp Asp
 35 40 45

aat caa ccc tta ccg ggg cag tat gac atc gat att tat gtc aat aag 192
 Asn Gln Pro Leu Pro Gly Gln Tyr Asp Ile Asp Ile Tyr Val Asn Lys
 50 55 60

caa tgg cgc ggg aaa tat gag att att gtt aaa gac aac ccg caa gaa 240
 Gln Trp Arg Gly Lys Tyr Glu Ile Ile Val Lys Asp Asn Pro Gln Glu
 65 70 75 80

aca tgt tta tca aga gaa gtt atc aag cgg tta ggc att aat agc gat 288
 Thr Cys Leu Ser Arg Glu Val Ile Lys Arg Leu Gly Ile Asn Ser Asp
 85 90 95

aac ttc gcc agc ggt aag caa tgt tta aca ttt gag caa ctt gtt cag 336
 Asn Phe Ala Ser Gly Lys Gln Cys Leu Thr Phe Glu Gln Leu Val Gln
 100 105 110

ggt ggg agc tat acc tgg gat atc ggg gtt ttt cgt ctc gat ttc agt 384
 Gly Gly Ser Tyr Thr Trp Asp Ile Gly Val Phe Arg Leu Asp Phe Ser
 115 120 125

gtc ccg cag gcc tgg gtg gaa gaa ctg gaa agt ggc tat gtt cca ccg 432
 Val Pro Gln Ala Trp Val Glu Glu Leu Glu Ser Gly Tyr Val Pro Pro

130	135	140	
gaa aac tgg gag cgg ggt att aat gcg ttt tat acc tct tat tat ctg			480
Glu Asn Trp Glu Arg Gly Ile Asn Ala Phe Tyr Thr Ser Tyr Tyr Leu			
145	150	155	160
agt cag tat tac agc gac tat aaa gcg tcg ggt aat aac aag agt aca			528
Ser Gln Tyr Tyr Ser Asp Tyr Lys Ala Ser Gly Asn Asn Lys Ser Thr			
	165	170	175
tat gta cgt ttt aac agc ggg tta aat tta ctg ggg tgg caa ctg cat			576
Tyr Val Arg Phe Asn Ser Gly Leu Thr Asn Leu Leu Gly Trp Gln Leu His			
	180	185	190
tct gat gcc agt ttc agt aaa aca aat aac aat cca ggg gtg tgg aaa			624
Ser Asp Ala Ser Phe Ser Lys Thr Asn Asn Asn Pro Gly Val Trp Lys			
	195	200	205
agc aat acc ctg tat ctg gaa cgt gga ttt gcc caa ctt ctc ggc acg			672
Ser Asn Thr Leu Tyr Leu Arg Gly Phe Ala Gln Leu Leu Gly Thr			
	210	215	220
ctt cgc gtg ggt gat atg tac aca tca agc gat att ttt gat tct gtt			720
Leu Arg Val Gly Asp Met Tyr Thr Ser Ser Asp Ile Phe Asp Ser Val			
	225	230	235
cgc ttc aga ggt gtg cgg ttg ttt cgt gat atg cag atg ttg cct aac			768
Arg Phe Arg Gly Val Arg Leu Phe Arg Asp Met Gln Met Leu Pro Asn			
	245	250	255
tcg aaa caa aat ttt acg cca cgg gtg cag ggg att gct cag agt aac			816
Ser Lys Gln Asn Phe Thr Pro Arg Val Gln Gly Ile Ala Gln Ser Asn			
	260	265	270
gcg ctg gta act att gaa cag aat ggt ttt gtg gtt tat cag aaa gag			864
Ala Leu Val Thr Ile Glu Gln Asn Gly Phe Val Val Tyr Gln Lys Glu			
	275	280	285
gtt cct cct ggc cgg ttc gcg att aca gat ttg cag ttg gcc ggt ggt			912
Val Pro Pro Gly Pro Phe Ala Ile Thr Asp Leu Gln Leu Ala Gly Gly			
	290	295	300
gga gca gat ctt gat gtc agc gtg aaa gag gcg gac ggc tcg gta acc			960
Gly Ala Asp Leu Asp Val Ser Val Lys Glu Ala Asp Gly Ser Val Thr			
	305	310	315
acc tat ctg gtg cct tat gca gcg gtg cca aat atg ctg caa ccc ggc			1008
Thr Tyr Leu Val Pro Tyr Ala Ala Val Pro Asn Met Leu Gln Pro Gly			
	325	330	335
gtg tcg aaa tat gat tta gcg gcg ggt cgt agc cat att gaa ggg gcg			1056
Val Ser Lys Tyr Asp Leu Ala Ala Gly Arg Ser His Ile Glu Gly Ala			
	340	345	350
agc aaa caa agt gat ttt gtc cag gcg ggt tat cag tat ggt ttt aat			1104
Ser Lys Gln Ser Asp Phe Val Gln Ala Gly Tyr Gln Tyr Gly Phe Asn			
	355	360	365
aat tta ttg acg ctg tat ggt ggc tcg atg gtc gcg aat aat tat tac			1152
Asn Leu Leu Thr Leu Tyr Gly Gly Ser Met Val Ala Asn Asn Tyr Tyr			
	370	375	380

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Ala Phe Thr Leu Gly Ala Gly Trp Asn Thr Arg Ile Gly Ala Ile Ser	
385 390 395 400	
gtc gat gcc act aag tcg cat agt aaa caa gac aac ggc gat gtg ttt	1248
Val Asp Ala Thr Lys Ser His Ser Lys Gln Asp Asn Gly Asp Val Phe	
405 410 415	
gac ggg caa agt tat caa att gcc tac aac aaa ttt gtg agc caa acg	1296
Asp Gly Gln Ser Tyr Gln Ile Ala Tyr Asn Lys Phe Val Ser Gln Thr	
420 425 430	
tcg acg cgt ttt ggt ctg gcg gcc tgg cgt tat tcg tcg cgt gat tac	1344
Ser Thr Arg Phe Gly Leu Ala Ala Trp Arg Tyr Ser Ser Arg Asp Tyr	
435 440 445	
cgg aca ttt aac gat cac gtt tgg gca aac aat aaa gat aat tat cgc	1392
Arg Thr Phe Asn Asp His Val Trp Ala Asn Asn Lys Asp Asn Tyr Arg	
450 455 460	
cgt gat gaa aac gat gtc tat gac att gcc gat tat tac cag aac gat	1440
Arg Asp Glu Asn Asp Val Tyr Asp Ile Ala Asp Tyr Tyr Gln Asn Asp	
465 470 475 480	
ttt ggc cgc aaa aat agc ttt tcc gcc aat atg agc cag tca ttg cca	1488
Phe Gly Arg Lys Asn Ser Phe Ser Ala Asn Met Ser Gln Ser Leu Pro	
485 490 495	
gaa ggt tgg ggg tct gtg tca tta agt acg tta tgg cga gat tac tgg	1536
Glu Gly Trp Gly Ser Val Ser Leu Ser Thr Leu Trp Arg Asp Tyr Trp	
500 505 510	
ggg cgt agc ggc agt agt aag gat tat cag ttg agt tat tcc aac aac	1584
Gly Arg Ser Gly Ser Ser Lys Asp Tyr Gln Leu Ser Tyr Ser Asn Asn	
515 520 525	
ctg cga cgg ata agc tat acc ctc gcg gca agc cag gct tat gac gag	1632
Leu Arg Arg Ile Ser Tyr Thr Leu Ala Ala Ser Gln Ala Tyr Asp Glu	
530 535 540	
aat cat cat gaa gag aaa cgt ttt aat att ttt ata tcg att ccc ttt	1680
Asn His His Glu Glu Lys Arg Phe Asn Ile Phe Ile Ser Ile Pro Phe	
545 550 555 560	
gat tgg ggt gat gac gtt tcg acg cct cgt cgg caa ata tat atg tct	1728
Asp Trp Gly Asp Asp Val Ser Thr Pro Arg Arg Gln Ile Tyr Met Ser	
565 570 575	
aac tca acg acg ttt gat gat cag ggg ttt gcc tca aat aat acg gga	1776
Asn Ser Thr Thr Phe Asp Asp Gln Gly Phe Ala Ser Asn Asn Thr Gly	
580 585 590	
tta tca gga aca gta ggg agt cgg gat cag ttc aat tat ggt gtc aac	1824
Leu Ser Gly Thr Val Gly Ser Arg Asp Gln Phe Asn Tyr Gly Val Asn	
595 600 605	
ctg agt cat caa cat cag gga aat gaa acg aca gct ggg gcg aat ttg	1872
Leu Ser His Gln His Gln Gly Asn Glu Thr Ala Gly Ala Asn Leu	
610 615 620	

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acc tgg aac gcg ccg gtt gcg aca gtg aat ggc agt tat agt cag tcg 1920
Thr Trp Asn Ala Pro Val Ala Thr Val Asn Gly Ser Tyr Ser Gln Ser
625                630                635                640

agt act tat cga cag gct gga gcc agt gtt tca ggg ggc att gtc gcc 1968
Ser Thr Tyr Arg Gln Ala Gly Ala Ser Val Ser Gly Gly Ile Val Ala
645                650                655

tgg tcg ggt ggc gtt aat ctg gcg aac cgt ctt tcc gaa acg ttt gct 2016
Trp Ser Gly Gly Val Asn Leu Ala Asn Arg Leu Ser Glu Thr Phe Ala
660                665                670

gtg atg aat gcg cca gga att aaa gat gct tat gtc aat ggg caa aaa 2064
Val Met Asn Ala Pro Gly Ile Lys Asp Ala Tyr Val Asn Gly Gln Lys
675                680                685

tat cgc aca aca aac cgt aat gga gtg gtg ata tac gac gga atg aca 2112
Tyr Arg Thr Thr Asn Arg Asn Gly Val Val Ile Tyr Asp Gly Met Thr
690                695                700

cct tat cgg gaa aat cac ctg atg ctg gat gtg tcg caa agc gat agc 2160
Pro Tyr Arg Glu Asn His Leu Met Leu Asp Val Ser Gln Ser Asp Ser
705                710                715                720

gaa gca gaa tta cgt ggc aac cgg aaa att gcc gcc cct tat cgc ggc 2208
Glu Ala Glu Leu Arg Gly Asn Arg Lys Ile Ala Ala Pro Tyr Arg Gly
725                730                735

gcg gtt gta ctg gtt aat ttt gat acc gat cag cgc aag cca tgg ttt 2256
Ala Val Val Leu Val Asn Phe Asp Thr Asp Gln Arg Lys Pro Trp Phe
740                745                750

ata aaa gcg tta aga gca gat ggg caa tca tta acg ttt ggt tat gaa 2304
Ile Lys Ala Leu Arg Ala Asp Gly Gln Ser Leu Thr Phe Gly Tyr Glu
755                760                765

gtc aat gat atc cat ggt cat aat att ggc gtt gtc ggc cag gga agt 2352
Val Asn Asp Ile His Gly His Asn Ile Gly Val Val Gly Gln Gly Ser
770                775                780

cag tta ttt att cgc acc aat gaa gta ccg cca tcg gtt aat gtg gca 2400
Gln Leu Phe Ile Arg Thr Asn Glu Val Pro Pro Ser Val Asn Val Ala
785                790                795                800

att gat aag caa caa gga ctt tca tgc aca atc acc ttc ggt aaa gag 2448
Ile Asp Lys Gln Gln Gly Leu Ser Cys Thr Ile Thr Phe Gly Lys Glu
805                810                815

att gat gaa agt aga aat tat att tgc cag taa 2481
Ile Asp Glu Ser Arg Asn Tyr Ile Cys Gln *
820                825

```

<210> 117

<211> 720

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(720)

```

<400> 117
atg gcc gct atc cca tgg cgg cct ttt aat tta aga ggc att aaa atg 48
Met Ala Ala Ile Pro Trp Arg Pro Phe Asn Leu Arg Gly Ile Lys Met
1 5 10 15

aaa gga tta tta tct tta ctc att ttt tct atg gtc ctt cct gca cat 96
Lys Gly Leu Leu Ser Leu Leu Ile Phe Ser Met Val Leu Pro Ala His
20 25 30

gcc gga att gtt atc tac ggg acg cgc att att tac ccg gca gaa aat 144
Ala Gly Ile Val Ile Tyr Gly Thr Arg Ile Ile Tyr Pro Ala Glu Asn
35 40 45

aaa gaa gtg atg gtg cag ttg atg aac cag gga aac cgt tct tcg ctg 192
Lys Glu Val Met Val Gln Leu Met Asn Gln Gly Asn Arg Ser Ser Leu
50 55 60

ctg cag gcg tgg att gat gat ggc gat acg tca tta cca cca gaa aaa 240
Leu Gln Ala Trp Ile Asp Asp Gly Asp Thr Ser Leu Pro Pro Glu Lys
65 70 75 80

att cag gtt cct ttc atg tta acg cca cca gtg gca aaa ata ggg gca 288
Ile Gln Val Pro Phe Met Leu Thr Pro Pro Val Ala Lys Ile Gly Ala
85 90 95

aat tcc ggg cag caa gta aaa atc aaa att atg ccg aat aaa ctg ccc 336
Asn Ser Gly Gln Gln Val Lys Ile Lys Ile Met Pro Asn Lys Leu Pro
100 105 110

act aat aaa gaa agc att ttt tat ctg aat gtt ctg gat att cca cca 384
Thr Asn Lys Glu Ser Ile Phe Tyr Leu Asn Val Leu Asp Ile Pro Pro
115 120 125

aat agt cca gag caa gaa ggt aag aat gca ctg aag ttt gcg atg caa 432
Asn Ser Pro Glu Gln Glu Gly Lys Asn Ala Leu Lys Phe Ala Met Gln
130 135 140

aac aga att aag ttg ttt tac cgg cca gcg ggt att gct ccg gta aat 480
Asn Arg Ile Lys Leu Phe Tyr Arg Pro Ala Gly Ile Ala Pro Val Asn
145 150 155 160

aaa gcg aca ttt aaa aaa ttg ctg gta aat cgc agt ggc aat ggt ttg 528
Lys Ala Thr Phe Lys Lys Leu Leu Val Asn Arg Ser Gly Asn Gly Leu
165 170 175

gtg ata aaa aat gac tca gct aat tgg gtg acg att tcg gat gtc aaa 576
Val Ile Lys Asn Asp Ser Ala Asn Trp Val Thr Ile Ser Asp Val Lys
180 185 190

gct aat aat gtc aaa gtc aat tat gaa act att atg att gcc ccc tta 624
Ala Asn Asn Val Lys Val Asn Tyr Glu Thr Ile Met Ile Ala Pro Leu
195 200 205

gaa agt cag agt gtt aat gtc aaa agt aat aat gca aat aac tgg cat 672
Glu Ser Gln Ser Val Asn Val Lys Ser Asn Asn Ala Asn Asn Trp His
210 215 220

ctg acc att atc gat gac cat ggc aac tat att agt gac aaa att taa 720
Leu Thr Ile Ile Asp Asp His Gly Asn Tyr Ile Ser Asp Lys Ile *
225 230 235

```

<210> 118
 <211> 543
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(543)

<400> 118
 atg aaa cgt tca att att gct gcc gct gtc ttt tct tct ttt ttt atg 48
 Met Lys Arg Ser Ile Ile Ala Ala Ala Val Phe Ser Ser Phe Phe Met
 1 5 10 15
 agc gct gga gta ttt gct gca gac gtt gat acc gga aca tta act att 96
 Ser Ala Gly Val Phe Ala Ala Asp Val Asp Thr Gly Thr Leu Thr Ile
 20 25 30
 aag ggg aat att gca gaa tct ccg tgt aaa ttc gaa gcg ggt ggt gat 144
 Lys Gly Asn Ile Ala Glu Ser Pro Cys Lys Phe Glu Ala Gly Gly Asp
 35 40 45
 tca gta agt att aat atg ccg act gta cca acc agt gtc ttt gaa ggt 192
 Ser Val Ser Ile Asn Met Pro Thr Val Pro Thr Ser Val Phe Glu Gly
 50 55 60
 aaa gct aaa tat tct acc tat gat gat gca gtc ggt gta acc agc agc 240
 Lys Ala Lys Tyr Ser Thr Tyr Asp Asp Ala Val Gly Val Thr Ser Ser
 65 70 75 80
 atg tta aaa att agc tgc ccg aaa gaa gtt gct ggt gta aaa ctc tcg 288
 Met Leu Lys Ile Ser Cys Pro Lys Glu Val Ala Gly Val Lys Leu Ser
 85 90 95
 ttg att acc aac gat aaa ata acc ggt aac gat aag gcg ata gcc agt 336
 Leu Ile Thr Asn Asp Lys Ile Thr Gly Asn Asp Lys Ala Ile Ala Ser
 100 105 110
 agc aac gat acc gtg ggt tac tat ctc tat tta ggt gat aac agc gat 384
 Ser Asn Asp Thr Val Gly Tyr Tyr Leu Tyr Leu Gly Asp Asn Ser Asp
 115 120 125
 gtc ctg gat gtt tct gca cct ttt aac att gag agt tat aaa aca gcg 432
 Val Leu Asp Val Ser Ala Pro Phe Asn Ile Glu Ser Tyr Lys Thr Ala
 130 135 140
 gaa ggt caa tat gct att ccg ttt aaa gca aaa tac ctg aaa ctg aca 480
 Glu Gly Gln Tyr Ala Ile Pro Phe Lys Ala Lys Tyr Leu Lys Leu Thr
 145 150 155 160
 gat aac tca gtg caa tca ggt gat gtg tta tct tct ctg gtt atg cgt 528
 Asp Asn Ser Val Gln Ser Gly Asp Val Leu Ser Ser Leu Val Met Arg
 165 170 175
 gtg gcg cag gat taa 543
 Val Ala Gln Asp *
 180

<210> 119
 <211> 288
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1) ... (288)

<400> 119
 atg ctg cac aca tta cat cgc tca ccc tgg ctg acg gat ttt gct gcg 48
 Met Leu His Thr Leu His Arg Ser Pro Trp Leu Thr Asp Phe Ala Ala
 1 5 10 15
 ctg ctg cgt ctg ctc agt gaa gga gac gaa ctg cta tta ttg caa gat 96
 Leu Leu Arg Leu Leu Ser Glu Gly Asp Glu Leu Leu Leu Leu Gln Asp
 20 25 30
 ggc gta act gcc gca gtt gac ggt aac cgc tac ctt gaa agt ctg cgt 144
 Gly Val Thr Ala Ala Val Asp Gly Asn Arg Tyr Leu Glu Ser Leu Arg
 35 40 45
 aat gcc ccc att aag gtc tat gcc ctg aac gaa gac ctt att gcc cgc 192
 Asn Ala Pro Ile Lys Val Tyr Ala Leu Asn Glu Asp Leu Ile Ala Arg
 50 55 60
 ggt ttg act ggt caa att tcg aac gac atc att ctc att gac tat act 240
 Gly Leu Thr Gly Gln Ile Ser Asn Asp Ile Ile Leu Ile Asp Tyr Thr
 65 70 75 80
 gat ttc gtc aga ctt acg gtt aag cac ccc agc cag atg gcc tgg tga 288
 Asp Phe Val Arg Leu Thr Val Lys His Pro Ser Gln Met Ala Trp *
 85 90 95

<210> 120
 <211> 360
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1) ... (360)

<400> 120
 atg aaa cga att gcg ttt gtt ttt tct act gca cct cat ggt aca gcc 48
 Met Lys Arg Ile Ala Phe Val Phe Ser Thr Ala Pro His Gly Thr Ala
 1 5 10 15
 gca ggc cgg gaa ggt tta gat gct tta ctg gca act tcc gca tta act 96
 Ala Gly Arg Glu Gly Leu Asp Ala Leu Leu Ala Thr Ser Ala Leu Thr
 20 25 30
 gac gat ctg gct gtc ttc ttt ata gct gat ggc gtt ttt cag ctg ctg 144
 Asp Asp Leu Ala Val Phe Phe Ile Ala Asp Gly Val Phe Gln Leu Leu
 35 40 45
 cca gga caa aag ccc gat gca gtg ctg gcg cgt gat tac att gcc act 192
 Pro Gly Gln Lys Pro Asp Ala Val Leu Ala Arg Asp Tyr Ile Ala Thr

50	55	60	
ttt aaa ttg ttg ggt ctg tac gac att gaa cag tgc tgg gtt tgt gcg			240
Phe Lys Leu Leu Gly Leu Tyr Asp Ile Glu Gln Cys Trp Val Cys Ala			
65	70	75	80
gct tca ctg cgc gaa cgc ggg tta gat ccg cag aca ccc ttt gtt gtc			288
Ala Ser Leu Arg Glu Arg Gly Leu Asp Pro Gln Thr Pro Phe Val Val			
	85	90	95
gaa gcc acg ccg ctc gaa gca gat gcc tta cgc cgc gaa ctc gcc aac			336
Glu Ala Thr Pro Leu Glu Ala Asp Ala Leu Arg Arg Glu Leu Ala Asn			
	100	105	110
tac gat gtt att ttg agg ttt tga			360
Tyr Asp Val Ile Leu Arg Phe *			
115			

<210> 121

<211> 387

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(387)

<400> 121

atg cgt ttt gcc atc gtg gtg acc ggg cca gca tac ggt acg caa cag	48
Met Arg Phe Ala Ile Val Val Thr Gly Pro Ala Tyr Gly Thr Gln Gln	
1	5 10 15

gcg agt agt gct ttt cag ttt gcg cag gcg ctg ata gca gat ggc cat	96
Ala Ser Ser Ala Phe Gln Phe Ala Gln Ala Leu Ile Ala Asp Gly His	
	20 25 30

gag tta agc agc gtc ttt ttc tat cgg gaa ggg gtc tat aac gct aac	144
Glu Leu Ser Ser Val Phe Phe Tyr Arg Glu Gly Val Tyr Asn Ala Asn	
	35 40 45

caa ttg acc tct ccg gca agt gac gaa ttt gac ctc gta cgg gcc tgg	192
Gln Leu Thr Ser Pro Ala Ser Asp Glu Phe Asp Leu Val Arg Ala Trp	
	50 55 60

caa caa ctg aat gcg caa cat ggt gtg gcg ctg aat atc tgc gta gcg	240
Gln Gln Leu Asn Ala Gln His Gly Val Ala Leu Asn Ile Cys Val Ala	
65	70 75 80

gca gca tta cgc cgt ggc gtt gtt gat gaa acg gag gcc gga aga ctg	288
Ala Ala Leu Arg Arg Gly Val Val Asp Glu Thr Glu Ala Gly Arg Leu	
	85 90 95

ggg ctg gct tcg tca aac ctt cag cag gga ttt acc tta agc gga ctt	336
Gly Leu Ala Ser Ser Asn Leu Gln Gln Gly Phe Thr Leu Ser Gly Leu	
	100 105 110

ggg gcg ctg gcg gaa gcc tcg ctg acc tgt gac agg gtg gta cag ttc	384
Gly Ala Leu Ala Glu Ala Ser Leu Thr Cys Asp Arg Val Val Gln Phe	
	115 120 125

tga

387

*

<210> 122

<211> 735

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (735)

<400> 122

gtg ttt ttt ttc atg tcc agg tcg ctt tta acc aac gaa acc agt gag	48
Met Phe Phe Phe Met Ser Arg Ser Leu Leu Thr Asn Glu Thr Ser Glu	
1 5 10 15	
ttg gat tta ctg gat caa cgt cct ttc gac cag acc gat ttt gat att	96
Leu Asp Leu Leu Asp Gln Arg Pro Phe Asp Gln Thr Asp Phe Asp Ile	
20 25 30	
ctg aaa tcc tac gaa gcg gtg gtg gac ggg tta gcg atg ctt att ggc	144
Leu Lys Ser Tyr Glu Ala Val Val Asp Gly Leu Ala Met Leu Ile Gly	
35 40 45	
tcc cac tgt gaa atc gtt ttg cac tct ttg cag gat cta aaa tgt tca	192
Ser His Cys Glu Ile Val Leu His Ser Leu Gln Asp Leu Lys Cys Ser	
50 55 60	
gcc att cgc att gct aac ggt gaa cat aca ggc cgg aag att ggt tcg	240
Ala Ile Arg Ile Ala Asn Gly Glu His Thr Gly Arg Lys Ile Gly Ser	
65 70 75 80	
cca att act gac ctg gcg cta cgt atg ctg cac gat atg acg gga gcg	288
Pro Ile Thr Asp Leu Ala Leu Arg Met Leu His Asp Met Thr Gly Ala	
85 90 95	
gat agc agc gtt tct aaa tgc tac ttt act cgc gcc aaa agc ggc gta	336
Asp Ser Ser Val Ser Lys Cys Tyr Phe Thr Arg Ala Lys Ser Gly Val	
100 105 110	
tta atg aag tcc ctg act atc gcg att cgt aac cgc gaa cag cgt gta	384
Leu Met Lys Ser Leu Thr Ile Ala Ile Arg Asn Arg Glu Gln Arg Val	
115 120 125	
att ggt ctg ctg tgc atc aat atg aat ctt gat gtt ccc ttc tcg cag	432
Ile Gly Leu Leu Cys Ile Asn Met Asn Leu Asp Val Pro Phe Ser Gln	
130 135 140	
att atg agc acc ttt gtg ccg cca gaa acc ccg gat gtc ggt tca agc	480
Ile Met Ser Thr Phe Val Pro Pro Glu Thr Pro Asp Val Gly Ser Ser	
145 150 155 160	
gtc aac ttt gcc tct tct gtt gaa gat ctg gtt acc caa acg ctg gag	528
Val Asn Phe Ala Ser Ser Val Glu Asp Leu Val Thr Gln Thr Leu Glu	
165 170 175	
ttc acc atc gaa gaa gtg aat gcc gat cgc aat gtt tct aat aac gcc	576
Phe Thr Ile Glu Glu Val Asn Ala Asp Arg Asn Val Ser Asn Asn Ala	

180	185	190	
aaa aat cgt cag atc gtg ctg aat ctc tac gag aaa ggg atc ttc gat			624
Lys Asn Arg Gln Ile Val Leu Asn Leu Tyr Glu Lys Gly Ile Phe Asp			
195	200	205	
att aaa gat gcg atc aac cag gtt gct gac cgc ctg aac atc tcc aaa			672
Ile Lys Asp Ala Ile Asn Gln Val Ala Asp Arg Leu Asn Ile Ser Lys			
210	215	220	
cac act gtc tat ctc tac atc cgc cag ttc aag agc ggt gat ttc cag			720
His Thr Val Tyr Leu Tyr Ile Arg Gln Phe Lys Ser Gly Asp Phe Gln			
225	230	235	240
ggg caa gat aag taa			735
Gly Gln Asp Lys *			

<210> 123
 <211> 255
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(255)

<400> 123	
atg acc gat aaa atc cgt act ctg caa ggt cgc gtt gtt agc gac aaa	48
Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys	
1 5 10 15	
atg gag aaa tcc att gtt gtt gct atc gaa cgt ttt gtg aaa cac ccg	96
Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro	
20 25 30	
atc tac ggt aaa ttc atc aag cgt acg acc aaa ctg cac gta cat gac	144
Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp	
35 40 45	
gag aac aac gaa tgc ggt atc ggt gac gtg gtt gaa atc cgc gaa tgc	192
Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys	
50 55 60	
cgt ccg ctg tcc aag act aaa tcc tgg acg ctg gtt cgc gtt gta gag	240
Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu	
65 70 75 80	
aaa gcg gtt ctg taa	255
Lys Ala Val Leu *	

<210> 124
 <211> 192
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS

<222> (1) ... (192)

<400> 124

```

atg aaa gca aaa gag ctg cgt gag aag agc gtt gaa gag ctg aac acc 48
Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
  1           5           10          15

gag ctg ctg aac ctg ctg cgt gag cag ttc aac ctg cgt atg cag gct 96
Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
          20           25           30

gca agt ggc cag ctg caa cag tct cac ctg ttg aag caa gtg cgt cgc 144
Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
          35           40           45

gat gtc gca cgc gtt aag act tta ctg aac gag aag gcg ggt gcg taa 192
Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala *
          50           55           60

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<210> 125

<211> 411

<212> DNA

<213> *Escherichia coli*

<220>

<221> CDS

<222> (1) ... (411)

<400> 125

```

atg tta caa cca aag cgt aca aaa ttc cgt aaa atg cac aaa ggc cgt 48
Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
  1           5           10          15

aac cgc ggt ctg gcg cag ggt acg gat gtt agc ttc ggc agc ttc ggt 96
Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
          20           25           30

ctg aaa gct gtt ggc cgt ggt cgt ctg act gcc cgt cag atc gaa gca 144
Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala
          35           40           45

gca cgt cgt gct atg acc cgt gca gtt aag cgt caa ggt aag atc tgg 192
Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
          50           55           60

atc cgt gtg ttc ccg gac aaa ccg atc act gaa aag ccg ctg gca gtg 240
Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val
          65           70           75           80

cgt atg ggt aaa ggt aaa ggt aac gtg gag tat tgg gtt gcc ttg att 288
Arg Met Gly Lys Gly Lys Gly Asn Val Glu Tyr Trp Val Ala Leu Ile
          85           90           95

cag ccg ggt aaa gtc ctg tat gaa atg gac ggt gtt ccg gaa gag ctg 336
Gln Pro Gly Lys Val Leu Tyr Glu Met Asp Gly Val Pro Glu Glu Leu
          100          105          110

gcc cgt gaa gca ttc aag ctg gca gca gcg aaa ctg ccg att aaa acc 384
Ala Arg Glu Ala Phe Lys Leu Ala Ala Ala Lys Leu Pro Ile Lys Thr

```

115 120 125
 acc ttt gta act aag acg gtg atg taa 411
 Thr Phe Val Thr Lys Thr Val Met *
 130 135

<210> 126
 <211> 702
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(702)

<400> 126
 atg ggt cag aaa gta cat cct aat ggt att cgc ctg ggt att gta aaa 48
 Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
 1 5 10 15
 cca tgg aac tct acc tgg ttt gcg aac acc aaa gaa ttc gct gac aac 96
 Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
 20 25 30
 ctg gac agc gat ttt aaa gta cgt cag tac ctg act aag gaa ctg gct 144
 Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
 35 40 45
 aaa gcg tcc gta tct cgt atc gtt atc gag cgt ccg gct aag agc atc 192
 Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
 50 55 60
 cgt gta acc att cac act gct cgc ccg ggt atc gtt atc ggt aaa aaa 240
 Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
 65 70 75 80
 ggt gaa gac gta gaa aaa ctg cgt aag gtc gta gcg gac atc gct ggc 288
 Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly
 85 90 95
 gtt cct gca cag atc aac atc gcc gaa gtt cgt aag cct gaa ctg gac 336
 Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp
 100 105 110
 gca aaa ctg gtt gct gac agc atc act tct cag ctg gaa cgt cgc gtt 384
 Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
 115 120 125
 atg ttc cgt cgt gct atg aag cgt gct gta cag aac gca atg cgt ctg 432
 Met Phe Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
 130 135 140
 ggc gct aaa ggt att aaa gtt gaa gtt agc ggc cgt ctg ggc ggc gcg 480
 Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
 145 150 155 160
 gaa atc gca cgt acc gaa tgg tac cgc gaa ggt cgc gta ccg ctg cac 528
 Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
 165 170 175

act ctg cgt gct gac atc gac tac aac acc tct gaa gcg cac acc act 576
 Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
 180 185 190

tac ggt gta atc ggc gtt aaa gtg tgg atc ttc aaa ggc gag atc ctg 624
 Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
 195 200 205

ggt ggt atg gct gct gtt gaa caa ccg gaa aaa ccg gct gct cag cct 672
 Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
 210 215 220

aaa aag cag cag cgt aaa ggc cgt aaa taa 702
 Lys Lys Gln Gln Arg Lys Gly Arg Lys *
 225 230

<210> 127

<211> 333

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(333)

<400> 127

atg gaa act atc gct aaa cat cgc cat gct cgt tct tct gct cag aag 48
 Met Glu Thr Ile Ala Lys His Arg His Ala Arg Ser Ser Ala Gln Lys
 1 5 10 15

gtt cgc ctt gtt gct gac ctg att cgc ggt aag aaa gtg tcg cag gct 96
 Val Arg Leu Val Ala Asp Leu Ile Arg Gly Lys Lys Val Ser Gln Ala
 20 25 30

ctg gat att ttg acc tac acc aac aag aaa gcg gct gta ctg gtc aag 144
 Leu Asp Ile Leu Thr Tyr Thr Asn Lys Lys Ala Ala Val Leu Val Lys
 35 40 45

aaa gtt ctg gaa tct gcc att gct aac gct gaa cac aac gat ggc gct 192
 Lys Val Leu Glu Ser Ala Ile Ala Asn Ala Glu His Asn Asp Gly Ala
 50 55 60

gac att gac gat ctg aaa gtt acg aaa att ttc gta gac gaa ggc ccg 240
 Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro
 65 70 75 80

agc atg aag cgc att atg ccg cgt gca aaa ggt cgt gca gat cgc atc 288
 Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile
 85 90 95

ctg aag cgc acc agc cac atc act gtg gtt gtg tcc gat cgc tga 333
 Leu Lys Arg Thr Ser His Ile Thr Val Val Val Ser Asp Arg *
 100 105 110

<210> 128

<211> 279

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(279)

<400> 128

atg cca cgt tct ctc aag aaa ggt cct ttt att gac ctg cac ttg ctg	48
Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu	
1 5 10 15	
aag aag gta gag aaa gcg gtg gaa agc gga gac aag aag ccc ctg cgc	96
Lys Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg	
20 25 30	
act tgg tcc cgt cgt tca acg atc ttt cct aac atg atc ggt ttg acc	144
Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr	
35 40 45	
atc gct gtc cat aat ggt cgt cag cac gtt ccg gta ttt gta acc gac	192
Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp	
50 55 60	
gaa atg gtt ggt cac aaa ctg ggt gaa ttc gca ccg act cgt act tat	240
Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr	
65 70 75 80	
cgc ggc cac gct gct gat aaa aaa gcg aag aag aaa taa	279
Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys Lys *	
85 90	

<210> 129

<211> 822

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(822)

<400> 129

atg gca gtt gtt aaa tgt aaa ccg aca tct ccg ggt cgt cgc cac gta	48
Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val	
1 5 10 15	
gtt aaa gtg gtt aac cct gag ctg cac aag ggc aaa cct ttt gct ccg	96
Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro	
20 25 30	
ttg ctg gaa aaa aac agc aaa tcc ggt ggt cgt aac aac aat ggc cgt	144
Leu Leu Glu Lys Asn Ser Lys Ser Gly Arg Asn Asn Asn Gly Arg	
35 40 45	
atc acc act cgt cat atc ggt ggt ggc cac aag cag gct tac cgt att	192
Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile	
50 55 60	
gtt gac ttc aaa cgc aac aaa gac ggt atc ccg gca gtt gtt gaa cgt	240
Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg	
65 70 75 80	


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ctt gag tac gat ccg aac cgt tcc gcg aac atc gcg ctg gtt ctg tac 288
Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr
      85                      90                      95

aaa gac ggt gaa cgc cgt tac atc ctg gcc cct aaa ggc ctg aaa gct 336
Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala
      100                      105                      110

ggc gac cag att cag tct ggc gtt gat gct gca atc aaa cca ggt aac 384
Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn
      115                      120                      125

acc ctg ccg atg cgc aac atc ccg gtt ggt tct act gtt cat aac gta 432
Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val
      130                      135                      140

gaa atg aaa cca ggt aaa ggc ggt cag ctg gca cgt tcc gct ggt act 480
Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr
      145                      150                      155                      160

tac gtt cag atc gtt gct cgt gat ggt gct tat gtc acc ctg cgt ctg 528
Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu
      165                      170                      175

cgt tct ggt gaa atg cgt aaa gta gaa gca gac tgc cgt gca act ctg 576
Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu
      180                      185                      190

ggc gaa gtt ggc aat gct gag cat atg ctg cgc gtt ctg ggt aaa gca 624
Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala
      195                      200                      205

ggg gct gca cgc tgg cgt ggt gtt cgt ccg acc gtt cgc ggt acc gcg 672
Gly Ala Ala Arg Trp Arg Gly Val Arg Pro Thr Val Arg Gly Thr Ala
      210                      215                      220

atg aac ccg gta gac cac cca cat ggt ggt ggt gaa ggt cgt aac ttt 720
Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Arg Asn Phe
      225                      230                      235                      240

ggg aag cac ccg gta act ccg tgg ggc gtt cag acc aaa ggt aag aag 768
Gly Lys His Pro Val Thr Pro Trp Gly Val Gln Thr Lys Gly Lys Lys
      245                      250                      255

acc cgc agc aac aag cgt act gat aaa ttc atc gta cgt cgc cgt agc 816
Thr Arg Ser Asn Lys Arg Thr Asp Lys Phe Ile Val Arg Arg Arg Ser
      260                      265                      270

aaa taa 822
Lys *
```

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<210> 130
<211> 303
<212> DNA
<213> Escherichia coli
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<220>
<221> CDS
<222> (1)...(303)
```

<400> 130

atg att cgt gaa gaa cgt ctg ctg aag gtg ctg cgt gca ccg cac gtt 48
 Met Ile Arg Glu Glu Arg Leu Leu Lys Val Leu Arg Ala Pro His Val
 1 5 10 15

tct gaa aaa gcg tct act gcg atg gaa aaa tcc aac acc atc gta ctc 96
 Ser Glu Lys Ala Ser Thr Ala Met Glu Lys Ser Asn Thr Ile Val Leu
 20 25 30

aaa gtt gct aaa gac gcg acc aaa gca gaa atc aaa gct gct gtg cag 144
 Lys Val Ala Lys Asp Ala Thr Lys Ala Glu Ile Lys Ala Ala Val Gln
 35 40 45

aaa ctg ttt gaa gtc gaa gtc gaa gtc gtt aac acc ctg gta gtt aaa 192
 Lys Leu Phe Glu Val Glu Val Glu Val Val Asn Thr Leu Val Val Lys
 50 55 60

ggg aaa gtt aaa cgt cac gga cag cgt atc ggt cgt cgt agc gac tgg 240
 Gly Lys Val Lys Arg His Gly Gln Arg Ile Gly Arg Arg Ser Asp Trp
 65 70 75 80

aaa aaa gct tac gtc acc ctg aaa gaa ggc cag aat ctg gac ttc gtt 288
 Lys Lys Ala Tyr Val Thr Leu Lys Glu Gly Gln Asn Leu Asp Phe Val
 85 90 95

ggc ggc gct gag taa 303
 Gly Gly Ala Glu *
 100

<210> 131

<211> 606

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(606)

<400> 131

atg gaa tta gta ttg aaa gac gcg cag agc gcg ctg act gtt tcc gaa 48
 Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu
 1 5 10 15

act acc ttc ggt cgt gat ttc aac gaa gcg ctg gtt cac cag gtt gtt 96
 Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val
 20 25 30

gtt gct tat gca gct ggt gct cgt cag ggt act cgt gct cag aag act 144
 Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr
 35 40 45

cgt gct gaa gta act ggt tcc ggt aaa aaa ccg tgg cgc cag aaa ggc 192
 Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly
 50 55 60

acc ggc cgt gcg cgt tct ggt tct atc aag agc ccg atc tgg cgt tct 240
 Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser
 65 70 75 80

```

ggt ggc gtg acc ttt gct gct cgt ccg cag gac cac agt caa aaa gtt 288
Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val
      85                      90                      95

aac aag aag atg tac cgc ggc gcg ctg aaa agc atc ctg tcc gaa ctg 336
Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu
      100                      105                      110

gta cgt cag gat cgt ctg atc gtt gtc gag aag ttc tct gta gaa gcg 384
Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala
      115                      120                      125

ccg aaa act aag ctg ctg gca cag aaa ctg aaa gac atg gct ctg gaa 432
Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu
      130                      135                      140

gat gtg ctg atc atc acc ggt gag ctg gac gaa aac ctg ttc ctg gct 480
Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala
      145                      150                      155                      160

gcg cgc aac ctg cac aag gtt gac gta cgc gat gca act ggt atc gac 528
Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp
      165                      170                      175

ccg gtt agc ctg atc gcc ttc gac aaa gtc gta atg act gct gat gct 576
Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
      180                      185                      190

ggt aag caa gtt gag gag atg ctg gca tga 606
Val Lys Gln Val Glu Glu Met Leu Ala *
      195                      200

```

<210> 132

<211> 630

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(630)

<400> 132

```

atg att ggt tta gtc ggt aaa aaa gtg ggt atg acc cgt atc ttc aca 48
Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr
      1                      5                      10                      15

gaa gac ggc gtt tct atc cca gta acc gta atc gaa gtt gaa gca aac 96
Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
      20                      25                      30

cgc gtt act cag gtt aaa gac ctg gct aac gat ggc tac cgt gct att 144
Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
      35                      40                      45

cag gtg acc acc ggt gct aaa aaa gct aac cgt gtg acc aag cct gaa 192
Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
      50                      55                      60

gct ggc cac ttc gct aaa gct ggc gta gaa gct ggc cgt ggt ctg tgg 240
Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp

```

65	70	75	80	
gaa ttc cgc ctg gct gaa ggc gaa gag ttc act gta ggt cag agc att	288			
Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile				
85	90	95		
agc gtt gaa ctg ttt gct gac gtt aaa aaa gtt gac gta act ggc acc	336			
Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr				
100	105	110		
tct aaa ggt aaa ggt ttc gca ggt acc gtt aag cgc tgg aac ttc cgt	384			
Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg				
115	120	125		
acc cag gac gct act cac ggt aac tcc ttg tct cac cgc gtt ccg ggt	432			
Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly				
130	135	140		
tct atc ggt cag aac cag act ccg ggc aaa gtg ttc aaa ggc aag aaa	480			
Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys				
145	150	155	160	
atg gca ggt cag atg ggt aac gaa cgt gta acc gtt cag agc ctt gac	528			
Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp				
165	170	175		
gta gta cgc gtt gac gct gag cgc aac ctg ctg ctg gtt aaa ggt gct	576			
Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala				
180	185	190		
gtc ccg ggt gca acc ggt agc gac ctg atc gtt aaa cca gct gtg aag	624			
Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys				
195	200	205		
gcg taa				630
Ala *				

<210> 133

<211> 312

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(312)

<400> 133

atg cag aac caa aga atc cgt atc cgc ctg aaa gcg ttt gat cat cgt	48
Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg	
1	5
10	15

ctg atc gat caa gca acc gcg gaa atc gtc gag act gcc aag cgc act	96
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr	
20	25
30	

ggc gcg cag gtc cgt ggt ccg atc ccg ctg ccg aca cgc aaa gag cgc	144
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg	
35	40
45	

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ttc act gtt ctg atc tcc ccg cac gtc aac aaa gac gcg cgc gat cag 192
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
   50                55                60

tac gaa atc cgt act cac ttg cgt ctg gtt gac atc gtt gag cca acc 240
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
   65                70                75                80

gag aaa acc gtt gat gct ctg atg cgt ctg gat ctg gct gcc ggt gta 288
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
                85                90                95

gac gtg cag atc agc ctg ggt taa 312
Asp Val Gln Ile Ser Leu Gly *
                100

```

<210> 134
 <211> 315
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(315)

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<400> 134
atg atc cgc aaa gcc ttt gtc atg cag gta aac ccc gac gcc cac gaa 48
Met Ile Arg Lys Ala Phe Val Met Gln Val Asn Pro Asp Ala His Glu
   1                5                10                15

gag tat cag cgt cgg cat aat ccc atc tgg cca gaa ctg gaa gca gtg 96
Glu Tyr Gln Arg Arg His Asn Pro Ile Trp Pro Glu Leu Glu Ala Val
                20                25                30

ctg aaa tct cac ggt gcg cat aac tac gcc atc tat ctc gac aaa gcg 144
Leu Lys Ser His Gly Ala His Asn Tyr Ala Ile Tyr Leu Asp Lys Ala
                35                40                45

cgt aat ctg ctg ttt gcc atg gta gag att gaa tct gaa gaa cgc tgg 192
Arg Asn Leu Leu Phe Ala Met Val Glu Ile Glu Ser Glu Glu Arg Trp
   50                55                60

aat gcg gtt gcc agc act gat gtt tgc caa cgt tgg tgg aaa tat atg 240
Asn Ala Val Ala Ser Thr Asp Val Cys Gln Arg Trp Trp Lys Tyr Met
   65                70                75                80

acc gat gtt atg ccc gct aac ccg gat aac agc ccg gtg agt agc gag 288
Thr Asp Val Met Pro Ala Asn Pro Asp Asn Ser Pro Val Ser Ser Glu
                85                90                95

ctg caa gaa gtg ttt tac ctg ccg taa 315
Leu Gln Glu Val Phe Tyr Leu Pro *
                100

```

<210> 135
 <211> 864
 <212> DNA
 <213> Escherichia coli

<220>

<221> CDS

<222> (1)...(864)

<400> 135

atg atc cgc agt atg acc gcc tac gcc cgg cgt gaa atc aag ggt gaa	48
Met Ile Arg Ser Met Thr Ala Tyr Ala Arg Arg Glu Ile Lys Gly Glu	
1 5 10 15	
tgg ggg agc gca acc tgg gaa atg cgc tcg gta aac cag cgt tat ctg	96
Trp Gly Ser Ala Thr Trp Glu Met Arg Ser Val Asn Gln Arg Tyr Leu	
20 25 30	
gaa act tac ttt cgt ctg ccg gag cag ttc cgt agc ctt gaa cct gtc	144
Glu Thr Tyr Phe Arg Leu Pro Glu Gln Phe Arg Ser Leu Glu Pro Val	
35 40 45	
gtt cgc gag cgt att cgt tct cgc ctg acg cgc ggt aaa gtg gaa tgt	192
Val Arg Glu Arg Ile Arg Ser Arg Leu Thr Arg Gly Lys Val Glu Cys	
50 55 60	
acc ctg cgc tat gag cca gat gtt agc gcg caa ggt gag ctg atc ctc	240
Thr Leu Arg Tyr Glu Pro Asp Val Ser Ala Gln Gly Glu Leu Ile Leu	
65 70 75 80	
aac gaa aaa ctg gct aaa cag ctg gta act gcc gcg aac tgg gta aaa	288
Asn Glu Lys Leu Lys Gln Leu Val Thr Ala Ala Asn Trp Val Lys	
85 90 95	
atg cag agt gac gaa ggg gaa atc aac ccg gtt gat att cta cgc tgg	336
Met Gln Ser Asp Glu Gly Glu Ile Asn Pro Val Asp Ile Leu Arg Trp	
100 105 110	
ccg ggc gtg atg gca gcc cag gag cag gat ctt gac gcc att gcc gct	384
Pro Gly Val Met Ala Ala Gln Glu Gln Asp Leu Asp Ala Ile Ala Ala	
115 120 125	
gaa att ctc gcg gcg ctg gat ggt acg ctg gac gac ttt att gtc gcg	432
Glu Ile Leu Ala Ala Leu Asp Gly Thr Leu Asp Asp Phe Ile Val Ala	
130 135 140	
cgc gaa acc gaa ggt cag gca ctg aaa gca ttg atc gag cag cgt ctg	480
Arg Glu Thr Glu Gly Gln Ala Leu Lys Ala Leu Ile Glu Gln Arg Leu	
145 150 155 160	
gaa ggc gtc acc gcc gaa gtg gtc aaa gtc cgc tcc cat atg ccg gaa	528
Glu Gly Val Thr Ala Glu Val Val Lys Val Arg Ser His Met Pro Glu	
165 170 175	
atc ctg caa tgg cag cgt gag cgt ctg gtc gcg aag ctg gaa gat gct	576
Ile Leu Gln Trp Gln Arg Glu Arg Leu Val Ala Lys Leu Glu Asp Ala	
180 185 190	
cag gtg caa ctg gaa aac aac cgt ctg gag cag gaa ctg gtt ctg ctg	624
Gln Val Gln Leu Glu Asn Asn Arg Leu Glu Gln Glu Leu Val Leu Leu	
195 200 205	
gca caa cga att gac gtt gcc gaa gaa ctg gat cgc ctc gaa gcg cat	672
Ala Gln Arg Ile Asp Val Ala Glu Glu Leu Asp Arg Leu Glu Ala His	
210 215 220	

gtc aaa gag acc tac aac att ctg aag aaa aaa gaa gcg gtt ggt cgt 720
 Val Lys Glu Thr Tyr Asn Ile Leu Lys Lys Lys Glu Ala Val Gly Arg
 225 230 235 240

cgt ctg gat ttt atg atg cag gag ttc aac cgc gag tcg aac act ctt 768
 Arg Leu Asp Phe Met Met Gln Glu Phe Asn Arg Glu Ser Asn Thr Leu
 245 250 255

gcg tcg aag tct atc aat gcc gaa gtg aca aac tcc gcc atc gag ctg 816
 Ala Ser Lys Ser Ile Asn Ala Glu Val Thr Asn Ser Ala Ile Glu Leu
 260 265 270

aaa gtg ttg att gag cag atg cgc gag cag att cag aac atc gaa taa 864
 Lys Val Leu Ile Glu Gln Met Arg Glu Gln Ile Gln Asn Ile Glu *
 275 280 285

<210> 136

<211> 492

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(492)

<400> 136

atg agc aca gaa aca att gaa ata ttc aat aat agt gat gaa tgg gca 48
 Met Ser Thr Glu Thr Ile Glu Ile Phe Asn Asn Ser Asp Glu Trp Ala
 1 5 10 15

aat caa cta aaa cac gca tta tcg aaa gga gaa aat ctg gca tta cta 96
 Asn Gln Leu Lys His Ala Leu Ser Lys Gly Glu Asn Leu Ala Leu Leu
 20 25 30

cat ggt tta act cct gat atc ctt gat aga ata tat gca tat gca ttc 144
 His Gly Leu Thr Pro Asp Ile Leu Asp Arg Ile Tyr Ala Tyr Ala Phe
 35 40 45

gac tac cat gaa aag ggt aat ata acg gac gca gaa att tat tat aaa 192
 Asp Tyr His Glu Lys Gly Asn Ile Thr Asp Ala Glu Ile Tyr Tyr Lys
 50 55 60

ttc ttg tgc att tat gcg ttc gaa aat cat gag tat cta aaa gat ttt 240
 Phe Leu Cys Ile Tyr Ala Phe Glu Asn His Glu Tyr Leu Lys Asp Phe
 65 70 75 80

gca tca gta tgt cag ccc aaa aag aaa tat caa caa gca tat gac ctt 288
 Ala Ser Val Cys Gln Pro Lys Lys Lys Tyr Gln Gln Ala Tyr Asp Leu
 85 90 95

tac aaa cta agt tac aat tac ttc ccg tat gat gac tat tca gtt att 336
 Tyr Lys Leu Ser Tyr Asn Tyr Phe Pro Tyr Asp Asp Tyr Ser Val Ile
 100 105 110

tat cgt atg ggt caa tgt cag att ggg gct aaa aat atc gat aac gca 384
 Tyr Arg Met Gly Gln Cys Gln Ile Gly Ala Lys Asn Ile Asp Asn Ala
 115 120 125

atg caa tgt ttc tat cac att att aac aat tgt gag gat gat agt gtt 432

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Met Gln Cys Phe Tyr His Ile Ile Asn Asn Cys Glu Asp Asp Ser Val
  130                               135                               140

aag agt aaa gcg cag gca tat att gaa ctc tta aac gat aat tca gaa 480
Lys Ser Lys Ala Gln Ala Tyr Ile Glu Leu Leu Asn Asp Asn Ser Glu
145                               150                               155                               160

gat aat ggc taa 492
Asp Asn Gly *

<210> 137
<211> 1947
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1947)

<400> 137
atg aat att tta ggt ttt ttc cag cga ctc ggt agg gcg tta cag ctc 48
Met Asn Ile Leu Gly Phe Phe Gln Arg Leu Gly Arg Ala Leu Gln Leu
  1                               5                               10                               15

cct atc gcg gtg ctg ccg gtg gcg gca ctg ttg ctg cga ttc ggt cag 96
Pro Ile Ala Val Leu Pro Val Ala Ala Leu Leu Leu Arg Phe Gly Gln
  20                               25                               30

cca gat tta ctt aac gtt gcg ttt att gcc cag gcg ggc ggt gcg att 144
Pro Asp Leu Leu Asn Val Ala Phe Ile Ala Gln Ala Gly Gly Ala Ile
  35                               40                               45

ttt gat aac ctc gca tta atc ttc gcc atc ggt gtg gca tcc agc tgg 192
Phe Asp Asn Leu Ala Leu Ile Phe Ala Ile Gly Val Ala Ser Ser Trp
  50                               55                               60

tcg aaa gac agc gct ggt gcg gcg gcg ctg gcg ggt gcg gta ggt tac 240
Ser Lys Asp Ser Ala Gly Ala Ala Ala Leu Ala Gly Ala Val Gly Tyr
  65                               70                               75                               80

ttt gtg tta acc aaa gcg atg gtg acc atc aac cca gaa att aac atg 288
Phe Val Leu Thr Lys Ala Met Val Thr Ile Asn Pro Glu Ile Asn Met
  85                               90                               95

ggt gta ctg gcg ggt atc att acc ggt ctg gtt ggt ggc gca gcc tat 336
Gly Val Leu Ala Gly Ile Ile Thr Gly Leu Val Gly Gly Ala Ala Tyr
  100                              105                              110

aac cgt tgg tcc gat att aaa ctg ccg gac ttc ctg agc ttc ttc ggc 384
Asn Arg Trp Ser Asp Ile Lys Leu Pro Asp Phe Leu Ser Phe Phe Gly
  115                              120                              125

ggc aaa cgc ttt gtg ccg att gcc acc gga ttc ttc tgc ctg gtg ctg 432
Gly Lys Arg Phe Val Pro Ile Ala Thr Gly Phe Phe Cys Leu Val Leu
  130                              135                              140

gcg gcc att ttt ggt tac gtc tgg ccg ccg gta cag cac gct atc cat 480
Ala Ala Ile Phe Gly Tyr Val Trp Pro Pro Val Gln His Ala Ile His
145                              150                              155                              160

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gca ggc ggc gag tgg atc gtt tct gcg ggc gcg ctg ggt tcc ggt atc	528
Ala Gly Gly Glu Trp Ile Val Ser Ala Gly Ala Leu Gly Ser Gly Ile	
165 170 175	
ttt ggt ttc atc aac cgt ctg ctg atc cca acc ggt ctg cat cag gta	576
Phe Gly Phe Ile Asn Arg Leu Leu Ile Pro Thr Gly Leu His Gln Val	
180 185 190	
ctg aac acc atc gcc tgg ttc cag att ggt gaa ttc acc aac gcg gcg	624
Leu Asn Thr Ile Ala Trp Phe Gln Ile Gly Glu Phe Thr Asn Ala Ala	
195 200 205	
ggt acg gtt ttc cac ggt gac att aac cgc ttc tat gcc ggt gac ggc	672
Gly Thr Val Phe His Gly Asp Ile Asn Arg Phe Tyr Ala Gly Asp Gly	
210 215 220	
acc gcg ggg atg ttc atg tcc ggc ttc ttc ccg atc atg atg ttc ggt	720
Thr Ala Gly Met Phe Met Ser Gly Phe Phe Pro Ile Met Met Phe Gly	
225 230 235 240	
ctg ccg ggt gcg gcg ctg gcg atg tac ttc gca gca ccg aaa gag cgt	768
Leu Pro Gly Ala Ala Leu Ala Met Tyr Phe Ala Ala Pro Lys Glu Arg	
245 250 255	
cgt ccg atg gtt ggc ggt atg ctg ctt tct gtt gct gtt act gcg ttc	816
Arg Pro Met Val Gly Gly Met Leu Leu Ser Val Ala Val Thr Ala Phe	
260 265 270	
ctg acc ggt gtg act gag ccg ctg gaa ttc ctg ttc atg ttc ctt gct	864
Leu Thr Gly Val Thr Glu Pro Leu Glu Phe Leu Phe Met Phe Leu Ala	
275 280 285	
ccg ctg ctg tac ctc ctg cac gca ctg ctg acc ggt atc agc ctg ttt	912
Pro Leu Leu Tyr Leu Leu His Ala Leu Leu Thr Gly Ile Ser Leu Phe	
290 295 300	
gtg gca acg ctg ctg ggt atc cac gcg ggc ttc tct ttc tct gcg ggg	960
Val Ala Thr Leu Leu Gly Ile His Ala Gly Phe Ser Phe Ser Ala Gly	
305 310 315 320	
gct atc gac tac gcg ttg atg tat aac ctg ccg gcc gcc agc cag aac	1008
Ala Ile Asp Tyr Ala Leu Met Tyr Asn Leu Pro Ala Ala Ser Gln Asn	
325 330 335	
gtc tgg atg ctg ctg gtg atg ggc gtt atc ttc ttc gct atc tac ttc	1056
Val Trp Met Leu Leu Val Met Gly Val Ile Phe Phe Ala Ile Tyr Phe	
340 345 350	
gtg gtg ttc agt ttg gtt atc cgc atg ttc aac ctg aaa acg ccg ggt	1104
Val Val Phe Ser Leu Val Ile Arg Met Phe Asn Leu Lys Thr Pro Gly	
355 360 365	
cgt gaa gat aaa gaa gac gag atc gtt act gaa gaa gcc aac agc aac	1152
Arg Glu Asp Lys Glu Asp Glu Ile Val Thr Glu Glu Ala Asn Ser Asn	
370 375 380	
act gaa gaa ggt ctg act caa ctg gca acc aac tat att gct gcg gtt	1200
Thr Glu Glu Gly Leu Thr Gln Leu Ala Thr Asn Tyr Ile Ala Ala Val	
385 390 395 400	

ggc ggc act gac aac ctg aaa gcg att gac gcc tgt atc acc cgt ctg	1248
Gly Gly Thr Asp Asn Leu Lys Ala Ile Asp Ala Cys Ile Thr Arg Leu	
405 410 415	
cgc ctt aca gtg gct gac tct gcc cgc gtt aac gat acg atg tgt aaa	1296
Arg Leu Thr Val Ala Asp Ser Ala Arg Val Asn Asp Thr Met Cys Lys	
420 425 430	
cgt ctg ggt gct tct ggg gta gtg aaa ctg aac aaa cag act att cag	1344
Arg Leu Gly Ala Ser Gly Val Val Lys Leu Asn Lys Gln Thr Ile Gln	
435 440 445	
gtg att gtt ggc gcg aaa gca gaa tcc atc ggc gat gcg atg aag aaa	1392
Val Ile Val Gly Ala Lys Ala Glu Ser Ile Gly Asp Ala Met Lys Lys	
450 455 460	
gtc gtt gcc cgt ggt ccg gta gcc gct gcg tca gct gaa gca act ccg	1440
Val Val Ala Arg Gly Pro Val Ala Ala Ala Ser Ala Glu Ala Thr Pro	
465 470 475 480	
gca act gcc gcg cct gta gca aaa ccg cag gct gta cca aac gcg gta	1488
Ala Thr Ala Ala Pro Val Ala Lys Pro Gln Ala Val Pro Asn Ala Val	
485 490 495	
tct atc gcg gag ctg gta tcc ccg att acc ggt gat gtc gtg gca ctg	1536
Ser Ile Ala Glu Leu Val Ser Pro Ile Thr Gly Asp Val Val Ala Leu	
500 505 510	
gat cag gtt cct gac gaa gca ttc gcc agc aaa gcg gtg ggt gac ggt	1584
Asp Gln Val Pro Asp Glu Ala Phe Ala Ser Lys Ala Val Gly Asp Gly	
515 520 525	
gtg gcg gtg aaa ccg aca gat aaa atc gtc gta tca cca gcc gca ggg	1632
Val Ala Val Lys Pro Thr Asp Lys Ile Val Val Ser Pro Ala Ala Gly	
530 535 540	
aca atc gtg aaa atc ttc aac acc aac cac gcg ttc tgc ctg gaa acc	1680
Thr Ile Val Lys Ile Phe Asn Thr Asn His Ala Phe Cys Leu Glu Thr	
545 550 555 560	
gaa aaa ggc gcg gag atc gtc gtc cat atg ggt atc gac acc gta gcg	1728
Glu Lys Gly Ala Glu Ile Val Val His Met Gly Ile Asp Thr Val Ala	
565 570 575	
ctg gaa ggt aaa ggc ttt aaa cgt ctg gtg gaa gag ggt gcg cag gta	1776
Leu Glu Gly Lys Gly Phe Lys Arg Leu Val Glu Glu Gly Ala Gln Val	
580 585 590	
agc gca ggg caa ccg att ctg gaa atg gat ctg gat tac ctg aac gct	1824
Ser Ala Gly Gln Pro Ile Leu Glu Met Asp Leu Asp Tyr Leu Asn Ala	
595 600 605	
aac gcc cgc tcc atg att agc ccg gtg gtt tgc agc aat atc gac gat	1872
Asn Ala Arg Ser Met Ile Ser Pro Val Val Cys Ser Asn Ile Asp Asp	
610 615 620	
ttc agt ggc ttg atc att aaa gct cag ggc cat att gtg gcg ggt caa	1920
Phe Ser Gly Leu Ile Ile Lys Ala Gln Gly His Ile Val Ala Gly Gln	
625 630 635 640	
aca ccg ctg tat gaa atc aaa aag taa	1947

Thr Pro Leu Tyr Glu Ile Lys Lys *
645

<210> 138
<211> 1239
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1239)

<400> 138
atg aag act atc ttc agg tac att ctt ttt tta gca ctg tat tct tgt 48
Met Lys Thr Ile Phe Arg Tyr Ile Leu Phe Leu Ala Leu Tyr Ser Cys
1 5 10 15
tgt aat aca gtc agt gca tat aca agt ttt att gtg gga aat aat gca 96
Cys Asn Thr Val Ser Ala Tyr Thr Ser Phe Ile Val Gly Asn Asn Ala
20 25 30
gga gtt gat aac tat cga ggc ccc tcc act gcc gca cag atg acc ttt 144
Gly Val Asp Asn Tyr Arg Gly Pro Ser Thr Ala Ala Gln Met Thr Phe
35 40 45
aat tac aca tca aca gca agc aac ttg gtt ttt tat aaa ccc acg cag 192
Asn Tyr Thr Ser Thr Ala Ser Asn Leu Val Phe Tyr Lys Pro Thr Gln
50 55 60
ctc ggc ccg act ggg gta aaa atg tac tgg tca tac ctg gat aca ggt 240
Leu Gly Pro Thr Gly Val Lys Met Tyr Trp Ser Tyr Leu Asp Thr Gly
65 70 75 80
acc ggt ggt ggt att ctt tac tgc aat aca tct ggc aga gcg aat cct 288
Thr Gly Gly Gly Ile Leu Tyr Cys Asn Thr Ser Gly Arg Ala Asn Pro
85 90 95
ggt cca ata act att gaa aat gcc atg gtc tat tca ggt aaa gat tat 336
Gly Pro Ile Thr Ile Glu Asn Ala Met Val Tyr Ser Gly Lys Asp Tyr
100 105 110
ggc gga cat aaa cta ttt aat aca tct gtt cct ggt ctg tat tac acc 384
Gly Gly His Lys Leu Phe Asn Thr Ser Val Pro Gly Leu Tyr Tyr Thr
115 120 125
atg tta ata tca agg gtc tgg tct gca tac gat aca ata act gac att 432
Met Leu Ile Ser Arg Val Trp Ser Ala Tyr Asp Thr Ile Thr Asp Ile
130 135 140
caa tcg cca gga atc tat atc gga gat cct tcc aac caa gaa ttt ttc 480
Gln Ser Pro Gly Ile Tyr Ile Gly Asp Pro Ser Asn Gln Glu Phe Phe
145 150 155 160
ttt tcc gtc aca gac agc gat cta caa act aag ggt tgc aac aaa gca 528
Phe Ser Val Thr Asp Ser Asp Leu Gln Thr Lys Gly Cys Asn Lys Ala
165 170 175
gac gac tac gat aag ttt tgg gct att ggt ggt ata gta cac aac ata 576
Asp Asp Tyr Asp Lys Phe Trp Ala Ile Gly Gly Ile Val His Asn Ile
180 185 190

```

act gtt gaa ttt tat aca gat act aat ttc gat cct aca ctt aat cag 624
Thr Val Glu Phe Tyr Thr Asp Thr Asn Phe Asp Pro Thr Leu Asn Gln
      195                200                205

caa gtc cag tta tcc agt tca tca aat tac ctt tat tcg ttt aag gcc 672
Gln Val Gln Leu Ser Ser Ser Ser Asn Tyr Leu Tyr Ser Phe Lys Ala
      210                215                220

tac agt cct ggt aca aaa gtt gta gat cac agc aac cac att tat gtc 720
Tyr Ser Pro Gly Thr Lys Val Val Asp His Ser Asn His Ile Tyr Val
      225                230                235                240

aat ttc aca ctg aat aat gtc aaa tta acc tta cca aca tgt ttt acc 768
Asn Phe Thr Leu Asn Asn Val Lys Leu Thr Leu Pro Thr Cys Phe Thr
      245                250                255

tcc ata ctt acc ggg cca tca gtc aat ggt tca acg gtt aga atg gga 816
Ser Ile Leu Thr Gly Pro Ser Val Asn Gly Ser Thr Val Arg Met Gly
      260                265                270

gaa tat agc tct ggg aca att aaa aat ggc gct tca cct gtt ccc ttt 864
Glu Tyr Ser Ser Gly Thr Ile Lys Asn Gly Ala Ser Pro Val Pro Phe
      275                280                285

gat atc tcg ctt cag aat tgt att cgt gtg cgt aat att gaa aca aaa 912
Asp Ile Ser Leu Gln Asn Cys Ile Arg Val Arg Asn Ile Glu Thr Lys
      290                295                300

ctc gtc act gga aaa gta ggt act caa aac aca caa ctg ctt ggt aat 960
Leu Val Thr Gly Lys Val Gly Thr Gln Asn Thr Gln Leu Leu Gly Asn
      305                310                315                320

acg ctt act gga agc act gcc gcc aaa ggc gtt ggc gta ctc att gaa 1008
Thr Leu Thr Gly Ser Thr Ala Ala Lys Gly Val Gly Val Leu Ile Glu
      325                330                335

ggg tta gca acc agt aaa aat ccg cta atg aca tta aaa cct aat gat 1056
Gly Leu Ala Thr Ser Lys Asn Pro Leu Met Thr Leu Lys Pro Asn Asp
      340                345                350

acg aat tct gtt tat ata gat tat gaa acc gaa gat gac acc tcc gat 1104
Thr Asn Ser Val Tyr Ile Asp Tyr Glu Thr Glu Asp Asp Thr Ser Asp
      355                360                365

ggg gtt tac cct aat caa ggt aac ggc aca tca cag cct ctt cat ttc 1152
Gly Val Tyr Pro Asn Gln Gly Asn Gly Thr Ser Gln Pro Leu His Phe
      370                375                380

cag gca aca tta aag caa gac ggg aat att gct atc gaa ccc ggc gaa 1200
Gln Ala Thr Leu Lys Gln Asp Gly Asn Ile Ala Ile Glu Pro Gly Glu
      385                390                395                400

ttt aaa gcc acc agt act ttc cag gta acc tat ccc tga 1239
Phe Lys Ala Thr Ser Thr Phe Gln Val Thr Tyr Pro *
      405                410

```

<210> 139

<211> 597

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(597)

<400> 139

```

atg cat ccc act caa cgt aag ctg atg aag aga ata att ctg ttt ctg 48
Met His Pro Thr Gln Arg Lys Leu Met Lys Arg Ile Ile Leu Phe Leu
  1           5           10           15

tca tta ctg ttt tgc atc gcc tgt cca gcc att gct gga cag gat att 96
Ser Leu Leu Phe Cys Ile Ala Cys Pro Ala Ile Ala Gly Gln Asp Ile
          20           25           30

gac ctt gtt gcc aat gta aaa aac agc acc tgc aaa agc gga atc agt 144
Asp Leu Val Ala Asn Val Lys Asn Ser Thr Cys Lys Ser Gly Ile Ser
          35           40           45

aac cag ggt aat att gat ctt ggc gtc gtt ggg gtg gga tat ttt tca 192
Asn Gln Gly Asn Ile Asp Leu Gly Val Val Gly Val Gly Tyr Phe Ser
          50           55           60

ggg aat gtt act cct gaa agt tat caa cca ggt gga aaa gag ttc act 240
Gly Asn Val Thr Pro Glu Ser Tyr Gln Pro Gly Gly Lys Glu Phe Thr
          65           70           75           80

atc act gta tcc gac tgt gca tta cag gga act ggc gat gtg cta aat 288
Ile Thr Val Ser Asp Cys Ala Leu Gln Gly Thr Gly Asp Val Leu Asn
          85           90           95

cag tta cat att gat ttt aga gcc ctt agc ggt gtc atg gct gct ggc 336
Gln Leu His Ile Asp Phe Arg Ala Leu Ser Gly Val Met Ala Ala Gly
          100          105          110

tct agg caa ata ttt gct aat gaa att tcg tca gga gca agt aat gta 384
Ser Arg Gln Ile Phe Ala Asn Glu Ile Ser Ser Gly Ala Ser Asn Val
          115          120          125

gga gta gtt ata ttt tct act cag gat tcg gcg aat aca ttc aat gtt 432
Gly Val Val Ile Phe Ser Thr Gln Asp Ser Ala Asn Thr Phe Asn Val
          130          135          140

ctt aat gct tca ggc gga tct cgt tcc gtt tat cca gta atg tcg gat 480
Leu Asn Ala Ser Gly Gly Ser Arg Ser Val Tyr Pro Val Met Ser Asp
          145          150          155          160

gac atg aat ggt tca tcc tgg aaa ttt agc acc cga atg caa aaa atc 528
Asp Met Asn Gly Ser Ser Trp Lys Phe Ser Thr Arg Met Gln Lys Ile
          165          170          175

gat cct gca ttg agt gtt aca tct ggt caa ctt atg agc cat gtg tta 576
Asp Pro Ala Leu Ser Val Thr Ser Gly Gln Leu Met Ser His Val Leu
          180          185          190

gtg gat att tac tac gaa taa 597
Val Asp Ile Tyr Tyr Glu *
          195

```

<210> 140

<211> 606

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(606)

<400> 140

```

atg atg aca ttt aaa aat tta cgt tat gga tta tcc agc agt gtc gtt 48
Met Met Thr Phe Lys Asn Leu Arg Tyr Gly Leu Ser Ser Ser Val Val
  1             5             10             15

ttg gct gcc tca ttg ttc agc gta ctc tct tat gcg gca aca gac agt 96
Leu Ala Ala Ser Leu Phe Ser Val Leu Ser Tyr Ala Ala Thr Asp Ser
             20             25             30

att gga ctg acc gtt att act act gta gaa atg ggt act tgt acc gct 144
Ile Gly Leu Thr Val Ile Thr Thr Val Glu Met Gly Thr Cys Thr Ala
             35             40             45

aca tta gta aat gac tct gat cag gac att tct gtt gtt gat ttt ggt 192
Thr Leu Val Asn Asp Ser Asp Gln Asp Ile Ser Val Val Asp Phe Gly
             50             55             60

gat gta tat att tct gaa atc aat gcc aag acc aaa gta aaa aca ttc 240
Asp Val Tyr Ile Ser Glu Ile Asn Ala Lys Thr Lys Val Lys Thr Phe
             65             70             75             80

aaa ctc aaa ttc aaa gac tgt gcg ggt atc ccc aat aaa aaa gcg caa 288
Lys Leu Lys Phe Lys Asp Cys Ala Gly Ile Pro Asn Lys Lys Ala Gln
             85             90             95

ata aaa tta acc aag cga gcc aca tgc gag gga act gct aat gac ggt 336
Ile Lys Leu Thr Lys Arg Ala Thr Cys Gly Thr Ala Asn Asp Gly
             100             105             110

gcg ggg ttt gca aat ggt tcc aca gcc gca gat aaa gca agt gct gtc 384
Ala Gly Phe Ala Asn Gly Ser Thr Ala Ala Asp Lys Ala Ser Ala Val
             115             120             125

gcc gtt gaa gtc tgg agc act gta act ccg gca aca ggg agt gca aca 432
Ala Val Glu Val Trp Ser Thr Val Thr Pro Ala Thr Gly Ser Ala Thr
             130             135             140

caa ttt agc tgt gta aca cca gca tca caa gag gta aca atc tcc act 480
Gln Phe Ser Cys Val Thr Pro Ala Ser Gln Glu Val Thr Ile Ser Thr
             145             150             155             160

gca gcc aat gcg gtc gtt tat tat ccg atg agt gca cgc ctg gtc gtg 528
Ala Ala Asn Ala Val Val Tyr Tyr Pro Met Ser Ala Arg Leu Val Val
             165             170             175

gaa aaa aat aaa acc gta aac aat gtc act gcg ggt aag ttt tct gca 576
Glu Lys Asn Lys Thr Val Asn Asn Val Thr Ala Gly Lys Phe Ser Ala
             180             185             190

cca gcc aca ttt aca gta acc tat aac taa 606
Pro Ala Thr Phe Thr Val Thr Tyr Asn *
             195             200

```

<210> 141

<211> 612

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (612)

<400> 141

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atg gaa ttc ggt gtc aga ttc agt aac tac aag gga cgt caa atg ata 48
Met Glu Phe Gly Val Arg Phe Ser Asn Tyr Lys Gly Arg Gln Met Ile
  1             5             10             15

aaa aca acg cca cat aaa ata gtg ata ctg atg gga ata tta tta tca 96
Lys Thr Thr Pro His Lys Ile Val Ile Leu Met Gly Ile Leu Leu Ser
          20             25             30

ccc tca gta ttt gca acg gat att aat gta gag ttt aca gcc act gtc 144
Pro Ser Val Phe Ala Thr Asp Ile Asn Val Glu Phe Thr Ala Thr Val
          35             40             45

aaa gcg aca acc tgt aac atc aca ctt act ggt aat aac gtc acg aat 192
Lys Ala Thr Thr Cys Asn Ile Thr Leu Thr Gly Asn Asn Val Thr Asn
          50             55             60

gat ggc aat aat aac tac aca ttg aga atc cct aag atg ggt ctg gat 240
Asp Gly Asn Asn Asn Tyr Thr Leu Arg Ile Pro Lys Met Gly Leu Asp
          65             70             75             80

aag atc gcg aat aaa acg aca gaa tct cag gct gat ttt aaa ctg gtt 288
Lys Ile Ala Asn Lys Thr Thr Glu Ser Gln Ala Asp Phe Lys Leu Val
          85             90             95

gcc agt ggg tgc agc agt ggc atc agt tgg att gat acc act ctg acc 336
Ala Ser Gly Cys Ser Ser Gly Ile Ser Trp Ile Asp Thr Thr Leu Thr
          100             105             110

gga aat gca tca tca agc tca cct aag ctt att ata ccg cag tct ggt 384
Gly Asn Ala Ser Ser Ser Ser Pro Lys Leu Ile Ile Pro Gln Ser Gly
          115             120             125

gat tca tct tcg acg aca agt aat atc ggt atg ggt ttc aaa aaa cgg 432
Asp Ser Ser Ser Thr Thr Ser Asn Ile Gly Met Gly Phe Lys Lys Arg
          130             135             140

act act gat gat gcc act ttc ctt aaa cct aac agt gcg gaa aag ata 480
Thr Thr Asp Asp Ala Thr Phe Leu Lys Pro Asn Ser Ala Glu Lys Ile
          145             150             155             160

cgc tgg agc aca gac gag atg cag ccc gat aag ggt ctt gaa atg acc 528
Arg Trp Ser Thr Asp Glu Met Gln Pro Asp Lys Gly Leu Glu Met Thr
          165             170             175

gtt gcg cta cgt gaa aca gat gca ggg caa ggc gta ccg ggg aat ttt 576
Val Ala Leu Arg Glu Thr Asp Ala Gly Gln Gly Val Pro Gly Asn Phe
          180             185             190

cgt gca ctg gcg acg ttt aat ttc atc tat caa taa 612
Arg Ala Leu Ala Thr Phe Asn Phe Ile Tyr Gln *
```

195

200

<210> 142
 <211> 420
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(420)

<400> 142
 atg gca atg act tac cac ctg gac gtc gtc agc gca gag caa caa atg 48
 Met Ala Met Thr Tyr His Leu Asp Val Val Ser Ala Glu Gln Gln Met
 1 5 10 15
 ttc tct ggt ctg gtc gag aaa atc cag gta acg ggt agc gaa ggt gaa 96
 Phe Ser Gly Leu Val Glu Lys Ile Gln Val Thr Gly Ser Glu Gly Glu
 20 25 30
 ctg ggg atc tac cct ggc cac gca ccg ctg ctc acc gcc att aag cct 144
 Leu Gly Ile Tyr Pro Gly His Ala Pro Leu Leu Thr Ala Ile Lys Pro
 35 40 45
 ggt atg att cgc atc gtg aaa cag cac ggt cac gaa gag ttt atc tat 192
 Gly Met. Ile Arg Ile Val Lys Gln His Gly His Glu Glu Phe Ile Tyr
 50 55 60
 ctg tct ggc ggc att ctt gaa gtg cag cct ggc aac gtg acc gtt ctg 240
 Leu Ser Gly Gly Ile Leu Glu Val Gln Pro Gly Asn Val Thr Val Leu
 65 70 75 80
 gcc gac acc gca att cgc ggc cag gat ctc gac gaa gcg cga gcc atg 288
 Ala Asp Thr Ala Ile Arg Gly Gln Asp Leu Asp Glu Ala Arg Ala Met
 85 90 95
 gaa gcg aaa cgt aag gct gaa gag cac att agc agc tct cac ggc gac 336
 Glu Ala Lys Arg Lys Ala Glu Glu His Ile Ser Ser Ser His Gly Asp
 100 105 110
 gta gat tac gct cag gcg tct gcg gaa ctg gcc aaa gcg atc gcg cag 384
 Val Asp Tyr Ala Gln Ala Ser Ala Glu Leu Ala Lys Ala Ile Ala Gln
 115 120 125
 ctg cgc gtt atc gag ttg acc aaa aaa gcg atg taa 420
 Leu Arg Val Ile Glu Leu Thr Lys Lys Ala Met *
 130 135

<210> 143
 <211> 1383
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1383)

<400> 143
 atg gct act gga aag att gtc cag gta atc ggc gcc gta gtt gac gtc 48

Met	Ala	Thr	Gly	Lys	Ile	Val	Gln	Val	Ile	Gly	Ala	Val	Val	Asp	Val	
1				5					10					15		
gaa ttc cct cag gat gcc gta ccg cgc gtg tac gat gct ctt gag gtg 96																
Glu Phe Pro Gln Asp Ala Val Pro Arg Val Tyr Asp Ala Leu Glu Val																
			20					25					30			
caa aat ggt aat gag cgt ctg gtg ctg gaa gtt cag cag cag ctc ggc 144																
Gln Asn Gly Asn Glu Arg Leu Val Leu Glu Val Gln Gln Gln Leu Gly																
			35				40					45				
ggc ggt atc gta cgt acc atc gca atg ggt tcc tcc gac ggt ctg cgt 192																
Gly Gly Ile Val Arg Thr Ile Ala Met Gly Ser Ser Asp Gly Leu Arg																
			50				55				60					
cgc ggt ctg gat gta aaa gac ctc gaa cac ccg att gaa gtc ccg gta 240																
Arg Gly Leu Asp Val Lys Asp Leu Glu His Pro Ile Glu Val Pro Val																
			65			70			75					80		
ggc aaa gcg act ctg ggc cgt atc atg aac gta ctg ggt gaa ccg gtc 288																
Gly Lys Ala Thr Leu Gly Arg Ile Met Asn Val Leu Gly Glu Pro Val																
				85				90					95			
gac atg aaa ggc gag atc ggt gaa gaa gag cgt tgg gcg att cac cgc 336																
Asp Met Lys Gly Glu Ile Gly Glu Glu Arg Trp Ala Ile His Arg																
			100				105					110				
gca gca cct tcc tac gaa gag ctg tca aac tct cag gaa ctg ctg gaa 384																
Ala Ala Pro Ser Tyr Glu Glu Leu Ser Asn Ser Gln Glu Leu Leu Glu																
			115				120					125				
acc ggt atc aaa gtt atc gac ctg atg tgt ccg ttc gct aag ggc ggt 432																
Thr Gly Ile Lys Val Ile Asp Leu Met Cys Pro Phe Ala Lys Gly Gly																
			130			135				140						
aaa gtt ggt ctg ttc ggt ggt gcg ggt gta ggt aaa acc gta aac atg 480																
Lys Val Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Asn Met																
			145			150			155				160			
atg gag ctc att cgt aac atc gcg atc gag cac tcc ggt tac tct gtg 528																
Met Glu Leu Ile Arg Asn Ile Ala Ile Glu His Ser Gly Tyr Ser Val																
				165				170					175			
ttt gcg ggc gta ggt gaa cgt act cgt gag ggt aac gac ttc tac cac 576																
Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Phe Tyr His																
			180				185					190				
gaa atg acc gac tcc aac gtt atc gac aaa gta tcc ctg gtg tat ggc 624																
Glu Met Thr Asp Ser Asn Val Ile Asp Lys Val Ser Leu Val Tyr Gly																
			195				200					205				
cag atg aac gag ccg ccg gga aac cgt ctg cgc gtt gct ctg acc ggt 672																
Gln Met Asn Glu Pro Pro Gly Asn Arg Leu Arg Val Ala Leu Thr Gly																
			210				215				220					
ctg acc atg gct gag aaa ttc cgt gac gaa ggt cgt gac gtt ctg ctg 720																
Leu Thr Met Ala Glu Lys Phe Arg Asp Glu Gly Arg Asp Val Leu Leu																
			225			230			235				240			
ttc gtt gac aac atc tat cgt tac acc ctg gcc ggt acg gaa gta tcc 768																
Phe Val Asp Asn Ile Tyr Arg Tyr Thr Leu Ala Gly Thr Glu Val Ser																

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<210> 144
<211> 864
<212> DNA
<213> Escherichia coli
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-80-

<221> CDS

<222> (1)...(864)

<400> 144

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atg gcc ggc gca aaa gag ata cgt agt aag atc gca agc gtc cag aac 48
Met Ala Gly Ala Lys Glu Ile Arg Ser Lys Ile Ala Ser Val Gln Asn
1 5 10 15

acg caa aag atc act aaa gcg atg gag atg gtc gcc gct tcc aaa atg 96
Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met
20 25 30

cgt aaa tcg cag gat cgc atg gcg gcc agc cgt cct tat gca gaa acc 144
Arg Lys Ser Gln Asp Arg Met Ala Ala Ser Arg Pro Tyr Ala Glu Thr
35 40 45

atg cgc aaa gtg att ggt cac ctt gca cac ggt aat ctg gaa tat aag 192
Met Arg Lys Val Ile Gly His Leu Ala His Gly Asn Leu Glu Tyr Lys
50 55 60

cac cct tac ctg gaa gac cgc gac gtt aaa cgc gtg ggc tac ctg gtg 240
His Pro Tyr Leu Glu Asp Arg Asp Val Lys Arg Val Gly Tyr Leu Val
65 70 75 80

gtg tcg acc gac cgt ggt ttg tgc ggt ggt ttg aac att aac ctg ttc 288
Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
85 90 95

aaa aaa ctg ctg gcg gaa atg aag acc tgg acc gac aaa ggc gtt caa 336
Lys Lys Leu Leu Ala Glu Met Lys Thr Trp Thr Asp Lys Gly Val Gln
100 105 110

tgc gac ctc gca atg atc ggc tcg aaa ggc gtg tcg ttc ttc aac tcc 384
Cys Asp Leu Ala Met Ile Gly Ser Lys Gly Val Ser Phe Phe Asn Ser
115 120 125

gtg ggc ggc aat gtt gtt gcc cag gtc acc ggc atg ggg gat aac cct 432
Val Gly Gly Asn Val Val Ala Gln Val Thr Gly Met Gly Asp Asn Pro
130 135 140

tcc ctg tcc gaa ctg atc ggt ccg gta aaa gtg atg ttg cag gcc tac 480
Ser Leu Ser Glu Leu Ile Gly Pro Val Lys Val Met Leu Gln Ala Tyr
145 150 155 160

gac gaa ggc cgt ctg gac aag ctt tac att gtc agc aac aaa ttt att 528
Asp Glu Gly Arg Leu Asp Lys Leu Tyr Ile Val Ser Asn Lys Phe Ile
165 170 175

aac acc atg tct cag gtt ccg acc atc agc cag ctg ctg ccg tta ccg 576
Asn Thr Met Ser Gln Val Pro Thr Ile Ser Gln Leu Leu Pro Leu Pro
180 185 190

gca tca gat gat gat gat ctg aaa cat aaa tcc tgg gat tac ctg tac 624
Ala Ser Asp Asp Asp Asp Leu Lys His Lys Ser Trp Asp Tyr Leu Tyr
195 200 205

gaa ccc gat ccg aag gcg ttg ctg gat acc ctg ctg cgt cgt tat gtc 672
Glu Pro Asp Pro Lys Ala Leu Leu Asp Thr Leu Leu Arg Arg Tyr Val
210 215 220

gaa tct cag gtt tat cag ggc gtg gtt gaa aac ctg gcc agc gag cag 720

```

```

Glu Ser Gln Val Tyr Gln Gly Val Val Glu Asn Leu Ala Ser Glu Gln
225                230                235                240

gcc gcc cgt atg gtg gcg atg aaa gcc gcg acc gac aat ggc ggc agc 768
Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Gly Gly Ser
                245                250                255

ctg att aaa gag ctg cag ttg gta tac aac aaa gct cgt cag gcc agc 816
Leu Ile Lys Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala Ser
                260                265                270

att act cag gaa ctc acc gag atc gtc tcg ggg gcc gcc gcg gtt taa 864
Ile Thr Gln Glu Leu Thr Glu Ile Val Ser Gly Ala Ala Ala Val *
                275                280                285

<210> 145
<211> 1542
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1542)

<400> 145
atg caa ctg aat tcc acc gaa atc agc gaa ctg atc aag cag cgc att 48
Met Gln Leu Asn Ser Thr Glu Ile Ser Glu Leu Ile Lys Gln Arg Ile
1                5                10                15

gct cag ttc aat gtt gtg agt gaa gct cac aac gaa ggt act att gtt 96
Ala Gln Phe Asn Val Val Ser Glu Ala His Asn Glu Gly Thr Ile Val
20                25                30

tct gta agt gac ggt gtt atc cgc att cac ggc ctg gcc gat tgt atg 144
Ser Val Ser Asp Gly Val Ile Arg Ile His Gly Leu Ala Asp Cys Met
35                40                45

cag ggt gaa atg atc tcc ctg ccg ggt aac cgt tac gct atc gca ctg 192
Gln Gly Glu Met Ile Ser Leu Pro Gly Asn Arg Tyr Ala Ile Ala Leu
50                55                60

aac ctc gag cgc gac tct gta ggt gcg gtt gtt atg ggt ccg tac gct 240
Asn Leu Glu Arg Asp Ser Val Gly Ala Val Val Met Gly Pro Tyr Ala
65                70                75                80

gac ctt gcc gaa ggc atg aaa gtt aag tgt act ggc cgt atc ctg gaa 288
Asp Leu Ala Glu Gly Met Lys Val Lys Cys Thr Gly Arg Ile Leu Glu
85                90                95

gtt ccg gtt ggc cgt ggc ctg ctg ggc cgt gtg gtt aac act ctg ggt 336
Val Pro Val Gly Arg Gly Leu Leu Gly Arg Val Val Asn Thr Leu Gly
100                105                110

gca cca atc gac ggt aaa ggt ccg ctg gat cac gac ggc ttc tct gct 384
Ala Pro Ile Asp Gly Lys Gly Pro Leu Asp His Asp Gly Phe Ser Ala
115                120                125

gta gaa gca atc gct ccg ggc gtt atc gaa cgt cag tcc gta gat cag 432
Val Glu Ala Ile Ala Pro Gly Val Ile Glu Arg Gln Ser Val Asp Gln

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130	135	140	
ccg gta cag acc ggt tat aaa gcc gtt gac tcc atg atc cca atc ggt			480
Pro Val Gln Thr Gly Tyr Lys Ala Val Asp Ser Met Ile Pro Ile Gly			
145	150	155	160
cgt ggt cag cgt gaa ttg atc atc ggt gac cgt cag aca ggt aaa acc			528
Arg Gly Gln Arg Glu Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr			
	165	170	175
gca ctg gct atc gat gcc atc atc aac cag cgc gat tcc ggt atc aaa			576
Ala Leu Ala Ile Asp Ala Ile Ile Asn Gln Arg Asp Ser Gly Ile Lys			
	180	185	190
tgt atc tat gtc gct atc ggc cag aaa gcg tcc acc att tct aac gtg			624
Cys Ile Tyr Val Ala Ile Gly Gln Lys Ala Ser Thr Ile Ser Asn Val			
	195	200	205
gta cgt aaa ctg gaa gag cac ggc gca ctg gct aac acc atc gtt gtg			672
Val Arg Lys Leu Glu Glu His Gly Ala Leu Ala Asn Thr Ile Val Val			
	210	215	220
gta gca acc gcg tct gaa tcc gct gca ctg caa tac ctg gca ccg tat			720
Val Ala Thr Ala Ser Glu Ser Ala Ala Leu Gln Tyr Leu Ala Pro Tyr			
	225	230	235
gcc ggt tgc gca atg ggc gaa tac ttc cgt gac cgc ggt gaa gat gcg			768
Ala Gly Cys Ala Met Gly Glu Tyr Phe Arg Asp Arg Gly Glu Asp Ala			
	245	250	255
ctg atc att tac gat gac ctg tct aaa cag gct gtt gct tac cgt cag			816
Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala Tyr Arg Gln			
	260	265	270
atc tcc ctg ctg ctc cgt cgt ccg cca gga cgt gaa gca ttc ccg ggc			864
Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala Phe Pro Gly			
	275	280	285
gac gtt ttc tac ctc cac tct cgt ctg ctg gag cgt gct gca cgt gtt			912
Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala Ala Arg Val			
	290	295	300
aac gcc gaa tac gtt gaa gcc ttc acc aaa ggt gaa gtg aaa ggg aaa			960
Asn Ala Glu Tyr Val Glu Ala Phe Thr Lys Gly Glu Val Lys Gly Lys			
	305	310	315
acc ggt tct ctg acc gca ctg ccg att atc gaa act cag gcg ggt gac			1008
Thr Gly Ser Leu Thr Ala Leu Pro Ile Ile Glu Thr Gln Ala Gly Asp			
	325	330	335
gtt tct gcg ttc gtt ccg acc aac gta atc tcc att acc gat ggt cag			1056
Val Ser Ala Phe Val Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln			
	340	345	350
atc ttc ctg gaa acc aac ctg ttc aac gcc ggt att cgt cct gcg gtt			1104
Ile Phe Leu Glu Thr Asn Leu Phe Asn Ala Gly Ile Arg Pro Ala Val			
	355	360	365
aac ccg ggt att tcc gta tcc cgt gtt ggt ggt gca gca cag acc aag			1152
Asn Pro Gly Ile Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys			
	370	375	380

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atc atg aaa aaa ctg tcc ggt ggt atc cgt acc gct ctg gca cag tat 1200
Ile Met Lys Lys Leu Ser Gly Gly Ile Arg Thr Ala Leu Ala Gln Tyr
385                      390                      395                      400

cgt gaa ctg gca gcg ttc tct cag ttt gca tcc gac ctt gac gat gca 1248
Arg Glu Leu Ala Ala Phe Ser Gln Phe Ala Ser Asp Leu Asp Asp Ala
                      405                      410                      415

aca cgt aag cag ctt gac cac ggt cag aaa gtg acc gaa ctg ctg aaa 1296
Thr Arg Lys Gln Leu Asp His Gly Gln Lys Val Thr Glu Leu Leu Lys
                      420                      425                      430

cag aaa cag tat gcg ccg atg tcc gtt gcg cag cag tct ctg gtt ctg 1344
Gln Lys Gln Tyr Ala Pro Met Ser Val Ala Gln Gln Ser Leu Val Leu
                      435                      440                      445

ttc gca gca gaa cgt ggt tac ctg gcg gat gtt gaa ctg tcg aaa att 1392
Phe Ala Ala Glu Arg Gly Tyr Leu Ala Asp Val Glu Leu Ser Lys Ile
                      450                      455                      460

ggc agc ttc gaa gcc gct ctg ctg gct tac gtc gac cgt gat cac gct 1440
Gly Ser Phe Glu Ala Ala Leu Leu Ala Tyr Val Asp Arg Asp His Ala
465                      470                      475                      480

ccg ttg atg caa gag atc aac cag acc ggt ggc tac aac gac gaa atc 1488
Pro Leu Met Gln Glu Ile Asn Gln Thr Gly Gly Tyr Asn Asp Glu Ile
                      485                      490                      495

gaa ggc aag ctg aaa ggc atc ctc gat tcc ttc aaa gca acc caa tcc 1536
Glu Gly Lys Leu Lys Gly Ile Leu Asp Ser Phe Lys Ala Thr Gln Ser
                      500                      505                      510

tgg taa
Trp * 1542

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<210> 146
 <211> 534
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(534)

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<400> 146
atg tct gaa ttt att acg gta gct cgc ccc tac gcc aaa gca gct ttt 48
Met Ser Glu Phe Ile Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
1                      5                      10                      15

gac ttt gcc gtc gaa cac caa agt gta gaa cgc tgg cag gac atg ctg 96
Asp Phe Ala Val Glu His Gln Ser Val Glu Arg Trp Gln Asp Met Leu
                      20                      25                      30

gcg ttt gcc gcc gag gta acc aaa aac gaa caa atg gca gag ctt ctc 144
Ala Phe Ala Ala Glu Val Thr Lys Asn Glu Gln Met Ala Glu Leu Leu
                      35                      40                      45

tct ggc gcg ctt gcg cca gaa acg ctc gcc gag tcg ttt atc gca gtt 192

```

Ser	Gly	Ala	Leu	Ala	Pro	Glu	Thr	Leu	Ala	Glu	Ser	Phe	Ile	Ala	Val	
50						55					60					
tgt	ggt	gag	caa	ctg	gac	gaa	aac	ggt	cag	aac	ctg	att	cgg	gtt	atg	240
Cys	Gly	Glu	Gln	Leu	Asp	Glu	Asn	Gly	Gln	Asn	Leu	Ile	Arg	Val	Met	
65					70				75						80	
gct	gaa	aat	ggt	cgt	ctt	aac	gcg	ctc	ccg	gat	gtt	ctg	gag	cag	ttt	288
Ala	Glu	Asn	Gly	Arg	Leu	Asn	Ala	Leu	Pro	Asp	Val	Leu	Glu	Gln	Phe	
				85				90					95			
att	cac	ctg	cgt	gcc	gtg	agt	gag	gct	acc	gct	gag	gta	gac	gtc	att	336
Ile	His	Leu	Arg	Ala	Val	Ser	Glu	Ala	Thr	Ala	Glu	Val	Asp	Val	Ile	
			100				105						110			
tcc	gct	gcc	gca	ctg	agt	gaa	caa	cag	ctc	gcg	aaa	att	tct	gct	gcg	384
Ser	Ala	Ala	Ala	Leu	Ser	Glu	Gln	Gln	Leu	Ala	Lys	Ile	Ser	Ala	Ala	
		115				120					125					
atg	gaa	aaa	cgt	ctg	tca	cgc	aaa	gtt	aag	ctg	aat	tgc	aaa	atc	gat	432
Met	Glu	Lys	Arg	Leu	Ser	Arg	Lys	Val	Lys	Leu	Asn	Cys	Lys	Ile	Asp	
		130				135				140						
aag	tct	gta	atg	gca	ggc	gtt	atc	atc	cga	gcg	ggt	gat	atg	gtc	att	480
Lys	Ser	Val	Met	Ala	Gly	Val	Ile	Ile	Arg	Ala	Gly	Asp	Met	Val	Ile	
		145			150				155					160		
gat	ggc	agc	gta	cgc	ggt	cgt	ctt	gag	cgc	ctt	gca	gac	gtc	ttg	cag	528
Asp	Gly	Ser	Val	Arg	Gly	Arg	Leu	Glu	Arg	Leu	Ala	Asp	Val	Leu	Gln	
				165				170						175		
tct	taa															534
Ser	*															

<210> 147
 <211> 471
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(471)

<400> 147																
gtg	aat	ctt	aac	gca	aca	atc	ctc	ggc	cag	gcc	atc	gcg	ttt	gtc	ctg	48
Met	Asn	Leu	Asn	Ala	Thr	Ile	Leu	Gly	Gln	Ala	Ile	Ala	Phe	Val	Leu	
1				5				10						15		
ttc	gtt	ctg	ttc	tgc	atg	aag	tac	gta	tgg	ccg	cca	tta	atg	gca	gcc	96
Phe	Val	Leu	Phe	Cys	Met	Lys	Tyr	Val	Trp	Pro	Pro	Leu	Met	Ala	Ala	
			20					25					30			
atc	gaa	aaa	cgt	caa	aaa	gaa	att	gct	gac	ggc	ctt	gct	tcc	gca	gaa	144
Ile	Glu	Lys	Arg	Gln	Lys	Glu	Ile	Ala	Asp	Gly	Leu	Ala	Ser	Ala	Glu	
		35				40					45					
cga	gca	cat	aag	gac	ctt	gac	ctt	gca	aag	gcc	agc	gcg	acc	gac	cag	192
Arg	Ala	His	Lys	Asp	Leu	Asp	Leu	Ala	Lys	Ala	Ser	Ala	Thr	Asp	Gln	
		50				55					60					

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ctg aaa aaa gcg aaa gcg gaa gcc cag gta atc atc gag cag gcg aac 240
Leu Lys Lys Ala Lys Ala Glu Ala Gln Val Ile Ile Glu Gln Ala Asn
 65                70                75                80

aaa cgc cgc tcg cag att ctg gac gaa gcg aaa gct gag gca gaa cag 288
Lys Arg Arg Ser Gln Ile Leu Asp Glu Ala Lys Ala Glu Ala Glu Gln
                85                90                95

gaa cgt act aaa atc gtg gcc cag gcg cag gcg gaa att gaa gcc gag 336
Glu Arg Thr Lys Ile Val Ala Gln Ala Gln Ala Glu Ile Glu Ala Glu
                100                105                110

cgt aaa cgt gcc cgt gaa gag ctg cgt aag caa gtt gct atc ctg gct 384
Arg Lys Arg Ala Arg Glu Glu Leu Arg Lys Gln Val Ala Ile Leu Ala
                115                120                125

gtt gct ggc gcc gag aag atc atc gaa cgt tcc gtg gat gaa gct gct 432
Val Ala Gly Ala Glu Lys Ile Ile Glu Arg Ser Val Asp Glu Ala Ala
                130                135                140

aac agc gac atc gtg gat aaa ctt gtc gct gaa ctg taa 471
Asn Ser Asp Ile Val Asp Lys Leu Val Ala Glu Leu *
145                150                155

```

<210> 148
 <211> 240
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1) ... (240)

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<400> 148
atg gaa aac ctg aat atg gat ctg ctg tac atg gct gcc gct gtg atg 48
Met Glu Asn Leu Asn Met Asp Leu Leu Tyr Met Ala Ala Ala Val Met
 1                5                10                15

atg ggt ctg gcg gca atc ggt gct gcg atc ggt atc ggc atc ctc ggg 96
Met Gly Leu Ala Ala Ile Gly Ala Ala Ile Gly Ile Gly Ile Leu Gly
                20                25                30

ggt aaa ttc ctg gaa ggc gca gcg cgt caa cct gat ctg att cct ctg 144
Gly Lys Phe Leu Glu Gly Ala Ala Arg Gln Pro Asp Leu Ile Pro Leu
                35                40                45

ctg cgt act cag ttc ttt atc gtt atg ggt ctg gtg gat gct atc ccg 192
Leu Arg Thr Gln Phe Phe Ile Val Met Gly Leu Val Asp Ala Ile Pro
                50                55                60

atg atc gct gta ggt ctg ggt ctg tac gtg atg ttc gct gtc gcg tag 240
Met Ile Ala Val Gly Leu Gly Leu Tyr Val Met Phe Ala Val Ala *
 65                70                75

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<210> 149
 <211> 816
 <212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(816)

<400> 149

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atg gct tca gaa aat atg acg ccg cag gat tac ata gga cac cac ctg 48
Met Ala Ser Glu Asn Met Thr Pro Gln Asp Tyr Ile Gly His His Leu
1 5 10 15

aat aac ctt cag ctg gac ctg cgt aca ttc tcg ctg gtg gat cca caa 96
Asn Asn Leu Gln Leu Asp Leu Arg Thr Phe Ser Leu Val Asp Pro Gln
20 25 30

aac ccc cca gcc acc ttc tgg aca atc aat att gac tcc atg ttc ttc 144
Asn Pro Pro Ala Thr Phe Trp Thr Ile Asn Ile Asp Ser Met Phe Phe
35 40 45

tcg gtg gtg ctg ggt ctg ttg ttc ctg gtt tta ttc cgt agc gta gcc 192
Ser Val Val Leu Gly Leu Leu Phe Leu Val Leu Phe Arg Ser Val Ala
50 55 60

aaa aag gcg acc agc ggt gtg cca ggt aag ttt cag acc gcg att gag 240
Lys Lys Ala Thr Ser Gly Val Pro Gly Lys Phe Gln Thr Ala Ile Glu
65 70 75 80

ctg gtg atc ggc ttt gtt aat ggt agc gtg aaa gac atg tac cat ggc 288
Leu Val Ile Gly Phe Val Asn Gly Ser Val Lys Asp Met Tyr His Gly
85 90 95

aaa agc aag ctg att gct ccg ctg gcc ctg acg atc ttc gtc tgg gta 336
Lys Ser Lys Leu Ile Ala Pro Leu Ala Leu Thr Ile Phe Val Trp Val
100 105 110

ttc ctg atg aac ctg atg gat tta ctg cct atc gac ctg ctg ccg tac 384
Phe Leu Met Asn Leu Met Asp Leu Leu Pro Ile Asp Leu Leu Pro Tyr
115 120 125

att gct gaa cat gta ctg ggt ctg cct gca ctg cgt gtg gtt ccg tct 432
Ile Ala Glu His Val Leu Gly Leu Pro Ala Leu Arg Val Val Pro Ser
130 135 140

gcg gac gtg aac gta acg ctg tct atg gca ctg ggc gta ttt atc ctg 480
Ala Asp Val Asn Val Thr Leu Ser Met Ala Leu Gly Val Phe Ile Leu
145 150 155 160

att ctg ttc tac agc atc aaa atg aaa ggc atc ggc ggc ttc acg aaa 528
Ile Leu Phe Tyr Ser Ile Lys Met Lys Gly Ile Gly Gly Phe Thr Lys
165 170 175

gag ttg acg ctg cag ccg ttc aat cac tgg gcg ttc att cct gtc aac 576
Glu Leu Thr Leu Gln Pro Phe Asn His Trp Ala Phe Ile Pro Val Asn
180 185 190

tta atc ctt gaa ggg gta agc ctg ctg tcc aaa cca gtt tca ctc ggt 624
Leu Ile Leu Glu Gly Val Ser Leu Leu Ser Lys Pro Val Ser Leu Gly
195 200 205

ttg cga ctg ttc ggt aac atg tat gcc ggt gag ctg att ttc att ctg 672
Leu Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile Leu

```

210	215	220	
att gct ggt ctg ttg ccg tgg tgg tca cag tgg atc ctg aat gtg ccg			720
Ile Ala Gly Leu Leu Pro Trp Trp Ser Gln Trp Ile Leu Asn Val Pro			
225	230	235	240
tgg gcc att ttc cac atc ctg atc att acg ctg caa gcc ttc atc ttc			768
Trp Ala Ile Phe His Ile Leu Ile Ile Thr Leu Gln Ala Phe Ile Phe			
	245	250	255
atg gtt ctg acg atc gtc tat ctg tgg atg ggg tct gaa gaa cat taa			816
Met Val Leu Thr Ile Val Tyr Leu Ser Met Ala Ser Glu Glu His *			
	260	265	270

<210> 150

<211> 393

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(393)

<400> 150

gtg aaa aac gtg atg tct gtg tgg ctc gtg agt cga aac gtt gct cgg	48
Met Lys Asn Val Met Ser Val Ser Leu Val Ser Arg Asn Val Ala Arg	
1 5 10 15	
aag ctt ctg ctc gtt cag tta ctg gtg gtg ata gca agt gga ttg ctg	96
Lys Leu Leu Leu Val Gln Leu Leu Val Val Ile Ala Ser Gly Leu Leu	
20 25 30	
ttc agc ctc aaa gac ccc ttc tgg ggc gtc tct gca ata agc ggg ggc	144
Phe Ser Leu Lys Asp Pro Phe Trp Gly Val Ser Ala Ile Ser Gly Gly	
35 40 45	
ctg gca gtc ttt ctg cct aac gtt ttg ttt atg ata ttt gcc tgg cgt	192
Leu Ala Val Phe Leu Pro Asn Val Leu Phe Met Ile Phe Ala Trp Arg	
50 55 60	
cac cag gcg cat aca cca gcg aaa ggc cgg gtg gcc tgg aca ttc gca	240
His Gln Ala His Thr Pro Ala Lys Gly Arg Val Ala Trp Thr Phe Ala	
65 70 75 80	
ttt ggc gaa gct ttc aaa gtt ctg gcg atg ttg gtg tta ctg gtg gtg	288
Phe Gly Glu Ala Phe Lys Val Leu Ala Met Leu Val Leu Leu Val Val	
85 90 95	
gcg ttg gcg gtt tta aag gcg gta ttc ttg ccg ctg atc gtt acg tgg	336
Ala Leu Ala Val Leu Lys Ala Val Phe Leu Pro Leu Ile Val Thr Trp	
100 105 110	
gtt ttg gtg ctg gtg gtt cag ata ctg gca ccg gct gta att aac aac	384
Val Leu Val Leu Val Val Gln Ile Leu Ala Pro Ala Val Ile Asn Asn	
115 120 125	
aaa ggg taa	393
Lys Gly *	
130	

<210> 151
 <211> 1242
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1242)

<400> 151
 atg caa aaa cac ggc gac cgc tat gtg tgg atc aac ccg cct gct att 48
 Met Gln Lys His Gly Asp Arg Tyr Val Trp Ile Asn Pro Pro Ala Ile
 1 5 10 15
 ccg ctt tct acc gaa gag atg gac agc gtt ttt gcg ctg cca tac aag 96
 Pro Leu Ser Thr Glu Glu Met Asp Ser Val Phe Ala Leu Pro Tyr Lys
 20 25 30
 cgc gtg cca cat ccg gcc tat ggc aat gcc cgt att ccg gct tac gaa 144
 Arg Val Pro His Pro Ala Tyr Gly Asn Ala Arg Ile Pro Ala Tyr Glu
 35 40 45
 atg atc cgt ttt tcg gtc aac att atg cgt gcc tgc ttt gcc gcc tgc 192
 Met Ile Arg Phe Ser Val Asn Ile Met Arg Gly Cys Phe Gly Gly Cys
 50 55 60
 tct ttc tgt tct atc acc gag cac gaa ggg cgc att att cag agc cgt 240
 Ser Phe Cys Ser Ile Thr Glu His Glu Gly Arg Ile Ile Gln Ser Arg
 65 70 75 80
 tcc gaa gat tcg atc att aat gag atc gaa gcg atc cgc gac acc gtt 288
 Ser Glu Asp Ser Ile Ile Asn Glu Ile Glu Ala Ile Arg Asp Thr Val
 85 90 95
 cca ggt ttt acg ggc gtg att tcc gat ctt ggt ggg cca act gcc aac 336
 Pro Gly Phe Thr Gly Val Ile Ser Asp Leu Gly Gly Pro Thr Ala Asn
 100 105 110
 atg tat atg ttg cgc tgc aaa tcg cca cgc gct gaa caa act tgt cgc 384
 Met Tyr Met Leu Arg Cys Lys Ser Pro Arg Ala Glu Gln Thr Cys Arg
 115 120 125
 cgt ttg tcg tgc gtt tat ccg gat att tgt ccg cac atg gac acg aac 432
 Arg Leu Ser Cys Val Tyr Pro Asp Ile Cys Pro His Met Asp Thr Asn
 130 135 140
 cac gaa cca acg atc aac ctc tat cgc cgt gcg cgt gat ctg aaa ggc 480
 His Glu Pro Thr Ile Asn Leu Tyr Arg Arg Ala Arg Asp Leu Lys Gly
 145 150 155 160
 att aaa aag atc ctg att gcc tct ggt gtg cgt tat gac ata gcc gta 528
 Ile Lys Lys Ile Leu Ile Ala Ser Gly Val Arg Tyr Asp Ile Ala Val
 165 170 175
 gaa gat ccg cgc tat atc aaa gaa ctg gcg acc cat cac gtc gcc ggt 576
 Glu Asp Pro Arg Tyr Ile Lys Glu Leu Ala Thr His His Val Gly Gly
 180 185 190
 tat ctg aag att gcc ccg gaa cat acc gaa gaa ggg ccg tta tcg aag 624

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Tyr Leu Lys Ile Ala Pro Glu His Thr Glu Glu Gly Pro Leu Ser Lys
195                                200                                205

atg atg aag ccg ggc atg ggc agc tat gac cgc ttt aaa gag ctg ttc 672
Met Met Lys Pro Gly Met Gly Ser Tyr Asp Arg Phe Lys Glu Leu Phe
210                                215                                220

gat act tac tca aaa cag gca ggt aaa gag cag tat ctg atc ccc tat 720
Asp Thr Tyr Ser Lys Gln Ala Gly Lys Glu Gln Tyr Leu Ile Pro Tyr
225                                230                                235                                240

ttc atc tcc gcg cac ccc ggt acg cgt gat gaa gat atg gtg aat ctg 768
Phe Ile Ser Ala His Pro Gly Thr Arg Asp Glu Asp Met Val Asn Leu
245                                250                                255

gcg ctg tgg ctg aaa aag cac cgc ttc cgc ctc gac cag gtg cag aac 816
Ala Leu Trp Leu Lys Lys His Arg Phe Arg Leu Asp Gln Val Gln Asn
260                                265                                270

ttc tat ccg tcg ccg ctg gcg aac tca acc acc atg tat tac acc ggg 864
Phe Tyr Pro Ser Pro Leu Ala Asn Ser Thr Thr Met Tyr Tyr Thr Gly
275                                280                                285

aaa aac ccg ctg gcg aag att ggt tat aag agc gaa gac gtc ttc gta 912
Lys Asn Pro Leu Ala Lys Ile Gly Tyr Lys Ser Glu Asp Val Phe Val
290                                295                                300

ccg aag ggc gac aaa cag cgt cgt ttg cat aaa gcg ttg ttg cgt tac 960
Pro Lys Gly Asp Lys Gln Arg Arg Leu His Lys Ala Leu Leu Arg Tyr
305                                310                                315                                320

cac gat ccg gca aac tgg ccg tta atc cgc cag gcg ctg gaa gcg atg 1008
His Asp Pro Ala Asn Trp Pro Leu Ile Arg Gln Ala Leu Glu Ala Met
325                                330                                335

ggc aaa aag cat ctg att ggc agc cgt cgc gat tgc tta gtg cct gcg 1056
Gly Lys Lys His Leu Ile Gly Ser Arg Arg Asp Cys Leu Val Pro Ala
340                                345                                350

cca acc att gaa gag atg cgt gaa gct cgt cgc cag aac cgc aat acc 1104
Pro Thr Ile Glu Glu Met Arg Glu Ala Arg Arg Gln Asn Arg Asn Thr
355                                360                                365

cgt ccg gcg ttg acg aaa cat acg ccg atg gcg acc cag cgt cag acg 1152
Arg Pro Ala Leu Thr Lys His Thr Pro Met Ala Thr Gln Arg Gln Thr
370                                375                                380

cct gct acg gca aaa aaa gcg tcg tct acg caa tct cgt ccg gtg aat 1200
Pro Ala Thr Ala Lys Lys Ala Ser Ser Thr Gln Ser Arg Pro Val Asn
385                                390                                395                                400

gct ggt gcg aag aaa cgg cct aaa gcg gcg gtt gga cgt taa 1242
Ala Gly Ala Lys Lys Arg Pro Lys Ala Ala Val Gly Arg *
405                                410

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<210> 152

<211> 978

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (978)

<400> 152

atg agc tct atc tcc ctg atc caa ccg gat cgc gac ctg ttc tcc tgg	48
Met Ser Ser Ile Ser Leu Ile Gln Pro Asp Arg Asp Leu Phe Ser Trp	
1 5 10 15	
ccg cag tac tgg gcc gcc tgt ttt gga ccg gca ccg ttt ttg ccg atg	96
Pro Gln Tyr Trp Ala Ala Cys Phe Gly Pro Ala Pro Phe Leu Pro Met	
20 25 30	
tct cgt gaa gag atg gat caa ctt ggc tgg gat agc tgc gac atc att	144
Ser Arg Glu Glu Met Asp Gln Leu Gly Trp Asp Ser Cys Asp Ile Ile	
35 40 45	
ttg gtt act ggc gac gcg tat gtc gat cac cca agc ttc ggg atg gcg	192
Leu Val Thr Gly Asp Ala Tyr Val Asp His Pro Ser Phe Gly Met Ala	
50 55 60	
att tgc ggt cgt atg ctg gaa gcg cag ggc ttt cgc gtc ggg atc atc	240
Ile Cys Gly Arg Met Leu Glu Ala Gln Gly Phe Arg Val Gly Ile Ile	
65 70 75 80	
gcc cag ccg gac tgg agc agc aaa gac gac ttt atg cgt ctg ggt aaa	288
Ala Gln Pro Asp Trp Ser Ser Lys Asp Asp Phe Met Arg Leu Gly Lys	
85 90 95	
ccg aat ctg ttt ttc ggt gtt act gct ggc aac atg gat tcg atg atc	336
Pro Asn Leu Phe Phe Gly Val Thr Ala Gly Asn Met Asp Ser Met Ile	
100 105 110	
aac cgt tat acc gcc gat cgc cgt tta cgt cat gac gat gcc tac acg	384
Asn Arg Tyr Thr Ala Asp Arg Arg Leu Arg His Asp Asp Ala Tyr Thr	
115 120 125	
ccg gat aac gtc gcg ggt aag cgc ccg gat cgc gcc aca ctg gtt tat	432
Pro Asp Asn Val Ala Gly Lys Arg Pro Asp Arg Ala Thr Leu Val Tyr	
130 135 140	
acc cag cgt tgt aaa gag gcg tgg aaa gat gta ccg gtg atc ctc ggc	480
Thr Gln Arg Cys Lys Glu Ala Trp Lys Asp Val Pro Val Ile Leu Gly	
145 150 155 160	
ggt att gag gct agt ctg cgc cgt acc gcg cat tat gat tac tgg tcc	528
Gly Ile Glu Ala Ser Leu Arg Arg Thr Ala His Tyr Asp Tyr Trp Ser	
165 170 175	
gat acc gtg cgc cgt tcc gtg ctg gtg gat tcg aaa gcc gac atg ctg	576
Asp Thr Val Arg Arg Ser Val Leu Val Asp Ser Lys Ala Asp Met Leu	
180 185 190	
atg ttt ggt aac ggt gag cgt ccg ctg gtg gaa gtg gcg cat cgt ctg	624
Met Phe Gly Asn Gly Glu Arg Pro Leu Val Glu Val Ala His Arg Leu	
195 200 205	
gcg atg ggc gag cca att agt gaa atc cgc gat gtg cgt aat acc gcg	672
Ala Met Gly Glu Pro Ile Ser Glu Ile Arg Asp Val Arg Asn Thr Ala	
210 215 220	

```

att atc gtg aaa gag gcg ctg cct ggc tgg agc ggc gtg gat tcc acc 720
Ile Ile Val Lys Glu Ala Leu Pro Gly Trp Ser Gly Val Asp Ser Thr
225                230                235                240

cgt ctt gat acc cct gga aaa atc gac cca atc ccg cat ccg tat ggt 768
Arg Leu Asp Thr Pro Gly Lys Ile Asp Pro Ile Pro His Pro Tyr Gly
                245                250                255

gaa gat ttg ccg tgc gcg gat aac aaa ccg gtg gca ccg aaa aag cag 816
Glu Asp Leu Pro Cys Ala Asp Asn Lys Pro Val Ala Pro Lys Lys Gln
                260                265                270

gaa gcc aaa gcc gta acc gtg cag cca ccg cgc ccg aaa ccg tgg gaa 864
Glu Ala Lys Ala Val Thr Val Gln Pro Pro Arg Pro Lys Pro Trp Glu
                275                280                285

aaa acc tac gtg ttg ctg cct tct ttc gag aaa gtg aag ggc gat aaa 912
Lys Thr Tyr Val Leu Leu Pro Ser Phe Glu Lys Val Lys Gly Asp Lys
                290                295                300

gtg ctg tac gcc cat gct tcg cgt att ctg cac cac gaa acc aac cca 960
Val Leu Tyr Ala His Ala Ser Arg Ile Leu His His Glu Thr Asn Pro
305                310                315                320

gct gtg ccc gcg cat tga
Ala Val Pro Ala His * 978
                325

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<210> 153
 <211> 681
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(681)

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<400> 153
atg att cag tat ctg aac gtc ttt ttt tac gat atc tac ccg tac att 48
Met Ile Gln Tyr Leu Asn Val Phe Phe Tyr Asp Ile Tyr Pro Tyr Ile
1                5                10                15

tgt gcg acg gtg ttt ttc ctc ggc agc tgg ctg cgc tac gac tac ggg 96
Cys Ala Thr Val Phe Phe Leu Gly Ser Trp Leu Arg Tyr Asp Tyr Gly
                20                25                30

cag tac acc tgg cgc gcc tcc tca agt caa atg ctc gat aaa cgc ggg 144
Gln Tyr Thr Trp Arg Ala Ser Ser Ser Gln Met Leu Asp Lys Arg Gly
                35                40                45

atg gtg ata tgg tcg aat ctg ttc cat atc ggc att ttg ggg att ttc 192
Met Val Ile Trp Ser Asn Leu Phe His Ile Gly Ile Leu Gly Ile Phe
50                55                60

ttc ggg cac ttg ttc ggc atg tta acg ccg cac tgg atg tac gcg tgg 240
Phe Gly His Leu Phe Gly Met Leu Thr Pro His Trp Met Tyr Ala Trp
65                70                75                80

ttt ttg cca gtg gca gcg aaa caa ctc atg gcg atg gtg ctc ggc ggt 288

```

Phe	Leu	Pro	Val	Ala	Ala	Lys	Gln	Leu	Met	Ala	Met	Val	Leu	Gly	Gly		
				85					90					95			
att	tgc	ggt	gtg	ttg	acg	ttg	att	ggc	ggc	gca	gga	ctg	ctg	tgg	cgc	336	
Ile	Cys	Gly	Val	Leu	Thr	Leu	Ile	Gly	Gly	Ala	Gly	Leu	Leu	Trp	Arg		
			100					105					110				
agg	ctg	aca	aat	cag	cgc	gtg	cgt	gcc	act	tcc	act	acg	ccg	gat	atc	384	
Arg	Leu	Thr	Asn	Gln	Arg	Val	Arg	Ala	Thr	Ser	Thr	Thr	Pro	Asp	Ile		
			115				120					125					
atc	atc	atg	agc	att	ttg	ctg	atc	cag	tgt	ctg	ttg	ggg	cta	agt	acc	432	
Ile	Ile	Met	Ser	Ile	Leu	Leu	Ile	Gln	Cys	Leu	Leu	Gly	Leu	Ser	Thr		
			130				135					140					
ata	ccg	ttt	tca	gca	cag	tat	cct	gat	ggg	agc	gaa	atg	atg	aag	ctg	480	
Ile	Pro	Phe	Ser	Ala	Gln	Tyr	Pro	Asp	Gly	Ser	Glu	Met	Met	Lys	Leu		
					150					155					160		
gtg	ggt	tgg	gcg	caa	agc	att	gtc	act	ttc	cgt	ggg	gga	tcg	tca	gag	528	
Val	Gly	Trp	Ala	Gln	Ser	Ile	Val	Thr	Phe	Arg	Gly	Gly	Ser	Ser	Glu		
				165					170						175		
atg	ctc	aac	ggc	gta	gcg	ttc	gtc	ttc	cgc	ctg	cat	ctg	gtg	ttg	gga	576	
Met	Leu	Asn	Gly	Val	Ala	Phe	Val	Phe	Arg	Leu	His	Leu	Val	Leu	Gly		
				180				185						190			
atg	acc	atc	ttc	ctg	ctc	ttc	ccg	ttc	acc	cga	ctg	gtg	cat	gtg	tgg	624	
Met	Thr	Ile	Phe	Leu	Leu	Phe	Pro	Phe	Thr	Arg	Leu	Val	His	Val	Trp		
				195				200					205				
agc	gcg	ccg	ttt	gag	tac	ttt	act	cgt	cga	tat	caa	att	gtg	cgt	tcg	672	
Ser	Ala	Pro	Phe	Glu	Tyr	Phe	Thr	Arg	Arg	Tyr	Gln	Ile	Val	Arg	Ser		
			210				215				220						
cgg	cga	taa														681	
Arg	Arg	*															
			225														
<210> 154																	
<211> 696																	
<212> DNA																	
<213> Escherichia coli																	
<220>																	
<221> CDS																	
<222> (1)...(696)																	
<400> 154																	
atg	cag	atc	ctc	aaa	gtg	atc	ggc	ctg	ttg	atg	gag	tat	ccg	gac	gag	48	
Met	Gln	Ile	Leu	Lys	Val	Ile	Gly	Leu	Leu	Met	Glu	Tyr	Pro	Asp	Glu		
				5				10						15			
ctg	ttg	tgg	gaa	tgc	aag	gag	gac	gcg	ctg	gcg	ttg	atc	cgc	cgc	gac	96	
Leu	Leu	Trp	Glu	Cys	Lys	Glu	Asp	Ala	Leu	Ala	Leu	Ile	Arg	Arg	Asp		
				20				25					30				
gcg	ccg	atg	ctt	acg	gat	ttc	acc	cac	aac	ctg	ctt	aac	gcg	ccg	ctg	144	
Ala	Pro	Met	Leu	Thr	Asp	Phe	Thr	His	Asn	Leu	Leu	Asn	Ala	Pro	Leu		
				35				40					45				

```

ctg gat aaa cag gcc gaa tgg tgc gaa gtg ttt gac cgc ggg cgc acc 192
Leu Asp Lys Gln Ala Glu Trp Cys Glu Val Phe Asp Arg Gly Arg Thr
  50                      55                      60

acg tcg ctg ctg ctg ttc gaa cat gtt cat gcc gag tcc cgc gat cgc 240
Thr Ser Leu Leu Leu Phe Glu His Val His Ala Glu Ser Arg Asp Arg
  65                      70                      75                      80

ggc cag gca atg gtg gac ctg ctg gcg gag tat gaa aag gtc ggc ctg 288
Gly Gln Ala Met Val Asp Leu Leu Ala Glu Tyr Glu Lys Val Gly Leu
                      85                      90                      95

cag ctg gat tgt cgg gaa ctg ccc gat tat cta ccg ctg tat ctg gag 336
Gln Leu Asp Cys Arg Glu Leu Pro Asp Tyr Leu Pro Leu Tyr Leu Glu
                      100                      105                      110

tat tta agc gta ctg cct gac gat cag gcg aaa gaa gga ttg ctc aat 384
Tyr Leu Ser Val Leu Pro Asp Gln Ala Lys Glu Gly Leu Leu Asn
                      115                      120                      125

gtt gcg ccg atc ctc gcc ctg ctt ggc ggt cgc tta aaa caa cgc gag 432
Val Ala Pro Ile Leu Ala Leu Leu Gly Gly Arg Leu Lys Gln Arg Glu
                      130                      135                      140

gca ccg tgg tac gcg ttg ttt gat gct ctg ctg caa ctg gcg gga agc 480
Ala Pro Trp Tyr Ala Leu Phe Asp Ala Leu Leu Gln Leu Ala Gly Ser
                      145                      150                      155                      160

tcc ctt tca agt gac agt gtc aca aaa caa gta aac agc gaa gag cgc 528
Ser Leu Ser Ser Asp Ser Val Thr Lys Gln Val Asn Ser Glu Glu Arg
                      165                      170                      175

gat gac acc cgc cag gcg ctt gat gca gtg tgg gaa gag gaa cag gtg 576
Asp Asp Thr Arg Gln Ala Leu Asp Ala Val Trp Glu Glu Glu Gln Val
                      180                      185                      190

aag ttt att gaa gat aac gcc acg gcg tgt gac agc tcg ccg ctt aat 624
Lys Phe Ile Glu Asp Asn Ala Thr Ala Cys Asp Ser Ser Pro Leu Asn
                      195                      200                      205

caa tat cag cga cgc ttt agc cag gat gtc gcg ccg caa tat gtc gac 672
Gln Tyr Gln Arg Arg Phe Ser Gln Asp Val Ala Pro Gln Tyr Val Asp
                      210                      215                      220

atc agt gcg gga ggt ggg aaa tga 696
Ile Ser Ala Gly Gly Gly Lys *
225                      230

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<210> 155

<211> 1545

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1545)

<400> 155

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atg aaa atc cgt tca caa gtc ggc atg gtg ctt aac ctc gac aaa tgt 48

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Met	Lys	Ile	Arg	Ser	Gln	Val	Gly	Met	Val	Leu	Asn	Leu	Asp	Lys	Cys	
1				5					10					15		
atc	ggc	tgc	cat	acc	tgt	tcg	gtg	acc	tgt	aaa	aac	gtc	tgg	acc	ggg	96
Ile	Gly	Cys	His	Thr	Cys	Ser	Val	Thr	Cys	Lys	Asn	Val	Trp	Thr	Gly	
			20					25					30			
cgc	gaa	ggc	atg	gag	tac	gca	tgg	ttt	aac	aac	gtc	gaa	acc	aaa	ccg	144
Arg	Glu	Gly	Met	Glu	Tyr	Ala	Trp	Phe	Asn	Asn	Val	Glu	Thr	Lys	Pro	
			35				40					45				
ggc	att	ggg	tat	ccg	aaa	aac	tgg	gaa	gat	cag	gaa	gag	tgg	caa	ggc	192
Gly	Ile	Gly	Tyr	Pro	Lys	Asn	Trp	Glu	Asp	Gln	Glu	Glu	Trp	Gln	Gly	
	50					55					60					
ggc	tgg	gtg	cgt	gat	gtg	aat	ggc	aag	ata	cgc	ccg	cgt	ctg	ggc	aac	240
Gly	Trp	Val	Arg	Asp	Val	Asn	Gly	Lys	Ile	Arg	Pro	Arg	Leu	Gly	Asn	
	65				70					75					80	
aag	atg	ggc	gta	ata	acc	aaa	atc	ttc	gcc	aac	ccg	gtg	gtg	ccg	cag	288
Lys	Met	Gly	Val	Ile	Thr	Lys	Ile	Phe	Ala	Asn	Pro	Val	Val	Pro	Gln	
				85					90					95		
att	gat	gat	tac	tac	gaa	cct	ttc	acc	ttc	gac	tac	gaa	cat	ttg	cat	336
Ile	Asp	Asp	Tyr	Tyr	Glu	Pro	Phe	Thr	Phe	Asp	Tyr	Glu	His	Leu	His	
			100					105					110			
agc	gca	ccg	gaa	ggc	aaa	cat	att	cct	act	gct	cgc	ccg	cgt	tca	ctg	384
Ser	Ala	Pro	Glu	Gly	Lys	His	Ile	Pro	Thr	Ala	Arg	Pro	Arg	Ser	Leu	
			115				120					125				
att	gac	ggc	aaa	cgg	atg	gac	aaa	gtg	atc	tgg	ggg	cca	aac	tgg	gaa	432
Ile	Asp	Gly	Lys	Arg	Met	Asp	Lys	Val	Ile	Trp	Gly	Pro	Asn	Trp	Glu	
	130					135					140					
gaa	ctg	ctg	ggc	ggg	gag	ttc	gaa	aaa	cgt	gcc	cgc	gac	cgc	aac	ttc	480
Glu	Leu	Leu	Gly	Gly	Glu	Phe	Glu	Lys	Arg	Ala	Arg	Asp	Arg	Asn	Phe	
	145				150					155					160	
gag	gcc	atg	caa	aag	gag	atg	tac	ggg	cag	ttt	gaa	aac	acc	ttc	atg	528
Glu	Ala	Met	Gln	Lys	Glu	Met	Tyr	Gly	Gln	Phe	Glu	Asn	Thr	Phe	Met	
				165				170						175		
atg	tac	ctg	ccg	cgc	ctg	tgc	gaa	cac	tgc	ctc	aat	ccc	agc	tgc	gtg	576
Met	Tyr	Leu	Pro	Arg	Leu	Cys	Glu	His	Cys	Leu	Asn	Pro	Ser	Cys	Val	
			180					185					190			
gcg	acc	tgc	cca	agc	ggc	gct	atc	tac	aaa	cgc	gaa	gaa	gac	ggc	att	624
Ala	Thr	Cys	Pro	Ser	Gly	Ala	Ile	Tyr	Lys	Arg	Glu	Glu	Asp	Gly	Ile	
			195				200					205				
gtg	ctg	att	gat	cag	gat	aaa	tgc	cgt	ggc	tgg	cgt	ttg	tgc	ata	agc	672
Val	Leu	Ile	Asp	Gln	Asp	Lys	Cys	Arg	Gly	Trp	Arg	Leu	Cys	Ile	Ser	
	210					215					220					
ggg	tgt	ccg	tac	aaa	aaa	atc	tac	ttc	aac	tgg	aaa	agc	ggc	aag	tca	720
Gly	Cys	Pro	Tyr	Lys	Lys	Ile	Tyr	Phe	Asn	Trp	Lys	Ser	Gly	Lys	Ser	
	225				230					235					240	
gaa	aaa	tgc	atc	ttc	tgt	tac	cca	cga	att	gag	tcc	ggg	caa	ccg	acc	768
Glu	Lys	Cys	Ile	Phe	Cys	Tyr	Pro	Arg	Ile	Glu	Ser	Gly	Gln	Pro	Thr	

-96-

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agc cgt atc gat gcc atc aac atc acc gaa gtg cgc gac aaa gcg gag 1536
Ser Arg Ile Asp Ala Ile Asn Ile Thr Glu Val Arg Asp Lys Ala Glu
          500                      505                      510

```

```

ggc gaa taa 1545
Gly Glu *

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<210> 156
<211> 3741
<212> DNA
<213> Escherichia coli

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<220>
<221> CDS
<222> (1)...(3741)

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<400> 156
atg agt aaa ctt ttg gat cgc ttt cgc tac ttc aaa caa aag ggc gaa 48
Met Ser Lys Leu Leu Asp Arg Phe Arg Tyr Phe Lys Gln Lys Gly Glu
  1              5              10              15

acc ttt gcc gat ggt cac gga cag gtg atg cat agc aac cgc gac tgg 96
Thr Phe Ala Asp Gly His Gly Gln Val Met His Ser Asn Arg Asp Trp
          20              25              30

gag gac agc tat cgc cag cgt tgg cag ttc gac aaa atc gtg cgt tcc 144
Glu Asp Ser Tyr Arg Gln Arg Trp Gln Phe Asp Lys Ile Val Arg Ser
          35              40              45

acc cac ggt gtt aac tgt aca ggc tcc tgt agc tgg aaa atc tac gtt 192
Thr His Gly Val Asn Cys Thr Gly Ser Cys Ser Trp Lys Ile Tyr Val
          50              55              60

aaa aat ggt ctg gtg acc tgg gaa atc caa cag acc gac tac ccg cgc 240
Lys Asn Gly Leu Val Thr Trp Glu Ile Gln Gln Thr Asp Tyr Pro Arg
          65              70              75              80

act cgc cct gac ctg ccc aat cat gaa cct cgc ggc tgc ccg cgt ggc 288
Thr Arg Pro Asp Leu Pro Asn His Glu Pro Arg Gly Cys Pro Arg Gly
          85              90              95

gca agt tac tcc tgg tat ctt tac agc gct aac cgc ctg aaa tac ccg 336
Ala Ser Tyr Ser Trp Tyr Leu Tyr Ser Ala Asn Arg Leu Lys Tyr Pro
          100              105              110

ctc att cgt aaa cga ctg att gaa ctg tgg cgc gaa gcc ctc aag caa 384
Leu Ile Arg Lys Arg Leu Ile Glu Leu Trp Arg Glu Ala Leu Lys Gln
          115              120              125

cac agc gat ccg gta ctg gcg tgg gca tcg att atg aac gat ccg caa 432
His Ser Asp Pro Val Leu Ala Trp Ala Ser Ile Met Asn Asp Pro Gln
          130              135              140

aag tgc ctg agc tac aaa caa gtg cgt ggg cgc ggc ggg ttt atc cgc 480
Lys Cys Leu Ser Tyr Lys Gln Val Arg Gly Arg Gly Gly Phe Ile Arg
          145              150              155              160

tcc aac tgg cag gaa cta aac cag ctg att gcc gcc gct aac gtc tgg 528

```

Ser	Asn	Trp	Gln	Glu	Leu	Asn	Gln	Leu	Ile	Ala	Ala	Ala	Asn	Val	Trp		
				165					170					175			
acc	atc	aaa	acc	tac	ggc	ccg	gat	cgc	gtt	gcc	ggg	ttc	tcg	ccg	atc	576	
Thr	Ile	Lys	Thr	Tyr	Gly	Pro	Asp	Arg	Val	Ala	Gly	Phe	Ser	Pro	Ile		
			180					185					190				
ccg	gcg	atg	tcg	atg	gtt	tct	tac	gcc	gcc	gga	acg	cgt	tat	ctg	tcg	624	
Pro	Ala	Met	Ser	Met	Val	Ser	Tyr	Ala	Ala	Gly	Thr	Arg	Tyr	Leu	Ser		
		195					200					205					
ctg	ctt	ggc	ggc	acc	tgt	tta	agt	ttc	tac	gac	tgg	tat	tgc	gac	ctg	672	
Leu	Leu	Gly	Gly	Thr	Cys	Leu	Ser	Phe	Tyr	Asp	Trp	Tyr	Cys	Asp	Leu		
	210					215					220						
ccg	ccc	gcc	tcg	ccg	atg	acc	tgg	ggc	gag	caa	acc	gac	gta	ccg	gaa	720	
Pro	Pro	Ala	Ser	Pro	Met	Thr	Trp	Gly	Glu	Gln	Thr	Asp	Val	Pro	Glu		
225					230				235					240			
tct	gcc	gac	tgg	tat	aac	tcc	agc	tac	atc	atc	gcc	tgg	ggg	tct	aac	768	
Ser	Ala	Asp	Trp	Tyr	Asn	Ser	Ser	Tyr	Ile	Ile	Ala	Trp	Gly	Ser	Asn		
				245					250					255			
gta	ccg	cag	aca	cgt	acg	ccg	gac	gcc	cac	ttc	ttt	acc	gaa	gta	cgc	816	
Val	Pro	Gln	Thr	Arg	Thr	Pro	Asp	Ala	His	Phe	Phe	Thr	Glu	Val	Arg		
			260					265					270				
tac	aaa	ggc	act	aaa	acc	atc	gcc	att	acc	cct	gac	tac	tct	gaa	gtg	864	
Tyr	Lys	Gly	Thr	Lys	Thr	Ile	Ala	Ile	Thr	Pro	Asp	Tyr	Ser	Glu	Val		
		275					280					285					
gcc	aaa	ttg	tgc	gac	cag	tgg	ctg	gca	ccg	aaa	caa	ggc	act	gat	agc	912	
Ala	Lys	Leu	Cys	Asp	Gln	Trp	Leu	Ala	Pro	Lys	Gln	Gly	Thr	Asp	Ser		
	290					295					300						
gcc	ctg	gcg	atg	gca	atg	ggc	cat	gtg	att	tta	aaa	gag	ttt	cat	ctc	960	
Ala	Leu	Ala	Met	Ala	Met	Gly	His	Val	Ile	Leu	Lys	Glu	Phe	His	Leu		
305					310					315					320		
gat	aat	ccc	agc	gac	tac	ttt	atc	aac	tac	tgc	cgc	cgc	tac	agc	gac	1008	
Asp	Asn	Pro	Ser	Asp	Tyr	Phe	Ile	Asn	Tyr	Cys	Arg	Arg	Tyr	Ser	Asp		
				325					330					335			
atg	ccg	atg	ctg	gta	atg	ctg	gag	cct	cgc	gac	gat	ggg	agc	tac	gtt	1056	
Met	Pro	Met	Leu	Val	Met	Leu	Glu	Pro	Arg	Asp	Asp	Gly	Ser	Tyr	Val		
			340					345					350				
ccc	ggg	cgc	atg	atc	cgc	gca	tct	gac	ctg	gtg	gat	gga	ctg	ggc	gaa	1104	
Pro	Gly	Arg	Met	Ile	Arg	Ala	Ser	Asp	Leu	Val	Asp	Gly	Leu	Gly	Glu		
		355					360					365					
agc	aac	aat	ccg	cag	tgg	aaa	acc	gta	gca	gtt	aat	acc	gca	ggg	gaa	1152	
Ser	Asn	Asn	Pro	Gln	Trp	Lys	Thr	Val	Ala	Val	Asn	Thr	Ala	Gly	Glu		
		370					375					380					
ttg	gta	gtg	ccg	aac	ggg	tcg	att	ggg	ttc	cgc	tgg	gga	gaa	aaa	ggc	1200	
Leu	Val	Val	Pro	Asn	Gly	Ser	Ile	Gly	Phe	Arg	Trp	Gly	Glu	Lys	Gly		
385					390					395					400		
aaa	tgg	aat	ctg	gaa	tcc	att	gcc	gcc	ggg	acg	gaa	acc	gaa	ttg	tcg	1248	
Lys	Trp	Asn	Leu	Glu	Ser	Ile	Ala	Ala	Gly	Thr	Glu	Thr	Glu	Leu	Ser		

405										410					415					
tta acc ctg ctc ggt caa cat gac gct gtt gca ggc gtg gcc ttc ccc	1296																			
Leu Thr Leu Leu Gly Gln His Asp Ala Val Ala Gly Val Ala Phe Pro																				
420 425 430																				
tac ttt ggc ggc att gaa aat ccg cat ttt cgc agc gta aaa cac aat	1344																			
Tyr Phe Gly Gly Ile Glu Asn Pro His Phe Arg Ser Val Lys His Asn																				
435 440 445																				
ccg gtg ctg gtg cgc caa ttg ccc gtt aaa aac ctg acg tta gtc gat	1392																			
Pro Val Leu Val Arg Gln Leu Pro Val Lys Asn Leu Thr Leu Val Asp																				
450 455 460																				
ggc aac acc tgt ccg gtg gtc agc gtt tat gat ttg gta ctg gcg aat	1440																			
Gly Asn Thr Cys Pro Val Val Ser Val Tyr Asp Leu Val Leu Ala Asn																				
465 470 475 480																				
tac ggc ctc gat cgc ggg ctg gaa gat gaa aac agt gcg aaa gat tac	1488																			
Tyr Gly Leu Asp Arg Gly Leu Glu Asp Glu Asn Ser Ala Lys Asp Tyr																				
485 490 495																				
gct gaa atc aaa ccg tac acc cca gcc tgg ggt gag caa att acc ggc	1536																			
Ala Glu Ile Lys Pro Tyr Thr Pro Ala Trp Gly Glu Gln Ile Thr Gly																				
500 505 510																				
gtg ccg cgc cag tat att gaa acc atc gcc cgt gaa ttt gcc gat acc	1584																			
Val Pro Arg Gln Tyr Ile Glu Thr Ile Ala Arg Glu Phe Ala Asp Thr																				
515 520 525																				
gcc cat aaa acg cat ggg cgc tcg atg att atc ctc ggc gca ggt gtt	1632																			
Ala His Lys Thr His Gly Arg Ser Met Ile Ile Leu Gly Ala Gly Val																				
530 535 540																				
aac cac tgg tat cac atg gac atg aac tac cgc ggg atg atc aat atg	1680																			
Asn His Trp Tyr His Met Asp Met Asn Tyr Arg Gly Met Ile Asn Met																				
545 550 555 560																				
ctg atc ttc tgc ggt tgt gtc ggg caa agc ggt ggc ggc tgg gca cac	1728																			
Leu Ile Phe Cys Gly Cys Val Gly Gln Ser Gly Gly Gly Trp Ala His																				
565 570 575																				
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Tyr Val Gly Gln Glu Lys Leu Arg Pro Gln Thr Gly Trp Leu Pro Leu																				
580 585 590																				
gcc ttt gcg ctc gac tgg aac cga cca ccg cgc caa atg aac agc acc	1824																			
Ala Phe Ala Leu Asp Trp Asn Arg Pro Pro Arg Gln Met Asn Ser Thr																				
595 600 605																				
tcg ttt ttc tac aat cat tcc agc caa tgg cgc tat gaa aaa gtc tct	1872																			
Ser Phe Phe Tyr Asn His Ser Ser Gln Trp Arg Tyr Glu Lys Val Ser																				
610 615 620																				
gct cag gag tta ctt tca ccg ctc gcc gat gcc agt aag tac agc ggt	1920																			
Ala Gln Glu Leu Leu Ser Pro Leu Ala Asp Ala Ser Lys Tyr Ser Gly																				
625 630 635 640																				
cat ctg att gat ttc aac gtt cgc gcc gaa cgt atg ggc tgg cta cct	1968																			
His Leu Ile Asp Phe Asn Val Arg Ala Glu Arg Met Gly Trp Leu Pro																				
645 650 655																				

tct gcg ccg cag ctg ggg cgt aac ccg ctc ggg att aaa gct gaa gcc	2016
Ser Ala Pro Gln Leu Gly Arg Asn Pro Leu Gly Ile Lys Ala Glu Ala	
660 665 670	
gac aag gcc gga tta tcc ccc aca gaa ttt acc gcc cag gcg ctg aaa	2064
Asp Lys Ala Gly Leu Ser Pro Thr Glu Phe Thr Ala Gln Ala Leu Lys	
675 680 685	
tcg ggc gat tta cgt atg gcc tgc gaa caa cca gat agc agc agc aat	2112
Ser Gly Asp Leu Arg Met Ala Cys Glu Gln Pro Asp Ser Ser Ser Asn	
690 695 700	
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His Pro Arg Asn Leu Phe Val Trp Arg Ser Asn Leu Leu Gly Ser Ser	
705 710 715 720	
ggc aaa ggc cac gag tat atg cag aag tat ctg ctg ggg acc gaa agc	2208
Gly Lys Gly His Glu Tyr Met Gln Lys Tyr Leu Leu Gly Thr Glu Ser	
725 730 735	
ggg att cag ggc gag gaa ctc ggt gcc agc gac ggg atc aaa ccg gaa	2256
Gly Ile Gln Gly Glu Glu Leu Gly Ala Ser Asp Gly Ile Lys Pro Glu	
740 745 750	
gaa gtc gag tgg caa act gca gcg att gaa ggc aag ctc gac ctg ctg	2304
Glu Val Glu Trp Gln Thr Ala Ala Ile Glu Gly Lys Leu Asp Leu Leu	
755 760 765	
gtg acg ctc gac ttc cgc atg tcc agt acc tgc ctg ttc tcc gat atc	2352
Val Thr Leu Asp Phe Arg Met Ser Ser Thr Cys Leu Phe Ser Asp Ile	
770 775 780	
gtt ctg ccc acc gcc acc tgg tac gaa aaa gac gat atg aac acc tcg	2400
Val Leu Pro Thr Ala Thr Trp Tyr Glu Lys Asp Asp Met Asn Thr Ser	
785 790 795 800	
gat atg cat ccg ttt att cat ccg ctt tct gcg gcg gtc gat ccg gcg	2448
Asp Met His Pro Phe Ile His Pro Leu Ser Ala Ala Val Asp Pro Ala	
805 810 815	
tgg gaa tca cgc agc gac tgg gaa atc tac aaa ggt atc gcc aaa gca	2496
Trp Glu Ser Arg Ser Asp Trp Glu Ile Tyr Lys Gly Ile Ala Lys Ala	
820 825 830	
ttt tcg caa gtg tgc gtg ggt cat ctt ggc aaa gaa acc gac gtg gta	2544
Phe Ser Gln Val Cys Val Gly His Leu Gly Lys Glu Thr Asp Val Val	
835 840 845	
tta caa ccc cta ctg cat gac tct ccg gca gag ctc tca cag ccg tgt	2592
Leu Gln Pro Leu Leu His Asp Ser Pro Ala Glu Leu Ser Gln Pro Cys	
850 855 860	
gaa gtg ctc gac tgg cgc aaa ggc gaa tgc gat ctg att cca ggc aaa	2640
Glu Val Leu Asp Trp Arg Lys Gly Glu Cys Asp Leu Ile Pro Gly Lys	
865 870 875 880	
acc gcg ccg aat att gtg gcg gtg gag cgc gac tac cct gct acg tat	2688
Thr Ala Pro Asn Ile Val Ala Val Glu Arg Asp Tyr Pro Ala Thr Tyr	
885 890 895	

gaa cgc ttt acc tcg ctc ggg cca ttg atg gac aaa ctt ggc aat ggc	2736
Glu Arg Phe Thr Ser Leu Gly Pro Leu Met Asp Lys Leu Gly Asn Gly	
900 905 910	
ggt aaa ggg att tcg tgg aat acc cag gat gaa atc gat ttc ctc ggc	2784
Gly Lys Gly Ile Ser Trp Asn Thr Gln Asp Glu Ile Asp Phe Leu Gly	
915 920 925	
aaa ctc aat tac acc aag cgt gat ggc ccg gca cag ggg cgt ccg ctg	2832
Lys Leu Asn Tyr Thr Lys Arg Asp Gly Pro Ala Gln Gly Arg Pro Leu	
930 935 940	
att gac acc gcc att gac gct tca gaa gtg att ctg gca ctg gca ccg	2880
Ile Asp Thr Ala Ile Asp Ala Ser Glu Val Ile Leu Ala Leu Ala Pro	
945 950 955 960	
gaa acc aac ggt cat gtt gca gtc aaa gcg tgg cag gcg ctg ggc gag	2928
Glu Thr Asn Gly His Val Ala Val Lys Ala Trp Gln Ala Leu Gly Glu	
965 970 975	
atc acc ggg cgc gaa cat acc cat ctg gcg ctg cac aaa gag gac gag	2976
Ile Thr Gly Arg Glu His Thr His Leu Ala Leu His Lys Glu Asp Glu	
980 985 990	
aag att cgc ttt cgc gat att cag gcg cag ccg cgt aaa att atc tcc	3024
Lys Ile Arg Phe Arg Asp Ile Gln Ala Gln Pro Arg Lys Ile Ile Ser	
995 1000 1005	
agc ccc acc tgg tcc ggt ctg gaa agc gat cac gtc tcc tat aac gcg	3072
Ser Pro Thr Trp Ser Gly Leu Glu Ser Asp His Val Ser Tyr Asn Ala	
1010 1015 1020	
gga tac acc aac gtt cat gag tta att ccg tgg cgc acg ctg tcg gga	3120
Gly Tyr Thr Asn Val His Glu Leu Ile Pro Trp Arg Thr Leu Ser Gly	
1025 1030 1035 1040	
cgc cag cag ctc tat cag gat cat ccg tgg atg cgt gct ttt ggt gaa	3168
Arg Gln Gln Leu Tyr Gln Asp His Pro Trp Met Arg Ala Phe Gly Glu	
1045 1050 1055	
agc ctg gtg gct tat cgc ccg cct atc gac acc cgt agc gtc agt gag	3216
Ser Leu Val Ala Tyr Arg Pro Ile Asp Thr Arg Ser Val Ser Glu	
1060 1065 1070	
atg cgc cag ata ccg cca aac ggc ttc ccg gaa aaa gca ctt aac ttc	3264
Met Arg Gln Ile Pro Pro Asn Gly Phe Pro Glu Lys Ala Leu Asn Phe	
1075 1080 1085	
ctg acg ccg cac cag aaa tgg ggc att cac tca acc tac agt gaa aac	3312
Leu Thr Pro His Gln Lys Trp Gly Ile His Ser Thr Tyr Ser Glu Asn	
1090 1095 1100	
ctg cta atg ctg acg ctc tct cgc ggt gga ccg att gtc tgg atc agc	3360
Leu Leu Met Leu Thr Leu Ser Arg Gly Gly Pro Ile Val Trp Ile Ser	
1105 1110 1115 1120	
gaa aca gat gcc cga gaa ctg acc att gtc gat aac gac tgg gtg gaa	3408
Glu Thr Asp Ala Arg Glu Leu Thr Ile Val Asp Asn Asp Trp Val Glu	
1125 1130 1135	
gta ttc aac gcc aac ggc gcg ctg act gcc cgc gcg gtg gtc agc caa	3456

Val	Phe	Asn	Ala	Asn	Gly	Ala	Leu	Thr	Ala	Arg	Ala	Val	Val	Ser	Gln	
			1140					1145					1150			
cgt	gta	ccg	ccg	ggc	atg	acc	atg	atg	tat	cac	gcc	cag	gaa	cgc	att	3504
Arg	Val	Pro	Pro	Gly	Met	Thr	Met	Met	Tyr	His	Ala	Gln	Glu	Arg	Ile	
		1155					1160					1165				
atg	aat	att	cct	ggg	tcg	gaa	gta	act	ggc	atg	cgc	ggc	ggc	att	cat	3552
Met	Asn	Ile	Pro	Gly	Ser	Glu	Val	Thr	Gly	Met	Arg	Gly	Gly	Ile	His	
	1170					1175					1180					
aac	tcg	gtt	acc	cgc	gtt	tgc	ccg	aaa	cca	acg	cat	atg	att	ggc	ggg	3600
Asn	Ser	Val	Thr	Arg	Val	Cys	Pro	Lys	Pro	Thr	His	Met	Ile	Gly	Gly	
1185					1190				1195					1200		
tac	gcg	cag	ctg	gcc	tgg	ggc	ttt	aac	tac	tac	ggc	acc	gtc	gga	tcg	3648
Tyr	Ala	Gln	Leu	Ala	Trp	Gly	Phe	Asn	Tyr	Tyr	Gly	Thr	Val	Gly	Ser	
			1205					1210					1215			
aac	cgc	gat	gag	ttc	atc	atg	atc	cgc	aag	atg	aag	aac	gtt	aac	tgg	3696
Asn	Arg	Asp	Glu	Phe	Ile	Met	Ile	Arg	Lys	Met	Lys	Asn	Val	Asn	Trp	
		1220					1225					1230				
ctg	gat	gat	gaa	ggg	cgc	gat	cag	gta	cag	gag	gcg	aaa	aaa	tga		3741
Leu	Asp	Asp	Glu	Gly	Arg	Asp	Gln	Val	Gln	Glu	Ala	Lys	Lys	*		
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Met	Asp	Leu	Ser	Gln	Leu	Thr	Pro	Arg	Arg	Pro	Tyr	Leu	Leu	Arg	Ala	
1				5					10					15		
ttc	tat	gag	tgg	ttg	ctg	gat	aac	cag	ctc	acg	ccg	cac	ctg	gtg	gtg	96
Phe	Tyr	Glu	Trp	Leu	Leu	Asp	Asn	Gln	Leu	Thr	Pro	His	Leu	Val	Val	
		20					25					30				
gat	gtg	acg	ctc	cct	ggc	gtg	cag	gtt	cct	atg	gaa	tat	gcg	cgt	gac	144
Asp	Val	Thr	Leu	Pro	Gly	Val	Gln	Val	Pro	Met	Glu	Tyr	Ala	Arg	Asp	
		35				40					45					
ggg	caa	atc	gta	ctc	aac	att	gcg	ccg	cgt	gct	gtc	ggc	aat	ctg	gaa	192
Gly	Gln	Ile	Val	Leu	Asn	Ile	Ala	Pro	Arg	Ala	Val	Gly	Asn	Leu	Glu	
	50				55				60							
ctg	gcg	aat	gat	gag	gtg	cgc	ttt	aac	gcg	cgc	ttt	ggg	ggc	att	ccg	240
Leu	Ala	Asn	Asp	Glu	Val	Arg	Phe	Asn	Ala	Arg	Phe	Gly	Gly	Ile	Pro	
	65				70				75					80		
cgt	cag	gtt	tct	gtg	ccg	ctg	gct	gcc	gtg	ctg	gct	atc	tac	gcc	cgt	288
Arg	Gln	Val	Ser	Val	Pro	Leu	Ala	Ala	Val	Leu	Ala	Ile	Tyr	Ala	Arg	

85	90	95	
gaa aat ggc gca ggc acg atg ttt gag cct gaa gct gcc tac gat gaa			336
Glu Asn Gly Ala Gly Thr Met Phe Glu Pro Glu Ala Ala Tyr Asp Glu			
100	105	110	
gat acc agc atc atg aat gat gaa gag gca tcg gca gac aac gaa acc			384
Asp Thr Ser Ile Met Asn Asp Glu Glu Ala Ser Ala Asp Asn Glu Thr			
115	120	125	
gtt atg tcg gtt att gat ggc gac aag cca gat cac gat gat gac act			432
Val Met Ser Val Ile Asp Gly Asp Lys Pro Asp His Asp Asp Asp Thr			
130	135	140	
cat cct gac gat gaa cct ccg cag cca cca cgc ggt ggt cga ccg gca			480
His Pro Asp Asp Glu Pro Pro Gln Pro Pro Arg Gly Gly Arg Pro Ala			
145	150	155	160
tta cgc gtt gtg aag taa			498
Leu Arg Val Val Lys *			
165			
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Met Ala Val Ala Ala Asn Lys Arg Ser Val Met Thr Leu Phe Ser Gly			
1	5	10	15
cct act gac atc tat agc cat cag gtc cgc att gtg ctg gct gag aaa			96
Pro Thr Asp Ile Tyr Ser His Gln Val Arg Ile Val Leu Ala Glu Lys			
20	25	30	
ggt gta agt ttc gag atc gaa cac gtg gaa aag gac aat ccg cct cag			144
Gly Val Ser Phe Glu Ile Glu His Val Glu Lys Asp Asn Pro Pro Gln			
35	40	45	
gat ctg att gac ctc aac ccg aat cag agc gtt ccg acc ctg gtg gat			192
Asp Leu Ile Asp Leu Asn Pro Asn Gln Ser Val Pro Thr Leu Val Asp			
50	55	60	
cgt gag ctg acc ctg tgg gaa tct cgc atc att atg gaa tat ctg gat			240
Arg Glu Leu Thr Leu Trp Glu Ser Arg Ile Ile Met Glu Tyr Leu Asp			
65	70	75	80
gag cgt ttc ccg cat ccg cca ctg atg cct gtt tac ccg gta gct cgc			288
Glu Arg Phe Pro His Pro Pro Leu Met Pro Val Tyr Pro Val Ala Arg			
85	90	95	
ggt gaa agc cgt ctg tac atg cat cgc atc gaa aaa gac tgg tac acg			336
Gly Glu Ser Arg Leu Tyr Met His Arg Ile Glu Lys Asp Trp Tyr Thr			
100	105	110	

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ctg atg aac acc atc atc aac ggt tca gct tct gaa gca gat gcc gca 384
Leu Met Asn Thr Ile Ile Asn Gly Ser Ala Ser Glu Ala Asp Ala Ala
      115              120              125

cgt aag caa ctg cgc gaa gaa ctg ctg gcg att gcg ccg gtc ttc ggt 432
Arg Lys Gln Leu Arg Glu Glu Leu Leu Ala Ile Ala Pro Val Phe Gly
      130              135              140

cag aag ccg tac ttc ctg agc gat gag ttc agc ctg gtc gat tgc tat 480
Gln Lys Pro Tyr Phe Leu Ser Asp Glu Phe Ser Leu Val Asp Cys Tyr
      145              150              155              160

ctt gct ccg ctg ctg tgg cgt ctg ccg caa ctg ggc atc gag ttc agc 528
Leu Ala Pro Leu Leu Trp Arg Leu Pro Gln Leu Gly Ile Glu Phe Ser
              165              170              175

ggc ccg ggt gcg aaa gag ctg aaa ggc tat atg acc cgc gtc ttt gag 576
Gly Pro Gly Ala Lys Glu Leu Lys Gly Tyr Met Thr Arg Val Phe Glu
              180              185              190

cgt gac tct ttc ctt gct tct tta act gaa gca gaa cgt gaa atg cgt 624
Arg Asp Ser Phe Leu Ala Ser Leu Thr Glu Ala Glu Arg Glu Met Arg
      195              200              205

ctg ggc ccg agt taa
Leu Gly Arg Ser *
      210

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<210> 159
<211> 1518
<212> DNA
<213> Escherichia coli

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<220>
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<222> (1)...(1518)

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Met Ser Glu Gln His Ala Gln Gly Ala Asp Ala Val Val Asp Leu Asn
      1              5              10              15

aat gaa ctg aaa acg cgt cgt gag aag ctg gcg aac ctg cgc gag cag 96
Asn Glu Leu Lys Thr Arg Arg Glu Lys Leu Ala Asn Leu Arg Glu Gln
              20              25              30

ggg att gcc ttc ccg aac gat ttc cgt cgc gat cat acc tct gac caa 144
Gly Ile Ala Phe Pro Asn Asp Phe Arg Arg Asp His Thr Ser Asp Gln
      35              40              45

ttg cac gca gaa ttc gac ggc aaa gag aac gaa gaa ctg gaa gcg ctg 192
Leu His Ala Glu Phe Asp Gly Lys Glu Asn Glu Glu Leu Glu Ala Leu
      50              55              60

aac atc gaa gtc gcc gtt gct ggc cgc atg atg acc cgt cgt att atg 240
Asn Ile Glu Val Ala Val Ala Gly Arg Met Met Thr Arg Arg Ile Met
      65              70              75              80

ggt aaa gcg tct ttc gtt acc ctg cag gac gtt ggc ggt cgc att cag 288
Gly Lys Ala Ser Phe Val Thr Leu Gln Asp Val Gly Gly Arg Ile Gln

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85								90				95					
ctg	tac	gtt	gcc	cgt	gac	gat	ctc	cgg	gaa	ggc	gtt	tat	aac	gag	cag	336	
Leu	Tyr	Val	Ala	Arg	Asp	Asp	Leu	Pro	Glu	Gly	Val	Tyr	Asn	Glu	Gln		
			100					105					110				
ttc	aaa	aaa	tgg	gac	ctc	ggc	gac	atc	ctc	ggc	gcg	aaa	ggg	aag	ctg	384	
Phe	Lys	Lys	Trp	Asp	Leu	Gly	Asp	Ile	Leu	Gly	Ala	Lys	Gly	Lys	Leu		
		115					120					125					
ttc	aaa	acc	aaa	acc	ggc	gaa	ctg	tct	atc	cac	tgc	acc	gag	ttg	cgt	432	
Phe	Lys	Thr	Lys	Thr	Gly	Glu	Leu	Ser	Ile	His	Cys	Thr	Glu	Leu	Arg		
		130					135				140						
ctg	ctg	acc	aaa	gca	ctg	cgt	cgg	ctg	cgg	gat	aaa	ttc	cac	ggc	ttg	480	
Leu	Leu	Thr	Lys	Ala	Leu	Arg	Pro	Leu	Pro	Asp	Lys	Phe	His	Gly	Leu		
145						150				155					160		
cag	gat	cag	gaa	gcg	cgc	tat	cgt	cag	cgt	tat	ctc	gat	ctc	atc	tcc	528	
Gln	Asp	Gln	Glu	Ala	Arg	Tyr	Arg	Gln	Arg	Tyr	Leu	Asp	Leu	Ile	Ser		
				165					170					175			
aac	gat	gaa	tcc	cgc	aac	acc	ttt	aaa	gtg	cgc	tcg	cag	atc	ctc	tct	576	
Asn	Asp	Glu	Ser	Arg	Asn	Thr	Phe	Lys	Val	Arg	Ser	Gln	Ile	Leu	Ser		
			180					185					190				
ggg	att	cgc	cag	ttc	atg	gtg	aac	cgc	ggc	ttt	atg	gaa	gtt	gaa	acg	624	
Gly	Ile	Arg	Gln	Phe	Met	Val	Asn	Arg	Gly	Phe	Met	Glu	Val	Glu	Thr		
		195					200					205					
cgg	atg	atg	cag	gtg	atc	cct	ggc	ggg	gcc	gct	gcg	cgt	cgg	ttt	atc	672	
Pro	Met	Met	Gln	Val	Ile	Pro	Gly	Gly	Ala	Ala	Ala	Arg	Pro	Phe	Ile		
	210					215					220						
acc	cac	cat	aac	gcg	ctg	gat	ctc	gac	atg	tac	ctg	cgt	atc	gcg	cgg	720	
Thr	His	His	Asn	Ala	Leu	Asp	Leu	Asp	Met	Tyr	Leu	Arg	Ile	Ala	Pro		
225					230					235				240			
gaa	ctg	tac	ctc	aag	cgt	ctg	gtg	gtt	ggg	ggc	ttc	gag	cgt	gta	ttc	768	
Glu	Leu	Tyr	Leu	Lys	Arg	Leu	Val	Val	Gly	Gly	Phe	Glu	Arg	Val	Phe		
				245					250					255			
gaa	atc	aac	cgt	aac	ttc	cgt	aac	gaa	ggg	att	tcc	gta	cgt	cat	aac	816	
Glu	Ile	Asn	Arg	Asn	Phe	Arg	Asn	Glu	Gly	Ile	Ser	Val	Arg	His	Asn		
			260					265					270				
cca	gag	ttc	acc	atg	atg	gaa	ctc	tac	atg	gct	tac	gca	gat	tac	aaa	864	
Pro	Glu	Phe	Thr	Met	Met	Glu	Leu	Tyr	Met	Ala	Tyr	Ala	Asp	Tyr	Lys		
		275					280					285					
gat	ctg	atc	gag	ctg	acc	gaa	tcg	ctg	ttc	cgt	act	ctg	gca	cag	gat	912	
Asp	Leu	Ile	Glu	Leu	Thr	Glu	Ser	Leu	Phe	Arg	Thr	Leu	Ala	Gln	Asp		
	290					295					300						
att	ctc	ggg	aag	acg	gaa	gtg	acc	tac	ggc	gac	gtg	acg	ctg	gac	ttc	960	
Ile	Leu	Gly	Lys	Thr	Glu	Val	Thr	Tyr	Gly	Asp	Val	Thr	Leu	Asp	Phe		
305					310					315				320			
ggg	aaa	cgg	ttc	gaa	aaa	ctg	acc	atg	cgt	gaa	gcg	atc	aag	aaa	tat	1008	
Gly	Lys	Pro	Phe	Glu	Lys	Leu	Thr	Met	Arg	Glu	Ala	Ile	Lys	Lys	Tyr		
				325					330					335			

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cgc ccg gaa acc gac atg gcg gat ctg gac aac ttc gac tct gcg aaa 1056
Arg Pro Glu Thr Asp Met Ala Asp Leu Asp Asn Phe Asp Ser Ala Lys
          340          345          350

gca att gct gaa tct atc ggc atc cac gtt gag aag agc tgg ggt ctg 1104
Ala Ile Ala Glu Ser Ile Gly Ile His Val Glu Lys Ser Trp Gly Leu
          355          360          365

ggc cgt atc gtt acc gag atc ttc gaa gaa gtg gca gaa gca cat ctg 1152
Gly Arg Ile Val Thr Glu Ile Phe Glu Glu Val Ala Glu Ala His Leu
          370          375          380

att cag ccg acc ttc att act gaa tat ccg gca gaa gtt tct ccg ctg 1200
Ile Gln Pro Thr Phe Ile Thr Glu Tyr Pro Ala Glu Val Ser Pro Leu
          385          390          395          400

gcg cgt cgt aac gac gtt aac ccg gaa atc aca gac cgc ttt gag ttc 1248
Ala Arg Arg Asn Asp Val Asn Pro Glu Ile Thr Asp Arg Phe Glu Phe
          405          410          415

ttc att ggt ggt cgt gaa atc ggt aac ggc ttt agc gag ctg aat gac 1296
Phe Ile Gly Gly Arg Glu Ile Gly Asn Gly Phe Ser Glu Leu Asn Asp
          420          425          430

gcg gaa gat cag gcg caa cgc ttc ctg gat cag gtt gcc gcg aaa gac 1344
Ala Glu Asp Gln Ala Gln Arg Phe Leu Asp Gln Val Ala Ala Lys Asp
          435          440          445

gca ggt gac gac gaa gcg atg ttc tac gat gaa gat tac gtc acc gca 1392
Ala Gly Asp Asp Glu Ala Met Phe Tyr Asp Glu Asp Tyr Val Thr Ala
          450          455          460

ctg gaa cat ggc tta ccg ccg aca gca ggt ctg gga att ggt atc gac 1440
Leu Glu His Gly Leu Pro Pro Thr Ala Gly Leu Gly Ile Gly Ile Asp
          465          470          475          480

cgt atg gta atg ctg ttc acc aac agc cat acc atc cgc gac gtt att 1488
Arg Met Val Met Leu Phe Thr Asn Ser His Thr Ile Arg Asp Val Ile
          485          490          495

ctg ttc ccg gcg atg cgt ccg gta aaa taa 1518
Leu Phe Pro Ala Met Arg Pro Val Lys *
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<210> 160

<211> 1098

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1098)

<400> 160

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Met Phe Glu Ile Asn Pro Val Asn Asn Arg Ile Gln Asp Leu Thr Glu
  1           5           10           15

cgc tcc gac gtt ctt agg ggg tat ctt gac tac gac gcc aag aaa gag 96

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Arg	Ser	Asp	Val	Leu	Arg	Gly	Tyr	Leu	Asp	Tyr	Asp	Ala	Lys	Lys	Glu	
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cgt	ctg	gaa	gaa	gta	aac	gcc	gag	ctg	gaa	cag	ccg	gat	gtc	tgg	aac	144
Arg	Leu	Glu	Glu	Val	Asn	Ala	Glu	Leu	Glu	Gln	Pro	Asp	Val	Trp	Asn	
		35					40					45				
gaa	ccc	gaa	cgc	gca	cag	gcg	ctg	ggt	aaa	gag	cgt	tcc	tcc	ctc	gaa	192
Glu	Pro	Glu	Arg	Ala	Gln	Ala	Leu	Gly	Lys	Glu	Arg	Ser	Ser	Leu	Glu	
	50					55				60						
gcc	gtt	gtc	gac	acc	ctc	gac	caa	atg	aaa	cag	ggg	ctg	gaa	gat	gtt	240
Ala	Val	Val	Asp	Thr	Leu	Asp	Gln	Met	Lys	Gln	Gly	Leu	Glu	Asp	Val	
	65				70				75						80	
tct	ggt	ctg	ctg	gaa	ctg	gct	gta	gaa	gct	gac	gac	gaa	gaa	acc	ttt	288
Ser	Gly	Leu	Leu	Glu	Leu	Ala	Val	Glu	Ala	Asp	Asp	Glu	Glu	Thr	Phe	
			85					90						95		
aac	gaa	gcc	gtt	gct	gaa	ctc	gac	gcc	ctg	gaa	gaa	aaa	ctg	gcg	cag	336
Asn	Glu	Ala	Val	Ala	Glu	Leu	Asp	Ala	Leu	Glu	Glu	Lys	Leu	Ala	Gln	
		100						105					110			
ctt	gag	ttc	cgc	cgt	atg	ttc	tct	ggc	gaa	tat	gac	agc	gcc	gac	tgc	384
Leu	Glu	Phe	Arg	Arg	Met	Phe	Ser	Gly	Glu	Tyr	Asp	Ser	Ala	Asp	Cys	
		115					120					125				
tac	ctc	gat	att	cag	gcg	ggg	tct	ggc	ggt	acg	gaa	gca	cag	gac	tgg	432
Tyr	Leu	Asp	Ile	Gln	Ala	Gly	Ser	Gly	Gly	Thr	Glu	Ala	Gln	Asp	Trp	
	130					135					140					
gcg	agc	atg	ctt	gag	cgt	atg	tat	ctg	cgc	tgg	gca	gaa	tcg	cgt	ggt	480
Ala	Ser	Met	Leu	Glu	Arg	Met	Tyr	Leu	Arg	Trp	Ala	Glu	Ser	Arg	Gly	
	145				150					155					160	
ttc	aaa	act	gaa	atc	atc	gaa	gag	tcg	gaa	ggt	gaa	gtg	gcg	ggt	att	528
Phe	Lys	Thr	Glu	Ile	Ile	Glu	Glu	Ser	Glu	Gly	Glu	Val	Ala	Gly	Ile	
			165					170						175		
aaa	tcc	gtg	acg	atc	aaa	atc	tcc	ggc	gat	tac	gct	tac	ggc	tgg	ctg	576
Lys	Ser	Val	Thr	Ile	Lys	Ile	Ser	Gly	Asp	Tyr	Ala	Tyr	Gly	Trp	Leu	
			180					185					190			
cgt	aca	gaa	acc	ggc	gtt	cac	cgc	ctg	gtg	cgt	aaa	agc	ccg	ttt	gac	624
Arg	Thr	Glu	Thr	Gly	Val	His	Arg	Leu	Val	Arg	Lys	Ser	Pro	Phe	Asp	
		195					200					205				
tcc	ggc	ggt	cgt	cgc	cac	acg	tcg	ttc	agc	tcc	gcg	ttt	gtt	tat	ccg	672
Ser	Gly	Gly	Arg	Arg	His	Thr	Ser	Phe	Ser	Ser	Ala	Phe	Val	Tyr	Pro	
	210					215					220					
gaa	gtt	gat	gat	gat	att	gat	atc	gaa	atc	aac	ccg	gcg	gat	ctg	cgc	720
Glu	Val	Asp	Asp	Asp	Ile	Asp	Ile	Glu	Ile	Asn	Pro	Ala	Asp	Leu	Arg	
	225				230					235				240		
att	gac	gtt	tat	cgc	acg	tcc	ggc	gcg	ggc	ggt	cag	cac	gtt	aac	cgt	768
Ile	Asp	Val	Tyr	Arg	Thr	Ser	Gly	Ala	Gly	Gly	Gln	His	Val	Asn	Arg	
				245				250						255		
acc	gaa	tct	gcg	gtg	cgt	att	acc	cac	atc	ccg	acc	ggg	atc	gtg	acc	816
Thr	Glu	Ser	Ala	Val	Arg	Ile	Thr	His	Ile	Pro	Thr	Gly	Ile	Val	Thr	

260	265	270	
cag tgc cag aac gac cgt tcc	cag cac aag aac aaa gat	cag gcc atg	864
Gln Cys Gln Asn Asp Arg Ser	Gln His Lys Asn Lys Asp	Gln Ala Met	
275	280	285	
aag cag atg aaa gcg aag ctt	tat gaa ctg gag atg cag	aag aaa aat	912
Lys Gln Met Lys Ala Lys Leu	Tyr Glu Leu Glu Met Gln	Lys Lys Asn	
290	295	300	
gcc gag aaa cag gcg atg gaa	gat aac aaa tcc gac atc	ggc tgg ggc	960
Ala Glu Lys Gln Ala Met Glu	Asp Asn Lys Ser Asp Ile	Gly Trp Gly	
305	310	315	320
agc cag att cgt tct tat gtc	ctt gat gac tcc cgc att	aaa gat ctg	1008
Ser Gln Ile Arg Ser Tyr Val	Leu Asp Asp Ser Arg Ile	Lys Asp Leu	
325	330	335	
cgc acc ggg gta gaa acc cgc	aac acg cag gcc gtg ctg	gac ggc agc	1056
Arg Thr Gly Val Glu Thr Arg	Asn Thr Gln Ala Val Leu	Asp Gly Ser	
340	345	350	
ctg gat caa ttt atc gaa gca	agt ttg aaa gca ggg tta	tga	1098
Leu Asp Gln Phe Ile Glu Ala	Ser Leu Lys Ala Gly Leu	*	
355	360	365	

<210> 161

<211> 1734

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1734)

<400> 161

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Met Lys Gln Gln Ile Gln Leu	Arg Arg Arg Glu Val Asp	Glu Thr Ala	
1	5	10	15
gac ttg ccc gct gaa ttg cct	ccc ttg ctg cgc cgt tta	tac gcc agc	96
Asp Leu Pro Ala Glu Leu Pro	Pro Leu Leu Arg Arg Leu	Tyr Ala Ser	
20	25	30	
cgg gga gta cgc agt gcg	caa gaa ctg gaa cgc agt	gtt aaa ggt atg	144
Arg Gly Val Arg Ser Ala Gln	Glu Leu Glu Arg Ser Val	Lys Gly Met	
35	40	45	
ctg ccc tgg cag caa ctg	agc ggc gtc gaa aag gcc	gtt gag atc ctt	192
Leu Pro Trp Gln Gln Leu Ser	Gly Val Glu Lys Ala Val	Glu Ile Leu	
50	55	60	
tac aac gct ttt cgc	gaa gga acg cgg att	att gtg gtc ggt gat	240
Tyr Asn Ala Phe Arg Glu	Gly Thr Arg Ile Ile	Val Val Gly Asp Phe	
65	70	75	80
gac gcc gac ggc gcg	acc agc acg gct cta	agc gtg ctg gcg atg	288
Asp Ala Asp Gly Ala Thr	Ser Thr Ala Leu Ser	Val Leu Ala Met Arg	
85	90	95	

tcg ctt ggt tgc agc aat atc gac tac ctg gta cca aac cgt ttc gaa	336
Ser Leu Gly Cys Ser Asn Ile Asp Tyr Leu Val Pro Asn Arg Phe Glu	
100 105 110	
gac ggt tac ggc tta agc ccg gaa gtg gtc gat cag gcc cat gcc cgt	384
Asp Gly Tyr Gly Leu Ser Pro Glu Val Val Asp Gln Ala His Ala Arg	
115 120 125	
ggc gcg cag tta att gtc acg gtg gat aac ggt att tcc tcc cat gcg	432
Gly Ala Gln Leu Ile Val Thr Val Asp Asn Gly Ile Ser Ser His Ala	
130 135 140	
ggg gtt gag cac gct cgc tcg ttg ggc atc ccg gtt att gtt acc gat	480
Gly Val Glu His Ala Arg Ser Leu Gly Ile Pro Val Ile Val Thr Asp	
145 150 155 160	
cac cat ttg cca ggc gac aca tta ccc gca gcg gaa gcg atc att aac	528
His His Leu Pro Gly Asp Thr Leu Pro Ala Ala Glu Ala Ile Ile Asn	
165 170 175	
cct aac ttg cgc gac tgt aat ttc ccg tcg aaa tca ctg gca ggc gtg	576
Pro Asn Leu Arg Asp Cys Asn Phe Pro Ser Lys Ser Leu Ala Gly Val	
180 185 190	
ggt gtg gcg ttt tat ctg atg ctg gcg ctg cgc acc ttt ttg cgc gat	624
Gly Val Ala Phe Tyr Leu Met Ala Leu Arg Thr Phe Leu Arg Asp	
195 200 205	
cag ggc tgg ttt gat gag cgt aac atc gca att cct aac ctg gca gaa	672
Gln Gly Trp Phe Asp Glu Arg Asn Ile Ala Ile Pro Asn Leu Ala Glu	
210 215 220	
ctg ctg gat ctg gtc gcg ctg ggg aca gtg gcg gac gtc gtg ccg ctg	720
Leu Leu Asp Leu Val Ala Leu Gly Thr Val Ala Asp Val Val Pro Leu	
225 230 235 240	
gac gct aat aat cgc att ctg acc tgg cag ggg atg agt cgc atc cga	768
Asp Ala Asn Asn Arg Ile Leu Thr Trp Gln Gly Met Ser Arg Ile Arg	
245 250 255	
gcc gga aag tgc cgt ccg ggg att aaa gcg ctg ctt gaa gtg gca aac	816
Ala Gly Lys Cys Arg Pro Gly Ile Lys Ala Leu Leu Glu Val Ala Asn	
260 265 270	
cgt gat gca caa aaa ctc gcc gcc agc gat tta ggt ttt gcg ctg ggg	864
Arg Asp Ala Gln Lys Leu Ala Ala Ser Asp Leu Gly Phe Ala Leu Gly	
275 280 285	
cca cgt ctc aat gct gcc gga cga ctg gac gat atg tcc gtc ggt gtg	912
Pro Arg Leu Asn Ala Ala Gly Arg Leu Asp Asp Met Ser Val Gly Val	
290 295 300	
gcg ctg ttg ttg tgc gac aac atc ggc gaa gcg cgc gtg ctg gca aat	960
Ala Leu Leu Leu Cys Asp Asn Ile Gly Glu Ala Arg Val Leu Ala Asn	
305 310 315 320	
gaa ctc gat gcg cta aac cag acg cga aaa gag atc gaa caa gga atg	1008
Glu Leu Asp Ala Leu Asn Gln Thr Arg Lys Glu Ile Glu Gln Gly Met	
325 330 335	

caa att gaa gcc ctg acc ctg tgc gag aaa ctg gag cgc agc cgt gac	1056
Gln Ile Glu Ala Leu Thr Leu Cys Glu Lys Leu Glu Arg Ser Arg Asp	
340 345 350	
acg cta ccc ggc ggg ctg gca atg tat cac ccc gaa tgg cat cag ggc	1104
Thr Leu Pro Gly Gly Leu Ala Met Tyr His Pro Glu Trp His Gln Gly	
355 360 365	
gtt gtc ggt att ctg gct tcg cgc atc aaa gag cgt ttt cac cgt ccg	1152
Val Val Gly Ile Leu Ala Ser Arg Ile Lys Glu Arg Phe His Arg Pro	
370 375 380	
gtt atc gcg ttt gcg cca gca ggt gac ggt acg ctg aaa ggt tcc ggt	1200
Val Ile Ala Phe Ala Pro Ala Gly Asp Gly Thr Leu Lys Gly Ser Gly	
385 390 395 400	
cgc tcc att cag ggg ctg cat atg cgt gat gcg ctg gag cga tta gac	1248
Arg Ser Ile Gln Gly Leu His Met Arg Asp Ala Leu Glu Arg Leu Asp	
405 410 415	
aca ctc tac cct ggc atg atg ctg aag ttt ggc ggt cat gcg atg gcg	1296
Thr Leu Tyr Pro Gly Met Met Leu Lys Phe Gly Gly His Ala Met Ala	
420 425 430	
gcg ggt ttg tcg ctg gaa gag gat aaa ttc aaa ctc ttt caa caa cgg	1344
Ala Gly Leu Ser Leu Glu Glu Asp Lys Phe Lys Leu Phe Gln Gln Arg	
435 440 445	
ttt ggc gaa ctg gtt act gag tgg ctg gac cct tcg cta ttg caa ggc	1392
Phe Gly Glu Leu Val Thr Glu Trp Leu Asp Pro Ser Leu Leu Gln Gly	
450 455 460	
gaa gtg gta tca gac ggt ccg tta agc ccg gcc gaa atg acc atg gaa	1440
Glu Val Val Ser Asp Gly Pro Leu Ser Pro Ala Glu Met Thr Met Glu	
465 470 475 480	
gtg gcg cag ctg ctg cgc gat gct ggc ccg tgg ggg cag atg ttc ccg	1488
Val Ala Gln Leu Leu Arg Asp Ala Gly Pro Trp Gly Gln Met Phe Pro	
485 490 495	
gag ccg ctg ttt gac ggt cat ttc cgt ctg ctg caa cag cgg ctg gtg	1536
Glu Pro Leu Phe Asp Gly His Phe Arg Leu Leu Gln Gln Arg Leu Val	
500 505 510	
ggc gaa cgt cat ttg aag gtg atg gtc gaa ccg gtc ggc ggc ggt cca	1584
Gly Glu Arg His Leu Lys Val Met Val Glu Pro Val Gly Gly Gly Pro	
515 520 525	
ctg ctg gat ggt att gct ttt aat gtc gat acc gcc ctc tgg ccg gat	1632
Leu Leu Asp Gly Ile Ala Phe Asn Val Asp Thr Ala Leu Trp Pro Asp	
530 535 540	
aac ggc gtg cgc gaa gtg caa ctg gct tat aag ctc gat atc aac gag	1680
Asn Gly Val Arg Glu Val Gln Leu Ala Tyr Lys Leu Asp Ile Asn Glu	
545 550 555 560	
ttt cgc ggc aac cgc agc ctg caa att atc atc gac aat atc tgg cca	1728
Phe Arg Gly Asn Arg Ser Leu Gln Ile Ile Ile Asp Asn Ile Trp Pro	
565 570 575	
att tag	1734

Ile *

<210> 162

<211> 711

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(711)

<400> 162

atg aag aaa ggt ttt atg ttg ttt act ttg tta gcg gcg ttt tca ggc	48
Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly	
1 5 10 15	
ttt gct cag gct gat gac gcg gca att caa caa acg tta gcc aaa atg	96
Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met	
20 25 30	
ggc atc aaa agc agc gat att cag ccc gcg cct gta gct ggc atg aag	144
Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys	
35 40 45	
aca gtt ctg act aac agc ggc gtg ttg tac atc acc gat gat ggt aaa	192
Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys	
50 55 60	
cat atc att cag ggg cca atg tat gac gtt agt ggc acg gct ccg gtc	240
His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val	
65 70 75 80	
aat gtc acc aat aag atg ctg tta aag cag ttg aat gcg ctt gaa aaa	288
Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys	
85 90 95	
gag atg atc gtt tat aaa gcg ccg cag gaa aaa cac gtc atc acc gtg	336
Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val	
100 105 110	
ttt act gat att acc tgt ggt tac tgc cac aaa ctg cat gag caa atg	384
Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met	
115 120 125	
gca gac tac aac gcg ctg ggg atc acc gtg cgt tat ctt gct ttc ccg	432
Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro	
130 135 140	
cgc cag ggg ctg gac agc gat gca gag aaa gaa atg aaa gct atc tgg	480
Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp	
145 150 155 160	
tgt gcg aaa gat aaa aac aaa gcg ttt gat gat gtg atg gca ggt aaa	528
Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys	
165 170 175	
agc gtc gca cca gcc agt tgc gac gtg gat att gcc gac cat tac gca	576
Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala	
180 185 190	

ctt ggc gtc cag ctt ggc gtt agc ggt act ccg gca gtt gtg ctg agc 624
 Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
 195 200 205

aat ggc aca ctt gtt ccg ggt tac cag ccg ccg aaa gag atg aaa gaa 672
 Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
 210 215 220

ttc ctc gac gaa cac caa aaa atg acc agc ggt aaa taa 711
 Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys *
 225 230 235

<210> 163

<211> 897

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(897)

<400> 163

gtg aaa cag gat ctg gca cgc atc gag cag ttt ctt gat gct ctg tgg 48
 Met Lys Gln Asp Leu Ala Arg Ile Glu Gln Phe Leu Asp Ala Leu Trp
 1 5 10 15

ctg gaa aaa aat ctg gct gaa aat acg ttg aac gct tac cgt cgc gat 96
 Leu Glu Lys Asn Leu Ala Glu Asn Thr Leu Asn Ala Tyr Arg Arg Asp
 20 25 30

ctg tca atg atg gtg gag tgg ttg cat cac cgc ggg ttg acg ctg gcg 144
 Leu Ser Met Met Val Glu Trp Leu His His Arg Gly Leu Thr Leu Ala
 35 40 45

acg gcg caa agt gac gat ttg cag gca tta ctg gca gaa cgg ctg gag 192
 Thr Ala Gln Ser Asp Asp Leu Gln Ala Leu Leu Ala Glu Arg Leu Glu
 50 55 60

ggc ggg tat aaa gcc acc agc tca gcg cgt ttg ctg agt gca gtg cgc 240
 Gly Gly Tyr Lys Ala Thr Ser Ser Ala Arg Leu Leu Ser Ala Val Arg
 65 70 75 80

cga ttg ttc cag tat ctt tat cgc gaa aag ttt cgt gaa gac gat ccc 288
 Arg Leu Phe Gln Tyr Leu Tyr Arg Glu Lys Phe Arg Glu Asp Asp Pro
 85 90 95

agt gcg cat ctc gct tca ccg aaa ttg ccc cag cgt ttg cca aaa gat 336
 Ser Ala His Leu Ala Ser Pro Lys Leu Pro Gln Arg Leu Pro Lys Asp
 100 105 110

tta agc gaa gcg cag gtc gaa cgt tta tta cag gca cca tta atc gat 384
 Leu Ser Glu Ala Gln Val Glu Arg Leu Leu Gln Ala Pro Leu Ile Asp
 115 120 125

cag cca ctg gag cta cgc gat aaa gcc atg ctt gaa gtg ttg tat gct 432
 Gln Pro Leu Glu Leu Arg Asp Lys Ala Met Leu Glu Val Leu Tyr Ala
 130 135 140

acc ggg ctg cgt gtc tct gaa ctg gtc gga ctg aca atg agt gat atc 480

Thr Gly Leu Arg Val Ser Glu Leu Val Gly Leu Thr Met Ser Asp Ile	
145 150 155 160	
agc ctg cgt cag ggc gtg gta cgg gtc att ggt aaa ggc aac aaa gag	528
Ser Leu Arg Gln Gly Val Val Arg Val Ile Gly Lys Gly Asn Lys Glu	
165 170 175	
cgt ctg gtg cgg tta ggt gaa gag gcg gtt tac tgg ctg gaa acc tat	576
Arg Leu Val Pro Leu Gly Glu Glu Ala Val Tyr Trp Leu Glu Thr Tyr	
180 185 190	
ctg gaa cat ggg cgt cgg tgg ctg ctg aat ggt gtg tca att gac gtg	624
Leu Glu His Gly Arg Pro Trp Leu Leu Asn Gly Val Ser Ile Asp Val	
195 200 205	
ttg ttt ccc agc cag cgt gcg cag cag atg acg cga cag acc ttc tgg	672
Leu Phe Pro Ser Gln Arg Ala Gln Gln Met Thr Arg Gln Thr Phe Trp	
210 215 220	
cac cgt att aaa cat tat gct gtg ctg gcg ggt atc gac agc gaa aag	720
His Arg Ile Lys His Tyr Ala Val Leu Ala Gly Ile Asp Ser Glu Lys	
225 230 235 240	
ctg tca cgg cat gtg ttg cgt cac gct ttt gcc act cat tta tta aat	768
Leu Ser Pro His Val Leu Arg His Ala Phe Ala Thr His Leu Leu Asn	
245 250 255	
cat ggt gcg gat tta cgc gtg gtg cag atg cta ctg gcc cac agc gat	816
His Gly Ala Asp Leu Arg Val Val Gln Met Leu Leu Gly His Ser Asp	
260 265 270	
ctc tcc acc acg caa att tat acg cat gtc gct acc gag cgt ctg cgg	864
Leu Ser Thr Thr Gln Ile Tyr Thr His Val Ala Thr Glu Arg Leu Arg	
275 280 285	
caa ctt cat caa cag cat cac ccg cgg gcg tga	897
Gln Leu His Gln Gln His His Pro Arg Ala *	
290 295	

<210> 164

<211> 1104

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1104)

<400> 164

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Met Ser Asp Ser Gln Thr Leu Val Val Lys Leu Gly Thr Ser Val Leu	
1 5 10 15	
aca gcc gga tcg cgc cgt ctg aac cgt gcc cat atc gtt gaa ctt gtt	96
Thr Gly Gly Ser Arg Arg Leu Asn Arg Ala His Ile Val Glu Leu Val	
20 25 30	
cgc cag tgc gcg cag tta cat gcc gcc ggg cat cgg att gtt att gtg	144
Arg Gln Cys Ala Gln Leu His Ala Ala Gly His Arg Ile Val Ile Val	
35 40 45	

acg tcg ggc gcg atc gcc gcc gga cgt gag cac ctg ggt tac ccg gaa	192
Thr Ser Gly Ala Ile Ala Ala Gly Arg Glu His Leu Gly Tyr Pro Glu	
50 55 60	
ctg cca gcg acc atc gcc tcg aaa caa ctg ctg gcg gcg gta ggg cag	240
Leu Pro Ala Thr Ile Ala Ser Lys Gln Leu Leu Ala Ala Val Gly Gln	
65 70 75 80	
agt cga ctg att caa ctg tgg gaa cag ctg ttt tcg att tat ggc att	288
Ser Arg Leu Ile Gln Leu Trp Glu Gln Leu Phe Ser Ile Tyr Gly Ile	
85 90 95	
cac gtc ggg caa atg ctg ctg acc cgt gct gat atg gaa gac cgt gaa	336
His Val Gly Gln Met Leu Leu Thr Arg Ala Asp Met Glu Asp Arg Glu	
100 105 110	
cgc ttc ctg aac gcc cgc gac acc ctg cga gcg ttg ctc gat aac aat	384
Arg Phe Leu Asn Ala Arg Asp Thr Leu Arg Ala Leu Leu Asp Asn Asn	
115 120 125	
atc gtt ccg gta atc aat gag aac gat gct gtc gct acg gca gag att	432
Ile Val Pro Val Ile Asn Glu Asn Asp Ala Val Ala Thr Ala Glu Ile	
130 135 140	
aag gtc ggc gat aac gat aac ctt tct gcg ctg gcg gcg att ctt gcg	480
Lys Val Gly Asp Asn Asp Asn Leu Ser Ala Leu Ala Ala Ile Leu Ala	
145 150 155 160	
ggg gcc gat aaa ctg ttg ctg ctg acc gat caa aaa ggt ttg tat acc	528
Gly Ala Asp Lys Leu Leu Leu Leu Thr Asp Gln Lys Gly Leu Tyr Thr	
165 170 175	
gct gac ccg cgc agc aat ccg cag gca gaa ctg att aaa gat gtt tac	576
Ala Asp Pro Arg Ser Asn Pro Gln Ala Glu Leu Ile Lys Asp Val Tyr	
180 185 190	
ggc att gat gac gca ctg cgc gcg att gcc ggt gac agc gtt tca ggc	624
Gly Ile Asp Asp Ala Leu Arg Ala Ile Ala Gly Asp Ser Val Ser Gly	
195 200 205	
ctc gga act ggc ggc atg agt acc aaa ttg cag gcc gct gac gtg gct	672
Leu Gly Thr Gly Gly Met Ser Thr Lys Leu Gln Ala Ala Asp Val Ala	
210 215 220	
tgc cgt gcg ggt atc gac acc att att gcc gcg ggc agc aag ccg ggc	720
Cys Arg Ala Gly Ile Asp Thr Ile Ile Ala Ala Gly Ser Lys Pro Gly	
225 230 235 240	
gtt att ggt gat gtg atg gaa ggc att tcc gtc ggt acg ctg ttc cat	768
Val Ile Gly Asp Val Met Glu Gly Ile Ser Val Gly Thr Leu Phe His	
245 250 255	
gcc cag gcg act ccg ctt gaa aac cgt aaa cgc tgg att ttc ggt gcg	816
Ala Gln Ala Thr Pro Leu Glu Asn Arg Lys Arg Trp Ile Phe Gly Ala	
260 265 270	
ccg ccg gcg ggt gaa atc acg gta gat gaa ggg gca act gcc gcc att	864
Pro Pro Ala Gly Glu Ile Thr Val Asp Glu Gly Ala Thr Ala Ala Ile	
275 280 285	

ctg gaa cgc ggc agc tcc ctg ttg ccg aaa ggc att aaa agc gtg act 912
 Leu Glu Arg Gly Ser Ser Leu Leu Pro Lys Gly Ile Lys Ser Val Thr
 290 295 300

ggc aat ttc tcg cgt ggt gaa gtc atc cgc att tgc aac ctc gaa ggc 960
 Gly Asn Phe Ser Arg Gly Glu Val Ile Arg Ile Cys Asn Leu Glu Gly
 305 310 315 320

cgc gat atc gcc cac ggc gtc agt cgt tac aac agc gat gca tta cgc 1008
 Arg Asp Ile Ala His Gly Val Ser Arg Tyr Asn Ser Asp Ala Leu Arg
 325 330 335

cgt att gcc gga cac cac tcg caa gaa att gat gca ata ctg gga tat 1056
 Arg Ile Ala Gly His His Ser Gln Glu Ile Asp Ala Ile Leu Gly Tyr
 340 345 350

gaa tac ggc ccg gtt gcc gtt cac cgt gat gac atg att acc cgt taa 1104
 Glu Tyr Gly Pro Val Ala Val His Arg Asp Asp Met Ile Thr Arg *
 355 360 365

<210> 165
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 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1254)

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 Met Leu Glu Gln Met Gly Ile Ala Ala Lys Gln Ala Ser Tyr Lys Leu
 1 5 10 15

gcg caa ctc tcc agc cgc gaa aaa aat cgc gtg ctg gaa aaa atc gcc 96
 Ala Gln Leu Ser Ser Arg Glu Lys Asn Arg Val Leu Glu Lys Ile Ala
 20 25 30

gat gaa ctg gaa gca caa agc gaa atc atc ctc aac gct aac gcc cag 144
 Asp Glu Leu Glu Ala Gln Ser Glu Ile Ile Leu Asn Ala Asn Ala Gln
 35 40 45

gat gtt gct gac gcg cga gcc aat ggc ctt agc gaa gcg atg ctt gac 192
 Asp Val Ala Asp Ala Arg Ala Asn Gly Leu Ser Glu Ala Met Leu Asp
 50 55 60

cgt ctg gca ctg acg ccc gca cgg ctg aaa ggc att gcc gac gat gta 240
 Arg Leu Ala Leu Thr Pro Ala Arg Leu Lys Gly Ile Ala Asp Asp Val
 65 70 75 80

cgt cag gtg tgc aac ctc gcc gat ccg gtg ggg cag gta atc gat ggc 288
 Arg Gln Val Cys Asn Leu Ala Asp Pro Val Gly Gln Val Ile Asp Gly
 85 90 95

ggc gta ctg gac agc ggc ctg cgt ctt gag cgt cgt cgc gta ccg ctg 336
 Gly Val Leu Asp Ser Gly Leu Arg Leu Glu Arg Arg Arg Val Pro Leu
 100 105 110

ggg gtt att ggc gtg att tat gaa gcg cgc ccg aac gtg acg gtt gat 384

Gly Val Ile Gly Val Ile Tyr Glu Ala Arg Pro Asn Val Thr Val Asp	
115 120 125	
gtc gct tcg ctg tgc ctg aaa acc ggt aat gcg gtg atc ctg cgc ggt	432
Val Ala Ser Leu Cys Leu Lys Thr Gly Asn Ala Val Ile Leu Arg Gly	
130 135 140	
ggc aaa gaa acg tgt cgc act aac gct gca acg gtg gcg gtg att cag	480
Gly Lys Glu Thr Cys Arg Thr Asn Ala Ala Thr Val Ala Val Ile Gln	
145 150 155 160	
gac gcc ctg aaa tcc tgc ggc tta ccg gcg ggt gcc gtg cag gcg att	528
Asp Ala Leu Lys Ser Cys Gly Leu Pro Ala Gly Ala Val Gln Ala Ile	
165 170 175	
gat aat cct gac cgt gcg ctg gtc agt gaa atg ctg cgt atg gat aaa	576
Asp Asn Pro Asp Arg Ala Leu Val Ser Glu Met Leu Arg Met Asp Lys	
180 185 190	
tac atc gac atg ctg atc ccg cgt ggt ggc gct ggt ttg cat aaa ctg	624
Tyr Ile Asp Met Leu Ile Pro Arg Gly Gly Ala Gly Leu His Lys Leu	
195 200 205	
tgc cgt gaa cag tcg aca atc ccg gtg atc aca ggt ggt ata ggc gta	672
Cys Arg Glu Gln Ser Thr Ile Pro Val Ile Thr Gly Gly Ile Gly Val	
210 215 220	
tgc cat att tac gtt gat gaa agt gta gag atc gct gaa gca tta aaa	720
Cys His Ile Tyr Val Asp Glu Ser Val Glu Ile Ala Glu Ala Leu Lys	
225 230 235 240	
gtg atc gtc aac gcg aaa act cag cgt ccg agc aca tgt aat acg gtt	768
Val Ile Val Asn Ala Lys Thr Gln Arg Pro Ser Thr Cys Asn Thr Val	
245 250 255	
gaa acg ttg ctg gtg aat aaa aac atc gcc gat agc ttc ctg ccc gca	816
Glu Thr Leu Leu Val Asn Lys Asn Ile Ala Asp Ser Phe Leu Pro Ala	
260 265 270	
tta agc aaa caa atg gcg gaa agc ggc gtg aca tta cac gca gat gca	864
Leu Ser Lys Gln Met Ala Glu Ser Gly Val Thr Leu His Ala Asp Ala	
275 280 285	
gct gca ctg gcg cag ttg cag gca ggc cct gcg aag gtg gtt gct gtt	912
Ala Ala Leu Ala Gln Leu Gln Ala Gly Pro Ala Lys Val Val Ala Val	
290 295 300	
aaa gcc gaa gag tat gac gat gag ttt ctg tca tta gat ttg aac gtc	960
Lys Ala Glu Glu Tyr Asp Asp Glu Phe Leu Ser Leu Asp Leu Asn Val	
305 310 315 320	
aaa atc gtc agc gat ctt gac gat gcc atc gcc cat att cgt gaa cac	1008
Lys Ile Val Ser Asp Leu Asp Asp Ala Ile Ala His Ile Arg Glu His	
325 330 335	
ggc aca caa cac tcc gat gcg atc ctg acc gcg gat atg cgc aac gcc	1056
Gly Thr Gln His Ser Asp Ala Ile Leu Thr Arg Asp Met Arg Asn Ala	
340 345 350	
cag cgt ttt gtt aac gaa gtg gat tcg tcc gct gtt tac gtt aac gcc	1104
Gln Arg Phe Val Asn Glu Val Asp Ser Ser Ala Val Tyr Val Asn Ala	

355	360	365	
tct acg cgt ttt acc gac ggc ggc cag ttt ggt ctg ggt gcg gaa gtg			1152
Ser Thr Arg Phe Thr Asp Gly Gly Gln Phe Gly Leu Gly Ala Glu Val			
370	375	380	
gcg gta agc aca caa aaa ctc cac gcg cgt ggc cca atg ggg ctg gaa			1200
Ala Val Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Gly Leu Glu			
385	390	395	400
gca ctg acc act tac aag tgg atc ggc att ggt gat tac acc att cgt			1248
Ala Leu Thr Thr Tyr Lys Trp Ile Gly Ile Gly Asp Tyr Thr Ile Arg			
	405	410	415
gcg taa			1254
Ala *			

<210> 166
 <211> 561
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(561)

<400> 166	
atg atg aca agg cag gca tca atg aaa ggc ttc cca att gcg cat att	48
Met Met Thr Arg Gln Ala Ser Met Lys Gly Phe Pro Ile Ala His Ile	
1 5 10 15	
ttt cac cct tca atc ccg cca atg cac gca gtg gtt aac aat cac aat	96
Phe His Pro Ser Ile Pro Pro Met His Ala Val Val Asn Asn His Asn	
20 25 30	
aga aat att gat tat tgg acg gta aaa aga aag ttt gca gaa att gtc	144
Arg Asn Ile Asp Tyr Trp Thr Val Lys Arg Lys Phe Ala Glu Ile Val	
35 40 45	
tcc acc aat gac gtt aat aaa att tac agt ata agt aat gaa ctg cgg	192
Ser Thr Asn Asp Val Asn Lys Ile Tyr Ser Ile Ser Asn Glu Leu Arg	
50 55 60	
aga gta tta tct gca ata act gca ttg aat ttc tat cat ggc gat gtt	240
Arg Val Leu Ser Ala Ile Thr Ala Leu Asn Phe Tyr His Gly Asp Val	
65 70 75 80	
cct tct gtc atg atc cga atc caa ccg gaa aat atg agt cca ttc att	288
Pro Ser Val Met Ile Arg Ile Gln Pro Glu Asn Met Ser Pro Phe Ile	
85 90 95	
ata gat att tct aca gga gaa cat gat gat tat atc ata caa aca tta	336
Ile Asp Ile Ser Thr Gly Glu His Asp Asp Tyr Ile Ile Gln Thr Leu	
100 105 110	
gat gta ggc act ttt gca cct ttt ggt gaa caa tgt act tgc tca gcc	384
Asp Val Gly Thr Phe Ala Pro Phe Gly Glu Gln Cys Thr Cys Ser Ala	
115 120 125	

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gtc aat aaa aaa gag ctg gaa tgt att aag gag acg att tct aag tat 432
Val Asn Lys Lys Glu Leu Glu Cys Ile Lys Glu Thr Ile Ser Lys Tyr
    130                135                140

tgt gca aaa ttc acc cga aaa gaa gcc atc tta acc ccc ctt gtg cac 480
Cys Ala Lys Phe Thr Arg Lys Glu Ala Ile Leu Thr Pro Leu Val His
    145                150                155                160

ttt aat aaa acc agc att act tca gat tgt tgg caa att ctc ttt ttt 528
Phe Asn Lys Thr Ser Ile Thr Ser Asp Cys Trp Gln Ile Leu Phe Phe
                165                170                175

tca ccc gat cat ttt aat aat gat ttt tat tga 561
Ser Pro Asp His Phe Asn Asn Asp Phe Tyr *
                180                185

<210> 167
<211> 1188
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1188)

<400> 167
atg ttc cct gtt tca tca att ggt aat gat att agt agt gat tta gtc 48
Met Phe Pro Val Ser Ser Ile Gly Asn Asp Ile Ser Ser Asp Leu Val
    1                5                10                15

cgt cga aaa atg aat gac ctt cct gaa agc cca aca gga aat aac ctc 96
Arg Arg Lys Met Asn Asp Leu Pro Glu Ser Pro Thr Gly Asn Asn Leu
                20                25                30

gaa gca cta gca cca ggt ata gaa aaa cta aaa cag acc tct att gaa 144
Glu Ala Leu Ala Pro Gly Ile Glu Lys Leu Lys Gln Thr Ser Ile Glu
                35                40                45

atg gtc act tta ctt aac acg tta caa cct ggt gga aaa tgc att atc 192
Met Val Thr Leu Leu Asn Thr Leu Gln Pro Gly Gly Lys Cys Ile Ile
    50                55                60

act ggt gat ttt caa aaa gaa tta gcg tac tta caa aat gta att ctt 240
Thr Gly Asp Phe Gln Lys Glu Leu Ala Tyr Leu Gln Asn Val Ile Leu
    65                70                75                80

tat aat gtc tcg tct ctt cgt ctg gat ttt tta ggt tat aac gcc caa 288
Tyr Asn Val Ser Ser Leu Arg Leu Asp Phe Leu Gly Tyr Asn Ala Gln
                85                90                95

att att caa cga tcg gac aat act tgt gaa ctt acc att aat gaa ccg 336
Ile Ile Gln Arg Ser Asp Asn Thr Cys Glu Leu Thr Ile Asn Glu Pro
                100                105                110

tta aaa aac cag gaa ata tcc aca ggt aat atc aat att aat tgc cca 384
Leu Lys Asn Gln Glu Ile Ser Thr Gly Asn Ile Asn Ile Asn Cys Pro
                115                120                125

tta aaa gat att tac aat gaa atc agg agg tta aac gta att ttt agt 432
Leu Lys Asp Ile Tyr Asn Glu Ile Arg Arg Leu Asn Val Ile Phe Ser

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130	135	140	
tgt ggg act gga gat atc gtt gat cta tcc tct ctg gac tta cgt aat			480
Cys Gly Thr Gly Asp Ile Val Asp Leu Ser Ser Leu Asp Leu Arg Asn			
145	150	155	160
gtc gat tta gat tat tat gat ttc aca gat aaa cat atg gct aat act			528
Val Asp Leu Asp Tyr Tyr Asp Phe Thr Asp Lys His Met Ala Asn Thr			
	165	170	175
att tta aat cct ttt aaa ttg aat tca aca aat ttt act aat gcc aac			576
Ile Leu Asn Pro Phe Lys Leu Asn Ser Thr Asn Phe Thr Asn Ala Asn			
	180	185	190
atg ttt cag gtt aat ttt gtt agt tca aca caa aac gcc aca atc tcc			624
Met Phe Gln Val Asn Phe Val Ser Ser Thr Gln Asn Ala Thr Ile Ser			
	195	200	205
tgg gat tat tta cta aaa ata acg cct gtt tta ata agc att agc gat			672
Trp Asp Tyr Leu Leu Lys Ile Thr Pro Val Leu Ile Ser Ile Ser Asp			
	210	215	220
atg tat tct gaa gaa aaa atc aag ttt gtc gaa agt tgt tta aat gag			720
Met Tyr Ser Glu Glu Lys Ile Lys Phe Val Glu Ser Cys Leu Asn Glu			
	225	230	240
cct gga gac att acc gaa gaa caa tta aaa att atg aga ttt gca att			768
Pro Gly Asp Ile Thr Glu Glu Gln Leu Lys Ile Met Arg Phe Ala Ile			
	245	250	255
ata aaa tct ata cca agg gca act ctt aca gat aaa tta gaa aat gaa			816
Ile Lys Ser Ile Pro Arg Ala Thr Leu Thr Asp Lys Leu Glu Asn Glu			
	260	265	270
tta aca aaa gaa ata tat aaa agc tca tctg aaa atc atc aat tgc ttg			864
Leu Thr Lys Glu Ile Tyr Lys Ser Ser Ser Lys Ile Ile Asn Cys Leu			
	275	280	285
aac aga att aaa tta aca gag atg aaa gaa ttc tca tca gaa aaa ata			912
Asn Arg Ile Lys Leu Thr Glu Met Lys Glu Phe Ser Ser Glu Lys Ile			
	290	295	300
tat gat tac atc gat ata atc att gaa gat tat gaa aat acc aaa gaa			960
Tyr Asp Tyr Ile Asp Ile Ile Ile Glu Asp Tyr Glu Asn Thr Lys Glu			
	305	310	320
aat gct tat ctg gtc gtc ccc caa att aat tat act atg gat tta aac			1008
Asn Ala Tyr Leu Val Val Pro Gln Ile Asn Tyr Thr Met Asp Leu Asn			
	325	330	335
ata gaa gac tct agc tca gaa gag tta ctt tca gat aat acc ctc gag			1056
Ile Glu Asp Ser Ser Ser Glu Glu Leu Leu Ser Asp Asn Thr Leu Glu			
	340	345	350
aaa gac gaa aat tct ccg gac aat ggc ttt gag gtc ggg gaa tat aac			1104
Lys Asp Glu Asn Ser Pro Asp Asn Gly Phe Glu Val Gly Glu Tyr Asn			
	355	360	365
aca tat gaa gca tat aac tca gag aag caa tat ttt acc aga gag gac			1152
Thr Tyr Glu Ala Tyr Asn Ser Glu Lys Gln Tyr Phe Thr Arg Glu Asp			
	370	375	380

tat acg tat gat tac gac ctt tta aat gca ata tag 1188
 Tyr Thr Tyr Asp Tyr Asp Leu Leu Asn Ala Ile *
 385 390 395

<210> 168
 <211> 948
 <212> DNA
 <213> *Escherichia coli*

<220>
 <221> CDS
 <222> (1)...(948)

<400> 168
 gtg tgt cat cgc gca ttt cga ctt cat ctt tgc aag gac tgg gtt ttc 48
 Met Cys His Arg Ala Phe Arg Leu His Leu Cys Lys Asp Trp Val Phe
 1 5 10 15
 atg ttt tct ggg ctg tta atc att ctg gtt ccc ctg att gtg ggt tac 96
 Met Phe Ser Gly Leu Leu Ile Ile Leu Val Pro Leu Ile Val Gly Tyr
 20 25 30
 ctc att ccg ctt cgc caa caa gct gcg tta aaa gtt att aat cag cta 144
 Leu Ile Pro Leu Arg Gln Gln Ala Ala Leu Lys Val Ile Asn Gln Leu
 35 40 45
 tta agc tgg atg gtt tac ctt att ctc ttt ttt atg ggt atc agt ctg 192
 Leu Ser Trp Met Val Tyr Leu Ile Leu Phe Phe Met Gly Ile Ser Leu
 50 55 60
 gcg ttt ctc gat aac ctc gcc agt aac ctg ttg gcg att ctg cat tat 240
 Ala Phe Leu Asp Asn Leu Ala Ser Asn Leu Leu Ala Ile Leu His Tyr
 65 70 75 80
 tct gcc gtc agt att acc gtt att tta ctg tgt aat att gcc gcc ctg 288
 Ser Ala Val Ser Ile Thr Val Ile Leu Leu Cys Asn Ile Ala Ala Leu
 85 90 95
 atg tgg ctg gag cga ggc ctg ccg tgg cgc aac cac cat cag caa gaa 336
 Met Trp Leu Glu Arg Gly Leu Pro Trp Arg Asn His His Gln Gln Glu
 100 105 110
 aaa ctc ccg tcg cgt att gcg atg gcg ctg gag tcg cta aaa ctg tgc 384
 Lys Leu Pro Ser Arg Ile Ala Met Ala Leu Glu Ser Leu Lys Leu Cys
 115 120 125
 ggc gta gta gtg att ggt ttt gcc att ggt cta agt gga ctg gct ttc 432
 Gly Val Val Val Ile Gly Phe Ala Ile Gly Leu Ser Gly Leu Ala Phe
 130 135 140
 tta caa cac gcg acc gaa gcc agt gaa tac acg tta att ttg cta ctt 480
 Leu Gln His Ala Thr Glu Ala Ser Glu Tyr Thr Leu Ile Leu Leu Leu
 145 150 155 160
 ttc ctc gtt ggt att cag ttg cgc aat aat ggc atg acc tta aag cag 528
 Phe Leu Val Gly Ile Gln Leu Arg Asn Asn Gly Met Thr Leu Lys Gln
 165 170 175
 att gtc ctt aat cgc ccg gga atg att gtc gcc gtg gtg gtg gtt gtc 576

Ile Val Leu Asn Arg Arg Gly Met Ile Val Ala Val Val Val Val Val	
180 185 190	
agt tca tta att ggt ggt tta att aac gcc ttt att ctt gat ctc ccc	624
Ser Ser Leu Ile Gly Gly Leu Ile Asn Ala Phe Ile Leu Asp Leu Pro	
195 200 205	
atc aat acc gcg ctg gca atg gcc tcc ggt ttc ggc tgg tat tct ctt	672
Ile Asn Thr Ala Leu Ala Met Ala Ser Gly Phe Gly Trp Tyr Ser Leu	
210 215 220	
tcc ggt att tta ttg acc gaa tct ttt ggt ccg gta atc ggg agc gcg	720
Ser Gly Ile Leu Leu Thr Glu Ser Phe Gly Pro Val Ile Gly Ser Ala	
225 230 235 240	
gcg ttt ttt aat gat ctg gcc cgt gaa ctg att gct att atg ttg atc	768
Ala Phe Phe Asn Asp Leu Ala Arg Glu Leu Ile Ala Ile Met Leu Ile	
245 250 255	
cct ggg ctg att cgc cgc agc cgc tct act gca ctg ggc tta tgc ggt	816
Pro Gly Leu Ile Arg Arg Ser Arg Ser Thr Ala Leu Gly Leu Cys Gly	
260 265 270	
gcc aca tca atg gat ttc acc ctg ccc gtt ctt caa cgt act ggc ggg	864
Ala Thr Ser Met Asp Phe Thr Leu Pro Val Leu Gln Arg Thr Gly Gly	
275 280 285	
ctg gat atg gtc ccg gcg gca att gtt cac ggt ttt att ctt agc ctg	912
Leu Asp Met Val Pro Ala Ala Ile Val His Gly Phe Ile Leu Ser Leu	
290 295 300	
tta gtg ccg atc ctc atc gcc ttt ttc tct gcg taa	948
Leu Val Pro Ile Leu Ile Ala Phe Phe Ser Ala *	
305 310 315	

<210> 169

<211> 291

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (291)

<400> 169

atg caa aac aca act cat gac aac gta att ctg gag ctc acc gtt cgc	48
Met Gln Asn Thr Thr His Asp Asn Val Ile Leu Glu Leu Thr Val Arg	
1 5 10 15	
aac cat ccg ggc gta atg acc cac gtt tgt ggc ctt ttt gcc cgc cgc	96
Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg	
20 25 30	
gct ttt aac gtt gaa ggc att ctt tgt ctg ccg att cag gac agc gac	144
Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp	
35 40 45	
aaa agc cat atc tgg cta ctg gtc aat gac gac cag cgt ctg gag cag	192
Lys Ser His Ile Trp Leu Leu Val Asn Asp Asp Gln Arg Leu Glu Gln	
50 55 60	

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atg ata agc caa atc gat aag ctg gaa gat gtc gtg aaa gtg cag cgt 240
Met Ile Ser Gln Ile Asp Lys Leu Glu Asp Val Val Lys Val Gln Arg
65 70 75 80

aat cag tcc gat ccg acg atg ttt aac aag atc gcg gtg ttt ttt cag 288
Asn Gln Ser Asp Pro Thr Met Phe Asn Lys Ile Ala Val Phe Phe Gln
85 90 95

taa 291
*
```

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<210> 170
<211> 1689
<212> DNA
<213> Escherichia coli
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<220>
<221> CDS
<222> (1)...(1689)
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<400> 170
atg gca agt tcg ggc aca aca tcg acg cgt aag cgc ttt acc ggc gca 48
Met Ala Ser Ser Gly Thr Thr Ser Thr Arg Lys Arg Phe Thr Gly Ala
1 5 10 15

gaa ttt atc gtt cat ttc ctg gaa cag cag ggc att aag att gtg aca 96
Glu Phe Ile Val His Phe Leu Glu Gln Gln Gly Ile Lys Ile Val Thr
20 25 30

ggc att ccg ggc ggt tct atc ctg cct gtt tac gat gcc tta agc caa 144
Gly Ile Pro Gly Gly Ser Ile Leu Pro Val Tyr Asp Ala Leu Ser Gln
35 40 45

agc acg caa atc cgc cat att ctg gcc cgt cat gaa cag ggc gcg ggc 192
Ser Thr Gln Ile Arg His Ile Leu Ala Arg His Glu Gln Gly Ala Gly
50 55 60

ttt atc gct cag gga atg gcg cgc acc gac ggt aaa ccg gcg gtc tgt 240
Phe Ile Ala Gln Gly Met Ala Arg Thr Asp Gly Lys Pro Ala Val Cys
65 70 75 80

atg gcc tgt agc gga ccg ggt gcg act aac ctg gtg acc gcc att gcc 288
Met Ala Cys Ser Gly Pro Gly Ala Thr Asn Leu Val Thr Ala Ile Ala
85 90 95

gat gcg cgg ctg gac tcc atc ccg ctg att tgc atc act ggt cag gtt 336
Asp Ala Arg Leu Asp Ser Ile Pro Leu Ile Cys Ile Thr Gly Gln Val
100 105 110

ccc gcc tcg atg atc ggc acc gac gcc ttc cag gaa gtg gac acc tac 384
Pro Ala Ser Met Ile Gly Thr Asp Ala Phe Gln Glu Val Asp Thr Tyr
115 120 125

ggc atc tct atc ccc atc acc aaa cac aac tat ctg gtc aga cat atc 432
Gly Ile Ser Ile Pro Ile Thr Lys His Asn Tyr Leu Val Arg His Ile
130 135 140

gaa gaa ctc ccg cag gtc atg agc gat gcc ttc cgc att gcg caa tca 480
```

Glu Glu Leu Pro Gln Val Met Ser Asp Ala Phe Arg Ile Ala Gln Ser	
145	150 155 160
ggc cgc cca ggc ccg gtg tgg ata gac att cct aag gat gtg caa acg	528
Gly Arg Pro Gly Pro Val Trp Ile Asp Ile Pro Lys Asp Val Gln Thr	
	165 170 175
gca gtt ttt gag att gaa aca cag ccc gct atg gca gaa aaa gcc gcc	576
Ala Val Phe Glu Ile Glu Thr Gln Pro Ala Met Ala Glu Lys Ala Ala	
	180 185 190
gcc ccc gcc ttt agc gaa gaa agc att cgt gac gca gcg gcg atg att	624
Ala Pro Ala Phe Ser Glu Glu Ser Ile Arg Asp Ala Ala Ala Met Ile	
	195 200 205
aac gct gcc aaa cgc ccg gtg ctt tat ctg ggc ggc ggt gtg atc aat	672
Asn Ala Ala Lys Arg Pro Val Leu Tyr Leu Gly Gly Gly Val Ile Asn	
	210 215 220
gcg ccc gca cgg gtg cgt gaa ctg gcg gag aaa gcg caa ctg cct acc	720
Ala Pro Ala Arg Val Arg Glu Leu Ala Glu Lys Ala Gln Leu Pro Thr	
	225 230 235 240
acc atg act tta atg gcg ctg ggc atg ttg cca aaa gcg cat ccg ttg	768
Thr Met Thr Leu Met Ala Leu Gly Met Leu Pro Lys Ala His Pro Leu	
	245 250 255
tcg ctg ggt atg ctg ggg atg cac ggc gtg cgc agc acc aac tat att	816
Ser Leu Gly Met Leu Gly Met His Gly Val Arg Ser Thr Asn Tyr Ile	
	260 265 270
ttg cag gag gcg gat ttg ttg ata gtg ctc ggt gcg cgt ttt gat gac	864
Leu Gln Glu Ala Asp Leu Leu Ile Val Leu Gly Ala Arg Phe Asp Asp	
	275 280 285
cgg gcg att ggc aaa acc gag cag ttc tgt ccg aat gcc aaa atc att	912
Arg Ala Ile Gly Lys Thr Glu Gln Phe Cys Pro Asn Ala Lys Ile Ile	
	290 295 300
cat gtc gat atc gac cgt gca gag ctg ggt aaa atc aag cag ccg cac	960
His Val Asp Ile Asp Arg Ala Glu Leu Gly Lys Ile Lys Gln Pro His	
	305 310 315 320
gtg gcg att cag gcg gat gtt gat gac gtg ctg gcg cag ttg atc ccg	1008
Val Ala Ile Gln Ala Asp Val Asp Asp Val Leu Ala Gln Leu Ile Pro	
	325 330 335
ctg gtg gaa gcg caa ccg cgt gca gag tgg cac cag ttg gta gcg gat	1056
Leu Val Glu Ala Gln Pro Arg Ala Glu Trp His Gln Leu Val Ala Asp	
	340 345 350
ttg cag cgt gag ttt ccg tgt cca atc ccg aaa gcg tgc gat ccg tta	1104
Leu Gln Arg Glu Phe Pro Cys Pro Ile Pro Lys Ala Cys Asp Pro Leu	
	355 360 365
agc cat tac ggc ctg atc aac gcc gtt gcc gcc tgt gtc gat gac aat	1152
Ser His Tyr Gly Leu Ile Asn Ala Val Ala Ala Cys Val Asp Asp Asn	
	370 375 380
gca att atc acc acc gac gtt ggt cag cat cag atg tgg acc gcg caa	1200
Ala Ile Ile Thr Thr Asp Val Gly Gln His Gln Met Trp Thr Ala Gln	

385	390	395	400	
gct tat ccg ctc aat cgc cca cgc cag tgg ctg acc tcc ggt ggg ctg				1248
Ala Tyr Pro Leu Asn Arg Pro Arg Gln Trp Leu Thr Ser Gly Gly Leu				
	405	410	415	
ggc acg atg ggt ttt ggc ctg cct gcg gcg att ggc gct gcg ctg gcg				1296
Gly Thr Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Ala Leu Ala				
	420	425	430	
aac ccg gat cgc aaa gtg ttg tgt ttc tcc ggc gac ggc agc ctg atg				1344
Asn Pro Asp Arg Lys Val Leu Cys Phe Ser Gly Asp Gly Ser Leu Met				
	435	440	445	
atg aat att cag gag atg gcg acc gcc agt gaa aat cag ctg gat gtc				1392
Met Asn Ile Gln Glu Met Ala Thr Ala Ser Glu Asn Gln Leu Asp Val				
	450	455	460	
aaa atc att ctg atg aac aac gaa gcg ctg ggg ctg gtg cat cag caa				1440
Lys Ile Ile Leu Met Asn Asn Glu Ala Leu Gly Leu Val His Gln Gln				
	465	470	475	480
cag agt ctg ttc tac gag caa ggc gtt ttt gcc gcc acc tat ccg ggc				1488
Gln Ser Leu Phe Tyr Glu Gln Gly Val Phe Ala Ala Thr Tyr Pro Gly				
	485	490	495	
aaa atc aac ttt atg cag att gcc gcc gga ttc ggc ctc gaa acc tgt				1536
Lys Ile Asn Phe Met Gln Ile Ala Ala Gly Phe Gly Leu Glu Thr Cys				
	500	505	510	
gat ttg aat aac gaa gcc gat ccg cag gct tca ttg cag gaa atc atc				1584
Asp Leu Asn Asn Glu Ala Asp Pro Gln Ala Ser Leu Gln Glu Ile Ile				
	515	520	525	
aat cgc cct ggc ccg gcg ctg atc cat gtg cgc att gat gcc gaa gaa				1632
Asn Arg Pro Gly Pro Ala Leu Ile His Val Arg Ile Asp Ala Glu Glu				
	530	535	540	
aaa gtt tac ccg atg gtg ccg cca ggt gcg gcg aat act gaa atg gtg				1680
Lys Val Tyr Pro Met Val Pro Pro Gly Ala Ala Asn Thr Glu Met Val				
	545	550	555	560
ggg gaa taa				1689
Gly Glu *				

<210> 171

<211> 99

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(99)

<400> 171

atg act act tcc atg ctc aac gca aaa cta cta cca act gcg cca tcc 48

Met Thr Thr Ser Met Leu Asn Ala Lys Leu Leu Pro Thr Ala Pro Ser

1

5

10

15

gcc gca gtg gtc gtc gtg cgt gtg gtg gtg gtc gtc ggc aat gcg ccg 96
Ala Ala Val Val Val Val Arg Val Val Val Val Val Gly Asn Ala Pro
20 25 30

tag 99
*

<210> 172
<211> 1017
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1017)

<400> 172
atg ttt gtc atc tgg agc cat aga aca ggg ttc atc atg agt cat caa 48
Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln
1 5 10 15

ctt acc ttc gcc gac agt gaa ttc agc agt aag cgc cgt cag acc aga 96
Leu Thr Phe Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg
20 25 30

aaa gag att ttc ttg tcc cgc atg gag cag att ctg cca tgg caa aac 144
Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn
35 40 45

atg gtg gaa gtc atc gag ccg ttt tac ccc aag gct ggt aat ggc cgg 192
Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg
50 55 60

cga cct tat ccg ctg gaa acc atg cta cgc att cac tgc atg cag cat 240
Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His
65 70 75 80

tgg tac aac ctg agc gat ggc gcg atg gaa gat gct ctg tac gaa atc 288
Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile
85 90 95

gcc tcc atg cgt ctg ttt gcc cgg tta tcc ctg gat agc gcc ttg ccg 336
Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro
100 105 110

gac cgc acc acc atc atg aat ttc cgc cac ctg ctg gag cag cat caa 384
Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln
115 120 125

ctg gcc cgc caa ttg ttc aag acc atc aat cgc tgg ctg gcc gaa gca 432
Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala
130 135 140

ggc gtc atg atg act caa ggc acc ttg gtc gat gcc acc atc att gag 480
Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu
145 150 155 160

gca ccc agc tcg acc aag aac aaa gag cag caa cgc gat ccg gag atg 528
Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met

165	170	175	
cat cag acc aag aaa ggc aat cag tgg cac ttt ggc atg aag gcc cac			576
His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His			
180	185	190	
att ggt gtc gat gcc aag agt ggc ctg acc cac agc ctg gtc acc acc			624
Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr			
195	200	205	
gcg gcc aac gag cat gac ctc aat cag ctg ggt aat ctg ctg cat gga			672
Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly			
210	215	220	
gag gag caa ttt gtc tca gcc gat gcc ggc tac caa ggg gcg cca cag			720
Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln			
225	230	235	240
cgc gag gag ctg gcc gag gtg gat gtg gac tgg ctg atc gcc gag cgc			768
Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg			
245	250	255	
ccc ggc aag gta aga acc ttg aaa cag cat cca cgc aag aac aaa acg			816
Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr			
260	265	270	
gcc atc aac atc gaa tac atg aaa gcc agc atc cgg gcc agg gtg gag			864
Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu			
275	280	285	
cac cca ttt cgc atc atc aag cga cag ttc ggc ttc gtg aaa gcc aga			912
His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg			
290	295	300	
tac aag ggg ttg ctg aaa aac gat aac caa ctg gcg atg tta ttc acg			960
Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr			
305	310	315	320
ctg gcc aac ctg ttt cgg gcg gac caa atg ata cgt cag tgg gag aga			1008
Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg			
325	330	335	
tct cac taa			1017
Ser His *			

<210> 173

<211> 474

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(474)

<400> 173

atg gta tat ata ata atc gtt tcc cac gga cat gaa gac tac atc aaa	48
Met Val Tyr Ile Ile Ile Val Ser His Gly His Glu Asp Tyr Ile Lys	
1	5
	10
	15

aaa tta ctc gaa aat ctt aat gct gac gat gag cac tac aag att atc 96
 Lys Leu Leu Glu Asn Leu Asn Ala Asp Asp Glu His Tyr Lys Ile Ile
 20 25 30

gta cgc gac aac aaa gac tct cta tta ttg aaa caa ata tgc cag cat 144
 Val Arg Asp Asn Lys Asp Ser Leu Leu Leu Lys Gln Ile Cys Gln His
 35 40 45

tat gca ggc ctg gac tat att agt gga ggt gta tac ggc ttt ggt cat 192
 Tyr Ala Gly Leu Asp Tyr Ile Ser Gly Gly Val Tyr Gly Phe Gly His
 50 55 60

aat aat aat att gcg gtg gcg tat gta aag gaa aaa tat aga ccc gca 240
 Asn Asn Asn Ile Ala Val Ala Tyr Val Lys Glu Lys Tyr Arg Pro Ala
 65 70 75 80

gat gat gat tac att ttg ttt ttg aat ccc gat atc atc atg aag cat 288
 Asp Asp Asp Tyr Ile Leu Phe Leu Asn Pro Asp Ile Ile Met Lys His
 85 90 95

gat gat ttg ctg aca tat att aaa tat gtc gaa agt aag cgt tat gct 336
 Asp Asp Leu Leu Thr Tyr Ile Lys Tyr Val Glu Ser Lys Arg Tyr Ala
 100 105 110

ttt agt aca tta tgc ctg ttc cga gat gaa gcg aaa tct tta cat gat 384
 Phe Ser Thr Leu Cys Leu Phe Arg Asp Glu Ala Lys Ser Leu His Asp
 115 120 125

tat tcc gta aga aaa ttt cct gtg ctt tct gat ttt att gtg tca ttt 432
 Tyr Ser Val Arg Lys Phe Pro Val Leu Ser Asp Phe Ile Val Ser Phe
 130 135 140

atg tta ggg att aag gaa ggt gcg aac aag tcc ctg ata tga 474
 Met Leu Gly Ile Lys Glu Gly Ala Asn Lys Ser Leu Ile *
 145 150 155

<210> 174

<211> 1119

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1119)

<400> 174

atg gga aaa agc ata gtc gtt gtt tct gcg gtc aat ttt acc act ggc 48
 Met Gly Lys Ser Ile Val Val Val Ser Ala Val Asn Phe Thr Thr Gly
 1 5 10 15

ggt cca ttt acc att ttg aaa aaa ttt ttg gca gca act aat aat aaa 96
 Gly Pro Phe Thr Ile Leu Lys Lys Phe Leu Ala Ala Thr Asn Asn Lys
 20 25 30

gaa aat gtc agt ttt atc gca tta gtc cat tct gct aaa gag tta aaa 144
 Glu Asn Val Ser Phe Ile Ala Leu Val His Ser Ala Lys Glu Leu Lys
 35 40 45

gaa agt tat cca tgg gtt aaa ttc att gag ttt cct gag gtt aaa ggg 192

Glu	Ser	Tyr	Pro	Trp	Val	Lys	Phe	Ile	Glu	Phe	Pro	Glu	Val	Lys	Gly		
50						55					60						
tcg	tgg	cta	aaa	cgt	ttg	cac	ttt	gaa	tat	gta	gtt	tgt	aaa	aaa	ctt	240	
Ser	Trp	Leu	Lys	Arg	Leu	His	Phe	Glu	Tyr	Val	Val	Cys	Lys	Lys	Leu		
65					70					75					80		
tca	aaa	gag	ctg	aat	gct	acg	cat	tgg	att	tgt	ctg	cat	gat	att	acg	288	
Ser	Lys	Glu	Leu	Asn	Ala	Thr	His	Trp	Ile	Cys	Leu	His	Asp	Ile	Thr		
				85					90					95			
gcc	aat	gtc	gtc	act	aaa	aaa	aga	tat	gtg	tat	tgt	cat	aac	cct	gca	336	
Ala	Asn	Val	Val	Thr	Lys	Lys	Arg	Tyr	Val	Tyr	Cys	His	Asn	Pro	Ala		
			100					105					110				
cct	ttt	tat	aaa	gga	att	tta	ttc	cgt	gaa	att	ctt	atg	gag	cct	agc	384	
Pro	Phe	Tyr	Lys	Gly	Ile	Leu	Phe	Arg	Glu	Ile	Leu	Met	Glu	Pro	Ser		
		115					120					125					
ttt	ttc	tta	ttt	aaa	atg	cta	tac	ggg	ctg	ata	tat	aaa	ata	aac	att	432	
Phe	Phe	Leu	Phe	Lys	Met	Leu	Tyr	Gly	Leu	Ile	Tyr	Lys	Ile	Asn	Ile		
	130					135					140						
aaa	aaa	aat	act	gca	gtg	ttt	gtt	caa	caa	ttc	tgg	atg	aaa	gaa	aaa	480	
Lys	Lys	Asn	Thr	Ala	Val	Phe	Val	Gln	Gln	Phe	Trp	Met	Lys	Glu	Lys		
145					150					155					160		
ttt	atc	aag	aaa	tat	tct	ata	aat	aac	atc	att	gtc	agt	cgg	cca	gaa	528	
Phe	Ile	Lys	Lys	Tyr	Ser	Ile	Asn	Asn	Ile	Ile	Val	Ser	Arg	Pro	Glu		
				165					170					175			
att	aaa	tta	tct	gat	aaa	agc	caa	ctt	act	gat	gat	gat	tct	caa	ttt	576	
Ile	Lys	Leu	Ser	Asp	Lys	Ser	Gln	Leu	Thr	Asp	Asp	Asp	Ser	Gln	Phe		
			180					185						190			
aag	aat	aac	cct	tct	gag	ttg	aca	ata	ttt	tac	cct	gct	gtt	cca	cga	624	
Lys	Asn	Asn	Pro	Ser	Glu	Leu	Thr	Ile	Phe	Tyr	Pro	Ala	Val	Pro	Arg		
		195					200					205					
gta	ttt	aaa	aat	tac	gag	ctt	att	att	agt	gca	gca	agg	aaa	ttg	aaa	672	
Val	Phe	Lys	Asn	Tyr	Glu	Leu	Ile	Ile	Ser	Ala	Ala	Arg	Lys	Leu	Lys		
	210					215					220						
gaa	caa	tcc	aat	att	aaa	ttt	ctg	ctt	act	atc	agt	ggt	aca	gaa	aat	720	
Glu	Gln	Ser	Asn	Ile	Lys	Phe	Leu	Leu	Thr	Ile	Ser	Gly	Thr	Glu	Asn		
225					230					235					240		
gcg	tat	gca	aaa	tat	att	atc	agt	ctt	gca	gaa	gga	ctg	gat	aat	gtt	768	
Ala	Tyr	Ala	Lys	Tyr	Ile	Ile	Ser	Leu	Ala	Glu	Gly	Leu	Asp	Asn	Val		
				245					250					255			
cat	ttc	ctc	ggg	tac	ttg	gat	aaa	gaa	aaa	atc	gat	cat	tgt	tat	aat	816	
His	Phe	Leu	Gly	Tyr	Leu	Asp	Lys	Glu	Lys	Ile	Asp	His	Cys	Tyr	Asn		
			260					265					270				
att	tca	gat	ata	gtt	tgt	ttt	ccc	tct	agg	tta	gaa	aca	tgg	gga	ttg	864	
Ile	Ser	Asp	Ile	Val	Cys	Phe	Pro	Ser	Arg	Leu	Glu	Thr	Trp	Gly	Leu		
		275					280					285					
ccg	ttg	tct	gaa	gct	aaa	gag	cga	ggt	aag	tgg	gta	tta	gca	tca	gat	912	
Pro	Leu	Ser	Glu	Ala	Lys	Glu	Arg	Gly	Lys	Trp	Val	Leu	Ala	Ser	Asp		

290	295	300	
ttc cca ttt act aga gaa act ctt ggt agt tat gaa aag aaa gct ttt			960
Phe Pro Phe Thr Arg Glu Thr Leu Gly Ser Tyr Glu Lys Lys Ala Phe			
305	310	315	320
ttt gat tct aat aac gat gac atg tta gtt aaa ctt att att gac ttc			1008
Phe Asp Ser Asn Asn Asp Asp Met Leu Val Lys Leu Ile Ile Asp Phe			
	325	330	335
aaa aaa ggt aac ctc aaa aaa gat atc tct gat gca aat ttc att tat			1056
Lys Lys Gly Asn Leu Lys Lys Asp Ile Ser Asp Ala Asn Phe Ile Tyr			
	340	345	350
cgt aat gaa aat gta tta gtt ggg ttt gat gaa cta gtt aat ttt att			1104
Arg Asn Glu Asn Val Leu Val Gly Phe Asp Glu Leu Val Asn Phe Ile			
	355	360	365
act gaa gaa cat tga			1119
Thr Glu Glu His *			
370			
/			
<210> 175			
<211> 591			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(591)			
<400> 175			
atg atc tta aaa ctc gct aaa cga tat ggt ctc tgt ggt ttt att cgg			48
Met Ile Leu Lys Leu Ala Lys Arg Tyr Gly Leu Cys Gly Phe Ile Arg			
1	5	10	15
ctt gtt aga gat gtc tta ttg act cgt gta ttt tac cgg aac tgt aga			96
Leu Val Arg Asp Val Leu Leu Thr Arg Val Phe Tyr Arg Asn Cys Arg			
	20	25	30
att att cga ttt ccc tgc tat att cgc aat gat ggt agc att aat ttt			144
Ile Ile Arg Phe Pro Cys Tyr Ile Arg Asn Asp Gly Ser Ile Asn Phe			
	35	40	45
ggt gaa aat ttc aca agt gga gtc ggt ctc agg ctg gat gca ttt gga			192
Gly Glu Asn Phe Thr Ser Gly Val Gly Leu Arg Leu Asp Ala Phe Gly			
	50	55	60
cgt ggc gtg att ttt ttt tcc gat aat gtg caa gtt aac gac tat gtt			240
Arg Gly Val Ile Phe Phe Ser Asp Asn Val Gln Val Asn Asp Tyr Val			
	65	70	75
cat atc gcc tca att gag agc gtt acg ata ggt cgg gat acg ctt att			288
His Ile Ala Ser Ile Glu Ser Val Thr Ile Gly Arg Asp Thr Leu Ile			
	85	90	95
gca agt aaa gta ttt att acc gat cat aat cac ggt tcc ttt aag cac			336
Ala Ser Lys Val Phe Ile Thr Asp His Asn His Gly Ser Phe Lys His			
	100	105	110

tct gat cca atg agt tct cca aat ata cct cca gac atg cgc acg ttg 384
 Ser Asp Pro Met Ser Ser Pro Asn Ile Pro Pro Asp Met Arg Thr Leu
 115 120 125

gaa tct tca gct gtt gta att ggc cag agg gtt tgg ttg ggt gag aat 432
 Glu Ser Ser Ala Val Val Ile Gly Gln Arg Val Trp Leu Gly Glu Asn
 130 135 140

gtg acg gtt ttg cct gga aca att att ggt aat gga gtc gta gtc ggc 480
 Val Thr Val Leu Pro Gly Thr Ile Ile Gly Asn Gly Val Val Val Gly
 145 150 155 160

gcc aat tct gtt gtt aga ggt tct att ccc gaa aat act gtc att gcg 528
 Ala Asn Ser Val Val Arg Gly Ser Ile Pro Glu Asn Thr Val Ile Ala
 165 170 175

gga gta cca gca aaa atc ata aag aaa tac aat cat gag acc aaa tta 576
 Gly Val Pro Ala Lys Ile Ile Lys Lys Tyr Asn His Glu Thr Lys Leu
 180 185 190

tgg gaa aaa gca tag 591
 Trp Glu Lys Ala *
 195

<210> 176

<211> 993

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(993)

<400> 176

atg tat ttt ttg aat gat tta aat ttc tct aga cgc gat gct gga ttt 48
 Met Tyr Phe Leu Asn Asp Leu Asn Phe Ser Arg Arg Asp Ala Gly Phe
 1 5 10 15

aaa gca aga aaa gat gca ctg gac att gct tca gat tat gaa aac att 96
 Lys Ala Arg Lys Asp Ala Leu Asp Ile Ala Ser Asp Tyr Glu Asn Ile
 20 25 30

tct gtt gtt aac att cct cta tgg ggt gga gta gtc cag aga att att 144
 Ser Val Val Asn Ile Pro Leu Trp Gly Gly Val Val Gln Arg Ile Ile
 35 40 45

agt tct gtt aag ctt agt aca ttt ctc tgc ggt ctt gaa aat aaa gat 192
 Ser Ser Val Lys Leu Ser Thr Phe Leu Cys Gly Leu Glu Asn Lys Asp
 50 55 60

gtt tta att ttc aat ttc ccg atg gcc aaa cca ttt tgg cat ata ttg 240
 Val Leu Ile Phe Asn Phe Pro Met Ala Lys Pro Phe Trp His Ile Leu
 65 70 75 80

tca ttc ttt cac cgc ctt cta aaa ttt aga ata gta cct ctg att cat 288
 Ser Phe Phe His Arg Leu Leu Lys Phe Arg Ile Val Pro Leu Ile His
 85 90 95

gat att gat gaa tta aga gga gga ggg ggt agt gat tct gtg cgg ctt 336
 Asp Ile Asp Glu Leu Arg Gly Gly Gly Gly Ser Asp Ser Val Arg Leu

100	105	110	
gct acc tgt gat atg gtc ata agt cac aat cca caa atg aca aag tac			384
Ala Thr Cys Asp Met Val Ile Ser His Asn Pro Gln Met Thr Lys Tyr			
115	120	125	
ctt agt aaa tat atg tct cag gat aaa atc aaa gac ata aaa ata ttt			432
Leu Ser Lys Tyr Met Ser Gln Asp Lys Ile Lys Asp Ile Lys Ile Phe			
130	135	140	
gat tac ctc gtc tca tct gat gtg gag cat cga gat gtt acg gat aag			480
Asp Tyr Leu Val Ser Ser Asp Val Glu His Arg Asp Val Thr Asp Lys			
145	150	155	160
caa cga ggg gtc ata tat gct ggc aac ctt tct agg cat aaa tgt tct			528
Gln Arg Gly Val Ile Tyr Ala Gly Asn Leu Ser Arg His Lys Cys Ser			
165	170	175	
ttc ata tat act gaa gga tgc gat ttt act ctc ttt ggt gtc aac tat			576
Phe Ile Tyr Thr Glu Gly Cys Asp Phe Thr Leu Phe Gly Val Asn Tyr			
180	185	190	
gaa aat aaa gat aat cct aaa tat ctt gga agt ttt gat gct caa tct			624
Glu Asn Lys Asp Asn Pro Lys Tyr Leu Gly Ser Phe Asp Ala Gln Ser			
195	200	205	
ccg gaa aag att aac ctc cca ggc atg caa ttt gga ctc att tgg gat			672
Pro Glu Lys Ile Asn Leu Pro Gly Met Gln Phe Gly Leu Ile Trp Asp			
210	215	220	
gga gat tct gtc gaa acc tgt agt ggt gcc ttt ggc gac tat tta aag			720
Gly Asp Ser Val Glu Thr Cys Ser Gly Ala Phe Gly Asp Tyr Leu Lys			
225	230	235	240
ttt aat aac cct cat aag aca tct ctt tat ctt tca atg gaa ctt cca			768
Phe Asn Asn Pro His Lys Thr Ser Leu Tyr Leu Ser Met Glu Leu Pro			
245	250	255	
gta ttt ata tgg gat aaa gcc gcc ctt gcg gat ttc att gta gat aat			816
Val Phe Ile Trp Asp Lys Ala Ala Leu Ala Asp Phe Ile Val Asp Asn			
260	265	270	
aga ata gga tat gca gtg gga tca atc aaa gaa atg caa gag att gtt			864
Arg Ile Gly Tyr Ala Val Gly Ser Ile Lys Glu Met Gln Glu Ile Val			
275	280	285	
gac tcc atg aca ata gaa act tat aag caa att agt gag aat aca aaa			912
Asp Ser Met Thr Ile Glu Thr Tyr Lys Gln Ile Ser Glu Asn Thr Lys			
290	295	300	
att att tct cag aaa att cga aca gga agt tac ttc agg gat gtt ctt			960
Ile Ile Ser Gln Lys Ile Arg Thr Gly Ser Tyr Phe Arg Asp Val Leu			
305	310	315	320
gaa gag gtg atc gat gat ctt aaa act cgc taa			993
Glu Glu Val Ile Asp Asp Leu Lys Thr Arg *			
325	330		

<210> 177

<211> 1167

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1167)

<400> 177

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atg atc tat ctt gta att agt gtc ttt ctc att aca gca ttt atc tgt 48
Met Ile Tyr Leu Val Ile Ser Val Phe Leu Ile Thr Ala Phe Ile Cys
 1             5             10             15

tta tat ctt aag aag gat ata ttt tat cca gcc gta tgc gtt aat atc 96
Leu Tyr Leu Lys Lys Asp Ile Phe Tyr Pro Ala Val Cys Val Asn Ile
             20             25             30

atc ttc gca ctg gtc tta ttg gga tat gaa ata acg tca gat ata tat 144
Ile Phe Ala Leu Val Leu Leu Gly Tyr Glu Ile Thr Ser Asp Ile Tyr
             35             40             45

gct ttt cag tta aat gac gct acg ttg att ttt cta ctt tgc aat gtt 192
Ala Phe Gln Leu Asn Asp Ala Thr Leu Ile Phe Leu Leu Cys Asn Val
             50             55             60

ttg aca ttt acc ctg tca tgt tta ttg acg gaa agt gta tta gat cta 240
Leu Thr Phe Thr Leu Ser Cys Leu Leu Thr Glu Ser Val Leu Asp Leu
             65             70             75             80

aat atc aga aaa gtc aat aat gct att tat agc ata cca tcg aag aaa 288
Asn Ile Arg Lys Val Asn Asn Ala Ile Tyr Ser Ile Pro Ser Lys Lys
             85             90             95

gtg cat aat gta ggc ttg tta gtt att tct ttt tcg atg ata tat ata 336
Val His Asn Val Gly Leu Leu Val Ile Ser Phe Ser Met Ile Tyr Ile
             100             105             110

tgc atg agg tta agt aac tac cag ttc ggg act agc tta ctt agc tat 384
Cys Met Arg Leu Ser Asn Tyr Gln Phe Gly Thr Ser Leu Leu Ser Tyr
             115             120             125

atg aat ttg ata aga gat gct gat gtt gaa gac aca tca aga aat ttc 432
Met Asn Leu Ile Arg Asp Ala Asp Val Glu Asp Thr Ser Arg Asn Phe
             130             135             140

tca gca tac atg cag cca atc att cta act act ttt gct tta ttt att 480
Ser Ala Tyr Met Gln Pro Ile Ile Leu Thr Thr Phe Ala Leu Phe Ile
             145             150             155             160

tgg tct aaa aaa ttt act aat aca aag gta agt aaa aca ttt act tta 528
Trp Ser Lys Lys Phe Thr Asn Thr Lys Val Ser Lys Thr Phe Thr Leu
             165             170             175

ctt gtt ttt att gta ttc atc ttt gca att ata ctg aat act ggt aag 576
Leu Val Phe Ile Val Phe Ile Phe Ala Ile Ile Leu Asn Thr Gly Lys
             180             185             190

caa att gtc ttt atg gtt atc atc tct tat gca ttc atc gta ggt gtt 624
Gln Ile Val Phe Met Val Ile Ile Ser Tyr Ala Phe Ile Val Gly Val
             195             200             205

aat aga gta aaa cat tat gtt tat ctt att aca gct gta ggt gtt cta 672

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Asn	Arg	Val	Lys	His	Tyr	Val	Tyr	Leu	Ile	Thr	Ala	Val	Gly	Val	Leu	
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ttc	tcc	ttg	tat	atg	ctc	ttt	tta	cgt	gga	ctg	cct	ggg	ggg	atg	gca	720
Phe	Ser	Leu	Tyr	Met	Leu	Phe	Leu	Arg	Gly	Leu	Pro	Gly	Gly	Met	Ala	
225					230					235					240	
tat	tat	cta	tcc	atg	tat	ttg	gtc	agc	cct	ata	atc	gcg	ttt	cag	gag	768
Tyr	Tyr	Leu	Ser	Met	Tyr	Leu	Val	Ser	Pro	Ile	Ile	Ala	Phe	Gln	Glu	
				245					250					255		
ttt	tat	ttt	cag	caa	gta	tct	aac	tct	gcc	agt	tct	cat	gtc	ttt	tgg	816
Phe	Tyr	Phe	Gln	Gln	Val	Ser	Asn	Ser	Ala	Ser	Ser	His	Val	Phe	Trp	
			260					265					270			
ttt	ttt	gaa	agg	ctg	atg	ggg	cta	tta	aca	ggg	gga	gtc	tct	atg	tcg	864
Phe	Phe	Glu	Arg	Leu	Met	Gly	Leu	Leu	Thr	Gly	Gly	Val	Ser	Met	Ser	
		275					280					285				
ttg	cat	aaa	gaa	ttt	gtg	tgg	gtg	ggg	ttg	cca	aca	aat	gtt	tat	act	912
Leu	His	Lys	Glu	Phe	Val	Trp	Val	Gly	Leu	Pro	Thr	Asn	Val	Tyr	Thr	
	290					295				300						
gct	ttt	tcg	gat	tat	gtt	tat	att	tcc	gcg	gag	cta	agc	tat	ttg	atg	960
Ala	Phe	Ser	Asp	Tyr	Val	Tyr	Ile	Ser	Ala	Glu	Leu	Ser	Tyr	Leu	Met	
305					310				315					320		
atg	gtt	att	cat	ggc	tgt	att	tca	ggg	gtt	tta	tgg	aga	ttg	tct	cga	1008
Met	Val	Ile	His	Gly	Cys	Ile	Ser	Gly	Val	Leu	Trp	Arg	Leu	Ser	Arg	
				325				330					335			
aat	tac	ata	tct	gtg	aaa	ata	ttt	tat	tca	tat	ttt	att	tat	acc	ttt	1056
Asn	Tyr	Ile	Ser	Val	Lys	Ile	Phe	Tyr	Ser	Tyr	Phe	Ile	Tyr	Thr	Phe	
			340				345						350			
tct	ttc	att	ttt	tat	cat	gaa	agc	ttc	atg	act	aat	att	agc	agt	tgg	1104
Ser	Phe	Ile	Phe	Tyr	His	Glu	Ser	Phe	Met	Thr	Asn	Ile	Ser	Ser	Trp	
		355				360						365				
ata	caa	ata	act	ctt	tgt	atc	ata	gta	ttc	tct	caa	ttt	ctt	aag	gcc	1152
Ile	Gln	Ile	Thr	Leu	Cys	Ile	Ile	Val	Phe	Ser	Gln	Phe	Leu	Lys	Ala	
		370				375					380					
cag	aaa	ata	aag	tga												1167
Gln	Lys	Ile	Lys	*												
385																

<210> 178

<211> 1104

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1104)

<400> 178

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Met	Tyr	Asp	Tyr	Ile	Ile	Val	Gly	Ser	Gly	Leu	Phe	Gly	Ala	Val	Cys	
1				5				10					15			

gcg aat gag tta aaa aag cta aac aaa aaa gtt tta gtg att gag aaa	96
Ala Asn Glu Leu Lys Lys Leu Asn Lys Lys Val Leu Val Ile Glu Lys	
20 25 30	
aga aat cat atc ggt gga aat gcg tac aca gag gac tgt gag ggt atc	144
Arg Asn His Ile Gly Gly Asn Ala Tyr Thr Glu Asp Cys Glu Gly Ile	
35 40 45	
cag att cat aaa tat ggt gca cat att ttt cat acc aat gat aaa tat	192
Gln Ile His Lys Tyr Gly Ala His Ile Phe His Thr Asn Asp Lys Tyr	
50 55 60	
ata tgg gat tac gtt aat gat tta gta gaa ttt aat cgt ttt act aat	240
Ile Trp Asp Tyr Val Asn Asp Leu Val Glu Phe Asn Arg Phe Thr Asn	
65 70 75 80	
tct cca ctg gcg att tat aaa gac aaa tta ttc aac ctt cct ttt aat	288
Ser Pro Leu Ala Ile Tyr Lys Asp Lys Leu Phe Asn Leu Pro Phe Asn	
85 90 95	
atg aat act ttc cac caa atg tgg gga gtt aaa gat cct caa gaa gct	336
Met Asn Thr Phe His Gln Met Trp Gly Val Lys Asp Pro Gln Glu Ala	
100 105 110	
caa aat atc att aat gct cag aaa aaa aag tat ggt gac aag gta cct	384
Gln Asn Ile Ile Asn Ala Gln Lys Lys Tyr Gly Asp Lys Val Pro	
115 120 125	
gaa aat ttg gag gag cag gcg att tca tta gtt ggg gag gac tta tac	432
Glu Asn Leu Glu Glu Gln Ala Ile Ser Leu Val Gly Glu Asp Leu Tyr	
130 135 140	
caa gca ttg ata aag ggt tat acg gag aag cag tgg gga aga agt gca	480
Gln Ala Leu Ile Lys Gly Tyr Thr Glu Lys Gln Trp Gly Arg Ser Ala	
145 150 155 160	
aaa gaa ttg cct gca ttt att att aag cga atc cca gtg aga ttt acg	528
Lys Glu Leu Pro Ala Phe Ile Ile Lys Arg Ile Pro Val Arg Phe Thr	
165 170 175	
ttt gat aac aat tat ttt tcc gat cgc tat caa ggt att ccg gtg gga	576
Phe Asp Asn Asn Tyr Phe Ser Asp Arg Tyr Gln Gly Ile Pro Val Gly	
180 185 190	
ggc tac act aag ctt att gaa aaa atg ctt gaa ggt gtg gac gta aaa	624
Gly Tyr Thr Lys Leu Ile Glu Lys Met Leu Glu Gly Val Asp Val Lys	
195 200 205	
tta ggc att gat ttt ttg aaa gac aaa gat tct cta gcg agt aaa gcc	672
Leu Gly Ile Asp Phe Leu Lys Asp Lys Asp Ser Leu Ala Ser Lys Ala	
210 215 220	
cat aga atc atc tac act gga ccc att gat cag tac ttc gac tat agg	720
His Arg Ile Ile Tyr Thr Gly Pro Ile Asp Gln Tyr Phe Asp Tyr Arg	
225 230 235 240	
ttt gga gcg tta gaa tat cgc tct tta aaa ttt gag acg gaa cgc cat	768
Phe Gly Ala Leu Glu Tyr Arg Ser Leu Lys Phe Glu Thr Glu Arg His	
245 250 255	

gaa ttt cca aac ttc caa ggg aat gca gta ata aat ttc act gat gct 816
 Glu Phe Pro Asn Phe Gln Gly Asn Ala Val Ile Asn Phe Thr Asp Ala
 260 265 270

aat gta cca tat acc aga ata att gag cat aaa cat ttt gac tat gtt 864
 Asn Val Pro Tyr Thr Arg Ile Ile Glu His Lys His Phe Asp Tyr Val
 275 280 285

gag aca aag cat acg gtt gtt aca aaa gaa tat cca tta gag tgg aaa 912
 Glu Thr Lys His Thr Val Thr Lys Glu Tyr Pro Leu Glu Trp Lys
 290 295 300

gtt ggc gac gaa ccc tac tat cca gtt aat gat aat aaa aac atg gag 960
 Val Gly Asp Glu Pro Tyr Tyr Pro Val Asn Asp Asn Lys Asn Met Glu
 305 310 315 320

ctt ttt aag aaa tat aga gag tta gct agc aga gaa gac aag gtt ata 1008
 Leu Phe Lys Lys Tyr Arg Glu Leu Ala Ser Arg Glu Asp Lys Val Ile
 325 330 335

ttt ggc ggg cgt ttg gcc gag tat aaa tat tat gat atg cat caa gtg 1056
 Phe Gly Gly Arg Leu Ala Glu Tyr Lys Tyr Tyr Asp Met His Gln Val
 340 345 350

ata tct gcc gct ctt tat caa gtg aaa aat ata atg agt acg gat taa 1104
 Ile Ser Ala Ala Leu Tyr Gln Val Lys Asn Ile Met Ser Thr Asp *
 355 360 365

<210> 179
 <211> 693
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(693)

<400> 179
 ttg aca tca tca ata acc aat gaa att atg caa tta tat acg gat agg 48
 Met Thr Ser Ser Ile Thr Asn Glu Ile Met Gln Leu Tyr Thr Asp Arg
 1 5 10 15

gag gtt ctt aac atg ggg ctt tgt agt cgt tat aaa agt ctt aca tgc 96
 Glu Val Leu Asn Met Gly Leu Cys Ser Arg Tyr Lys Ser Leu Thr Cys
 20 25 30

aat agt tgc tca atg cat tgc caa ata atg cca gaa gag tca ccg cgt 144
 Asn Ser Cys Ser Met His Cys Gln Ile Met Pro Glu Glu Ser Pro Arg
 35 40 45

ttg cag tat tgc gca aac tcg tgt ttt tgt atg tgg ccc gaa gaa agt 192
 Leu Gln Tyr Cys Ala Asn Ser Cys Phe Cys Met Trp Pro Glu Glu Ser
 50 55 60

tca tat ttt aat cgt ggt gtg gta gaa ggt atc tta aca aaa aac cac 240
 Ser Tyr Phe Asn Arg Gly Val Val Glu Gly Ile Leu Thr Lys Asn His
 65 70 75 80

aat gcg aga tta agc gga tat att ttt gtc gat ttt tca gta agt ttt 288

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Asn Ala Arg Leu Ser Gly Tyr Ile Phe Val Asp Phe Ser Val Ser Phe
      85                      90                      95

tta cgt cta ttc ctt gaa aaa gac tgg att gac tat ctt gca agt act 336
Leu Arg Leu Phe Leu Glu Lys Asp Trp Ile Asp Tyr Leu Ala Ser Thr
      100                      105                      110

gac atg ggg att gtt tta gtc agc gac cgc aat atg caa tcg tta gct 384
Asp Met Gly Ile Val Leu Val Ser Asp Arg Asn Met Gln Ser Leu Ala
      115                      120                      125

aat tac tgg cga aaa cac aac tca gca ata tct gct gtc ata tat aat 432
Asn Tyr Trp Arg Lys His Asn Ser Ala Ile Ser Ala Val Ile Tyr Asn
      130                      135                      140

gat gat ggt ctt gat gtt gcc aat gaa aag atc aga caa cta ttt att 480
Asp Asp Gly Leu Asp Val Ala Asn Glu Lys Ile Arg Gln Leu Phe Ile
      145                      150                      155                      160

ggt cgt tat tta tca ttt acc gga ggt aac aca tta act cag atg gaa 528
Gly Arg Tyr Leu Ser Phe Thr Gly Gly Asn Thr Leu Thr Gln Met Glu
      165                      170                      175

ttc acc ata atg ggg tat atg gtt tct ggt tat aat cca tat cag att 576
Phe Thr Ile Met Gly Tyr Met Val Ser Gly Tyr Asn Pro Tyr Gln Ile
      180                      185                      190

gct gaa gtt ctg gat atg gat atc cgt agc atc tac gcg tac aag caa 624
Ala Glu Val Leu Asp Met Asp Ile Arg Ser Ile Tyr Ala Tyr Lys Gln
      195                      200                      205

cga atc gaa aag aga atg ggt ggt aaa ata aac gaa tta ttt att cgt 672
Arg Ile Glu Lys Arg Met Gly Gly Lys Ile Asn Glu Leu Phe Ile Arg
      210                      215                      220

tca cat tcg gtc caa cat tga 693
Ser His Ser Val Gln His *
      225                      230

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<210> 180

<211> 1176

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (1176)

<400> 180

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atg caa aaa ctg att aac tca gtg caa aac tat gcc tgg ggc agc aaa 48
Met Gln Lys Leu Ile Asn Ser Val Gln Asn Tyr Ala Trp Gly Ser Lys
      1                      5                      10                      15

acg gcg ttg act gaa ctt tat ggt atg gaa aat ccg tcc agc cag ccg 96
Thr Ala Leu Thr Glu Leu Tyr Gly Met Glu Asn Pro Ser Ser Gln Pro
      20                      25                      30

atg gcc gag ctg tgg atg ggc gca cat ccg aaa agc agt tca cga gtg 144
Met Ala Glu Leu Trp Met Gly Ala His Pro Lys Ser Ser Ser Arg Val
      35                      40                      45

```

cag aat gcc gcc gga gat atc gtt tca ctg cgt gat gtg att gag agt	192
Gln Asn Ala Ala Gly Asp Ile Val Ser Leu Arg Asp Val Ile Glu Ser	
50 55 60	
gat aaa tcg act ctg ctc gga gag gcc gtt gcc aaa cgc ttt ggc gaa	240
Asp Lys Ser Thr Leu Leu Gly Glu Ala Val Ala Lys Arg Phe Gly Glu	
65 70 75 80	
ctg cct ttc ctg ttc aaa gta tta tgc gca gca cag cca ctc tcc att	288
Leu Pro Phe Leu Phe Lys Val Leu Cys Ala Ala Gln Pro Leu Ser Ile	
85 90 95	
cag gtt cat cca aac aaa cac aat tct gaa atc ggt ttt gcc aaa gaa	336
Gln Val His Pro Asn Lys His Asn Ser Glu Ile Gly Phe Ala Lys Glu	
100 105 110	
aat gcc gca ggt atc ccg atg gat gcc gcc gag cgt aac tat aaa gat	384
Asn Ala Ala Gly Ile Pro Met Asp Ala Ala Glu Arg Asn Tyr Lys Asp	
115 120 125	
cct aac cac aag ccg gag ctg gtt ttt gcg ctg acg cct ttc ctt gcg	432
Pro Asn His Lys Pro Glu Leu Val Phe Ala Leu Thr Pro Phe Leu Ala	
130 135 140	
atg aac gcg ttt cgt gaa ttt tcc gag att gtc tcc cta ctc cag ccg	480
Met Asn Ala Phe Arg Glu Phe Ser Glu Ile Val Ser Leu Leu Gln Pro	
145 150 155 160	
gtc gca ggt gca cat ccg gcg att gct cac ttt tta caa cag cct gat	528
Val Ala Gly Ala His Pro Ala Ile Ala His Phe Leu Gln Gln Pro Asp	
165 170 175	
gcc gaa cgt tta agc gaa ctg ttc gcc agc ctg ttg aat atg cag ggt	576
Ala Glu Arg Leu Ser Glu Leu Phe Ala Ser Leu Leu Asn Met Gln Gly	
180 185 190	
gaa gaa aaa tcc cgc gcg ctg gcg att tta aaa tcg gcc ctc gat agc	624
Glu Glu Lys Ser Arg Ala Leu Ala Ile Leu Lys Ser Ala Leu Asp Ser	
195 200 205	
cag cag ggt gaa ccg tgg caa acg att cgt tta att tct gaa ttt tac	672
Gln Gln Gly Glu Pro Trp Gln Thr Ile Arg Leu Ile Ser Glu Phe Tyr	
210 215 220	
ccg gaa gac agc ggt ctg ttc tcc ccg cta ttg ctg aat gtg gtg aaa	720
Pro Glu Asp Ser Gly Leu Phe Ser Pro Leu Leu Leu Asn Val Val Lys	
225 230 235 240	
ttg aac cct ggc gaa gcg atg ttc ctg ttc gct gaa aca ccg cac gct	768
Leu Asn Pro Gly Glu Ala Met Phe Leu Phe Ala Glu Thr Pro His Ala	
245 250 255	
tac ctg caa ggc gtg gcg ctg gaa gtg atg gca aac tcc gat aac gtg	816
Tyr Leu Gln Gly Val Ala Leu Glu Val Met Ala Asn Ser Asp Asn Val	
260 265 270	
ctg cgt gcg ggt ctg acg cct aaa tac att gat att ccg gaa ctg gtt	864
Leu Arg Ala Gly Leu Thr Pro Lys Tyr Ile Asp Ile Pro Glu Leu Val	
275 280 285	

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gcc aat gtg aaa ttc gaa gcc aaa ccg gct aac cag ttg ttg acc cag 912
Ala Asn Val Lys Phe Glu Ala Lys Pro Ala Asn Gln Leu Leu Thr Gln
290 295 300

ccg gtg aaa caa ggt gca gaa ctg gac ttc ccg att cca gtg gat gat 960
Pro Val Lys Gln Gly Ala Glu Leu Asp Phe Pro Ile Pro Val Asp Asp
305 310 315 320

ttt gcc ttc tcg ctg cat gac ctt agt gat aaa gaa acc acc att agc 1008
Phe Ala Phe Ser Leu His Asp Leu Ser Asp Lys Glu Thr Thr Ile Ser
325 330 335

cag cag agt gcc gcc att ttg ttc tgc gtc gaa ggc gat gca acg ttg 1056
Gln Gln Ser Ala Ala Ile Leu Phe Cys Val Glu Gly Asp Ala Thr Leu
340 345 350

tgg aaa ggt tct cag cag tta cag ctt aaa ccg ggt gaa tca gcg ttt 1104
Trp Lys Gly Ser Gln Gln Leu Gln Leu Lys Pro Gly Glu Ser Ala Phe
355 360 365

att gcc gcc aac gaa tca ccg gtg act gtc aaa ggc cac ggc cgt tta 1152
Ile Ala Ala Asn Glu Ser Pro Val Thr Val Lys Gly His Gly Arg Leu
370 375 380

gcg cgt gtt tac aac aag ctg taa 1176
Ala Arg Val Tyr Asn Lys Leu *
385 390

<210> 181
<211> 795
<212> DNA
<213> Escherichia coli .

<220>
<221> CDS
<222> (1)...(795)

<400> 181
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Met Lys Gln Tyr Leu Glu Leu Met Gln Lys Val Leu Asp Glu Gly Thr
1 5 10 15

cag aaa aac gac cgt acc gga acc gga acg ctt tcc att ttt ggt cat 96
Gln Lys Asn Asp Arg Thr Gly Thr Gly Thr Leu Ser Ile Phe Gly His
20 25 30

cag atg cgt ttt aac ctg caa gat gga ttc ccg ctg gtg aca act aaa 144
Gln Met Arg Phe Asn Leu Gln Asp Gly Phe Pro Leu Val Thr Thr Lys
35 40 45

cgt tgc cac ctg cgt tcc atc atc cat gaa ctg ctg tgg ttt ctg cag 192
Arg Cys His Leu Arg Ser Ile Ile His Glu Leu Leu Trp Phe Leu Gln
50 55 60

ggc gac act aac att gct tat cta cac gaa aac aat gtc acc atc tgg 240
Gly Asp Thr Asn Ile Ala Tyr Leu His Glu Asn Asn Val Thr Ile Trp
65 70 75 80

gac gaa tgg gcc gat gaa aac ggc gac ctc ggg cca gtg tat ggt aaa 288
Asp Glu Trp Ala Asp Glu Asn Gly Asp Leu Gly Pro Val Tyr Gly Lys

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85	90	95	
cag tgg cgc gcc tgg cca acg cca gat ggt cgt cat att gac cag atc			336
Gln Trp Arg Ala Trp Pro Thr Pro Asp Gly Arg His Ile Asp Gln Ile			
100	105	110	
act acg gta ctg aac cag ctg aaa aac gac ccg gat tcc cgc cgc att			384
Thr Thr Val Leu Asn Gln Leu Lys Asn Asp Pro Asp Ser Arg Arg Ile			
115	120	125	
att gtt tca gcg tgg aac gta ggc gaa ctg gat aaa atg gcg ctg gca			432
Ile Val Ser Ala Trp Asn Val Gly Glu Leu Asp Lys Met Ala Leu Ala			
130	135	140	
ccg tgc cat gca ttc ttc cag ttc tat gtg gca gac ggc aaa ctc tct			480
Pro Cys His Ala Phe Phe Gln Phe Tyr Val Ala Asp Gly Lys Leu Ser			
145	150	155	160
tgc cag ctt tat cag cgc tcc tgt gac gtc ttc ctc ggc ctg ccg ttc			528
Cys Gln Leu Tyr Gln Arg Ser Cys Asp Val Phe Leu Gly Leu Pro Phe			
165	170	175	
aac att gcc agc tac gcg tta ttg gtg cat atg atg gcg cag cag tgc			576
Asn Ile Ala Ser Tyr Ala Leu Leu Val His Met Met Ala Gln Gln Cys			
180	185	190	
gat ctg gaa gtg ggt gat ttt gtc tgg acc ggt ggc gac acg cat ctg			624
Asp Leu Glu Val Gly Asp Phe Val Trp Thr Gly Gly Asp Thr His Leu			
195	200	205	
tac agc aac cat atg gat caa act cat ctg caa tta agc cgc gaa ccg			672
Tyr Ser Asn His Met Asp Gln Thr His Leu Gln Leu Ser Arg Glu Pro			
210	215	220	
cgt ccg ctg ccg aag ttg att atc aaa cgt aaa ccc gaa tcc atc ttc			720
Arg Pro Leu Pro Lys Leu Ile Ile Lys Arg Lys Pro Glu Ser Ile Phe			
225	230	235	240
gac tac cgt ttc gaa gac ttt gag att gaa ggc tac gat ccg cat ccg			768
Asp Tyr Arg Phe Glu Asp Phe Glu Ile Glu Gly Tyr Asp Pro His Pro			
245	250	255	
ggc att aaa gcg ccg gtg gct atc taa			795
Gly Ile Lys Ala Pro Val Ala Ile *			
260			

<210> 182

<211> 876

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(876)

<400> 182

atg acc agt agc tat ctg cat ttt ccg gag ttt gat ccg gtc att ttc	48
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1	5
10	15

tca ata gga ccc gtg gcg ctt cac tgg tac ggc ctg atg tat ctg gtg	96
Ser Ile Gly Pro Val Ala Leu His Trp Tyr Gly Leu Met Tyr Leu Val	
20 25 30	
ggt ttc att ttt gca atg tgg ctg gca aca cga cgg gcg aat cgt ccg	144
Gly Phe Ile Phe Ala Met Trp Leu Ala Thr Arg Arg Ala Asn Arg Pro	
35 40 45	
ggc agc ggc tgg acc aaa aat gaa gtt gaa aac tta ctc tat gcg ggc	192
Gly Ser Gly Trp Thr Lys Asn Glu Val Glu Asn Leu Leu Tyr Ala Gly	
50 55 60	
ttc ctc ggc gtc ttc ctc ggg gga cgt att ggt tat gtt ctg ttc tac	240
Phe Leu Gly Val Phe Leu Gly Gly Arg Ile Gly Tyr Val Leu Phe Tyr	
65 70 75 80	
aat ttc ccg cag ttt atg gcc gat ccg ctg tat ctg ttc cgt gtc tgg	288
Asn Phe Pro Gln Phe Met Ala Asp Pro Leu Tyr Leu Phe Arg Val Trp	
85 90 95	
gac ggc ggc atg tct ttc cac ggc ggc ctg att ggc gtt atc gtg gtg	336
Asp Gly Gly Met Ser Phe His Gly Gly Leu Ile Gly Val Ile Val Val	
100 105 110	
atg att atc ttc gcc cgc cgt act aaa cgt tcc ttc ttc cag gtc tct	384
Met Ile Ile Phe Ala Arg Arg Thr Lys Arg Ser Phe Phe Gln Val Ser	
115 120 125	
gat ttt atc gca cca ctc att ccg ttt ggt ctt ggt gcc ggg cgt ctg	432
Asp Phe Ile Ala Pro Leu Ile Pro Phe Gly Leu Gly Ala Gly Arg Leu	
130 135 140	
ggc aac ttt att aac ggt gaa ttg tgg ggc cgc gtt gac ccg aac ttc	480
Gly Asn Phe Ile Asn Gly Glu Leu Trp Gly Arg Val Asp Pro Asn Phe	
145 150 155 160	
ccg ttt gcc atg ctg ttc cct ggc tcc cgt aca gaa gat att ttg ctg	528
Pro Phe Ala Met Leu Phe Pro Gly Ser Arg Thr Glu Asp Ile Leu Leu	
165 170 175	
ctg caa acc aac ccg cag tgg caa tcc att ttc gac act tac ggt gtg	576
Leu Gln Thr Asn Pro Gln Trp Gln Ser Ile Phe Asp Thr Tyr Gly Val	
180 185 190	
ctg ccg cgc cac cca tca cag ctt tac gag ctg ctg ctg gaa ggt gtg	624
Leu Pro Arg His Pro Ser Gln Leu Tyr Glu Leu Leu Leu Glu Gly Val	
195 200 205	
gtg ctg ttt att atc ctc aac ctg tat att cgt aaa cca cgc cca atg	672
Val Leu Phe Ile Ile Leu Asn Leu Tyr Ile Arg Lys Pro Arg Pro Met	
210 215 220	
gga gct gtc tca ggt ttg ttc ctg att ggt tac ggc gcg ttt cgc atc	720
Gly Ala Val Ser Gly Leu Phe Leu Ile Gly Tyr Gly Ala Phe Arg Ile	
225 230 235 240	
att gtt gag ttt ttc cgc cag ccc gac gcg cag ttt acc ggt gcc tgg	768
Ile Val Glu Phe Phe Arg Gln Pro Asp Ala Gln Phe Thr Gly Ala Trp	
245 250 255	
gtg cag tac atc agc atg ggg caa att ctt tcc atc ccg atg att gtc	816

Val Gln Tyr Ile Ser Met Gly Gln Ile Leu Ser Ile Pro Met Ile Val
260 265 270

gcg ggt gtg atc atg atg gtc tgg gca tat cgt cgc agc cca cag caa 864
Ala Gly Val Ile Met Met Val Trp Ala Tyr Arg Arg Ser Pro Gln Gln
275 280 285

cac gtt tcc tga 876
His Val Ser *
290

<210> 183
<211> 726
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(726)

<400> 183

atg gac agt ctc aat ctt aat aaa cat att tcc ggc cag ttc aac gcc 48
Met Asp Ser Leu Asn Leu Asn Lys His Ile Ser Gly Gln Phe Asn Ala
1 5 10 15

gaa ctg gaa agt atc cgc acg cag gtg atg acc atg ggc ggc atg gtg 96
Glu Leu Glu Ser Ile Arg Thr Gln Val Met Thr Met Gly Gly Met Val
20 25 30

gag cag cag ctt tct gat gca atc acc gcg atg cat aac cag gac agc 144
Glu Gln Gln Leu Ser Asp Ala Ile Thr Ala Met His Asn Gln Asp Ser
35 40 45

gat ctg gcg aag cgc gtc atc gaa ggc gac aag aac gtc aac atg atg 192
Asp Leu Ala Lys Arg Val Ile Glu Gly Asp Lys Asn Val Asn Met Met
50 55 60

gaa gtg gcg atc gat gaa gcc tgc gtg cgc att atc gcc aaa cgt cag 240
Glu Val Ala Ile Asp Glu Ala Cys Val Arg Ile Ile Ala Lys Arg Gln
65 70 75 80

ccg acg gcg agc gac ctg cga ctg gtt atg gtg atc agt aaa acc att 288
Pro Thr Ala Ser Asp Leu Arg Leu Val Met Val Ile Ser Lys Thr Ile
85 90 95

gcc gag ctg gag cgt att ggc gac gtg gcg gac aaa atc tgc cgt act 336
Ala Glu Leu Glu Arg Ile Gly Asp Val Ala Asp Lys Ile Cys Arg Thr
100 105 110

gcg ctg gag aaa ttc tcc cag cag cat cag ccg ttg ctg gta agt ctg 384
Ala Leu Glu Lys Phe Ser Gln Gln His Gln Pro Leu Leu Val Ser Leu
115 120 125

gag tcg ctg ggc cgt cat acc atc cag atg ctg cac gac gtg ctg gac 432
Glu Ser Leu Gly Arg His Thr Ile Gln Met Leu His Asp Val Leu Asp
130 135 140

gcg ttc gcg cgg atg gac att gac gaa gcg gta cgt att tat cgt gaa 480
Ala Phe Ala Arg Met Asp Ile Asp Glu Ala Val Arg Ile Tyr Arg Glu
145 150 155 160

```

gat aaa aaa gtc gat cag gaa tac gaa ggt att gtt cgt caa ctg atg 528
Asp Lys Lys Val Asp Gln Glu Tyr Glu Gly Ile Val Arg Gln Leu Met
      165              170              175

acc tac atg atg gaa gat tcg cgt acc att ccg agc gta ctt act gcg 576
Thr Tyr Met Met Glu Asp Ser Arg Thr Ile Pro Ser Val Leu Thr Ala
      180              185              190

ctg ttc tgc gcg cgt tct atc gaa cgt att ggc gac cgc tgc cag aat 624
Leu Phe Cys Ala Arg Ser Ile Glu Arg Ile Gly Asp Arg Cys Gln Asn
      195              200              205

att tgt gag ttt atc ttc tac tac gtg aag ggg cag gat ttc cgt cac 672
Ile Cys Glu Phe Ile Phe Tyr Tyr Val Lys Gly Gln Asp Phe Arg His
      210              215              220

gtc ggt ggc gat gag ctg gat aaa ctg ctg gcg ggg aaa gat agc gac 720
Val Gly Gly Asp Glu Leu Asp Lys Leu Leu Ala Gly Lys Asp Ser Asp
      225              230              235              240

aaa taa 726
Lys *

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<210> 184
<211> 774
<212> DNA
<213> Escherichia coli

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<220>
<221> CDS
<222> (1)...(774)

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<400> 184
atg agt atg gtt gaa act gcc ccg agt aaa att cag gtt cgt aat ttg 48
Met Ser Met Val Glu Thr Ala Pro Ser Lys Ile Gln Val Arg Asn Leu
  1              5              10              15

aac ttc tac tac ggc aaa ttc cat gcc ctg aaa aac atc aac ctg gat 96
Asn Phe Tyr Tyr Gly Lys Phe His Ala Leu Lys Asn Ile Asn Leu Asp
      20              25              30

atc gct aaa aac cag gta acg gcg ttt atc ggg ccg tcc ggc tgc ggt 144
Ile Ala Lys Asn Gln Val Thr Ala Phe Ile Gly Pro Ser Gly Cys Gly
      35              40              45

aaa tcg acg ctg ctg cgt acc ttc aac aaa atg ttt gaa ctg tac ccg 192
Lys Ser Thr Leu Leu Arg Thr Phe Asn Lys Met Phe Glu Leu Tyr Pro
      50              55              60

gag cag cgt gcg gaa ggt gaa att ctg ctt gat ggc gac aac atc ctg 240
Glu Gln Arg Ala Glu Gly Glu Ile Leu Leu Asp Gly Asp Asn Ile Leu
      65              70              75              80

acc aac tct cag gat atc gca ctg ctg cgt gcg aaa gtg ggc atg gtg 288
Thr Asn Ser Gln Asp Ile Ala Leu Leu Arg Ala Lys Val Gly Met Val
      85              90              95

ttc cag aaa ccg acg ccg ttt ccg atg tcc atc tac gac aac atc gct 336

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Phe	Gln	Lys	Pro	Thr	Pro	Phe	Pro	Met	Ser	Ile	Tyr	Asp	Asn	Ile	Ala		
			100					105					110				
ttt	ggc	gtt	cgt	ctg	ttt	gag	aag	ctc	tcc	cgt	gcc	gac	atg	gac	gag	384	
Phe	Gly	Val	Arg	Leu	Phe	Glu	Lys	Leu	Ser	Arg	Ala	Asp	Met	Asp	Glu		
		115					120					125					
cgc	gtg	cag	tggt	gca	ttg	acc	aaa	gcc	gca	ttg	tggt	aac	gaa	acc	aaa	432	
Arg	Val	Gln	Trp	Ala	Leu	Thr	Lys	Ala	Ala	Leu	Trp	Asn	Glu	Thr	Lys		
		130				135					140						
gat	aaa	ttg	cac	cag	agc	ggg	tac	tct	ctc	tct	ggg	ggg	cag	caa	cag	480	
Asp	Lys	Leu	His	Gln	Ser	Gly	Tyr	Ser	Leu	Ser	Gly	Gly	Gln	Gln	Gln		
		145			150					155					160		
cgt	ctg	tgt	att	gcg	cgt	ggg	atc	gcc	att	cgc	ccg	gaa	gtg	ctg	ctg	528	
Arg	Leu	Cys	Ile	Ala	Arg	Gly	Ile	Ala	Ile	Arg	Pro	Glu	Val	Leu	Leu		
			165					170						175			
ctc	gac	gaa	ccg	tgt	tgc	gcg	ctc	gac	cct	atc	tct	acc	ggg	cgt	att	576	
Leu	Asp	Glu	Pro	Cys	Ser	Ala	Leu	Asp	Pro	Ile	Ser	Thr	Gly	Arg	Ile		
			180					185					190				
gaa	gag	ctg	atc	acc	gaa	ctg	aag	cag	gat	tac	acc	gtg	gtg	atc	gtc	624	
Glu	Glu	Leu	Ile	Thr	Glu	Leu	Lys	Gln	Asp	Tyr	Thr	Val	Val	Ile	Val		
		195					200					205					
acc	cac	aac	atg	cag	cag	gct	gcg	cgt	tgt	tcc	gac	cac	acg	gcg	ttt	672	
Thr	His	Asn	Met	Gln	Gln	Ala	Ala	Arg	Cys	Ser	Asp	His	Thr	Ala	Phe		
		210				215					220						
atg	tac	ctg	ggc	gaa	ttg	att	gag	ttc	agc	aac	acg	gac	gat	ctg	ttc	720	
Met	Tyr	Leu	Gly	Glu	Leu	Ile	Glu	Phe	Ser	Asn	Thr	Asp	Asp	Leu	Phe		
		225			230					235				240			
acc	aag	cca	gcg	aag	aaa	caa	aca	gaa	gac	tac	atc	acc	ggg	cgt	tac	768	
Thr	Lys	Pro	Ala	Lys	Lys	Gln	Thr	Glu	Asp	Tyr	Ile	Thr	Gly	Arg	Tyr		
			245					250					255				
ggg	tga															774	
Gly	*																

<210> 185

<211> 891

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(891)

<400> 185

atg	gct	atg	gtt	gaa	atg	caa	acc	act	gcg	gcg	ctg	gct	gaa	tct	cgc	48	
Met	Ala	Met	Val	Glu	Met	Gln	Thr	Thr	Ala	Ala	Leu	Ala	Glu	Ser	Arg		
1			5					10					15				

cgc	aaa	atg	cag	gcg	cgt	cgc	cgc	ctc	aaa	aac	cgt	att	gcg	ctg	acg	96	
Arg	Lys	Met	Gln	Ala	Arg	Arg	Arg	Leu	Lys	Asn	Arg	Ile	Ala	Leu	Thr		
			20					25					30				

ctc tgc atg gcg acg atg gcc ttc ggc ctg ttc tgg ctg atc tgg att	144
Leu Ser Met Ala Thr Met Ala Phe Gly Leu Phe Trp Leu Ile Trp Ile	
35 40 45	
tta atg tcc acc atc act cgc ggt atc gac ggt atg tgc ctg gcg ctg	192
Leu Met Ser Thr Ile Thr Arg Gly Ile Asp Gly Met Ser Leu Ala Leu	
50 55 60	
ttc act gaa atg acg ccg ccg ccc aat acg gaa ggt ggt ggt ctg gcg	240
Phe Thr Glu Met Thr Pro Pro Asn Thr Glu Gly Gly Gly Leu Ala	
65 70 75 80	
aac gct ctg gcg ggt agc ggg ctg tta att ttg tgg gcc acg gta ttc	288
Asn Ala Leu Ala Gly Ser Gly Leu Leu Ile Leu Trp Ala Thr Val Phe	
85 90 95	
ggt acg ccg ctg ggc att atg gcg ggg att tat ctg gcg gaa tat ggt	336
Gly Thr Pro Leu Gly Ile Met Ala Gly Ile Tyr Leu Ala Glu Tyr Gly	
100 105 110	
cgt aaa tcc tgg ctg gca gaa gtg att cgc ttc att aac gac att ctg	384
Arg Lys Ser Trp Leu Ala Glu Val Ile Arg Phe Ile Asn Asp Ile Leu	
115 120 125	
ctc tct gcg ccg tgc att gtg gtt ggt ctg ttt gtt tac acc att gtg	432
Leu Ser Ala Pro Ser Ile Val Val Gly Leu Phe Val Tyr Thr Ile Val	
130 135 140	
gtg gcg cag atg gag cac ttc tcc ggc tgg gcg ggc gtg att gcc ctg	480
Val Ala Gln Met Glu His Phe Ser Gly Trp Ala Gly Val Ile Ala Leu	
145 150 155 160	
gcg ttg ttg cag gtg ccg att gtt atc cgc acc acc gag aac atg ctg	528
Ala Leu Leu Gln Val Pro Ile Val Ile Arg Thr Thr Glu Asn Met Leu	
165 170 175	
aaa ctg gtg ccg tac agc ctg cgt gaa gcg gct tat gcg ctg ggt aca	576
Lys Leu Val Pro Tyr Ser Leu Arg Glu Ala Ala Tyr Ala Leu Gly Thr	
180 185 190	
ccg aag tgg aag atg atc tct gcg att acg ctg aaa gcg tgc gtg tcc	624
Pro Lys Trp Lys Met Ile Ser Ala Ile Thr Leu Lys Ala Ser Val Ser	
195 200 205	
ggg att atg acc ggt atc ctg ctg gcg att gcc cgt att gct ggt gaa	672
Gly Ile Met Thr Gly Ile Leu Leu Ala Ile Ala Arg Ile Ala Gly Glu	
210 215 220	
acc gcg ccg ctg ctg ttt acc gcg ctc tcc aac cag ttc tgg agc acg	720
Thr Ala Pro Leu Leu Phe Thr Ala Leu Ser Asn Gln Phe Trp Ser Thr	
225 230 235 240	
gac atg atg cag ccg atc gcc aac ctg ccg gtg acg atc ttt aag ttt	768
Asp Met Met Gln Pro Ile Ala Asn Leu Pro Val Thr Ile Phe Lys Phe	
245 250 255	
gcg atg agc ccg ttt gcg gaa tgg cag caa ttg gcc tgg gcc ggg gta	816
Ala Met Ser Pro Phe Ala Glu Trp Gln Gln Leu Ala Trp Ala Gly Val	
260 265 270	

ttg atc att acc ctg tgc gta ctg ctg ctg aac att ctg gcg cgc gtt 864
 Leu Ile Ile Thr Leu Cys Val Leu Leu Leu Asn Ile Leu Ala Arg Val
 275 280 285

gtt ttt gcg aag aat aaa cac ggt tga 891
 Val Phe Ala Lys Asn Lys His Gly *
 290 295

<210> 186

<211> 960

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(960)

<400> 186

atg gct gca acc aag cct gct ttt aac cca ccg ggt aaa aag ggc gac 48
 Met Ala Ala Thr Lys Pro Ala Phe Asn Pro Pro Gly Lys Lys Gly Asp
 1 5 10 15

ata att ttc agc gtg ctg gta aaa ctg gcg gcg ctg att gtg cta ttg 96
 Ile Ile Phe Ser Val Leu Val Lys Leu Ala Ala Leu Ile Val Leu Leu
 20 25 30

atg ttg ggt ggc att att gtc tct ctg atc atc tcc tcc tgg ccg agc 144
 Met Leu Gly Gly Ile Ile Val Ser Leu Ile Ile Ser Ser Trp Pro Ser
 35 40 45

att cag aaa ttt ggt ctg gct ttc cta tgg acc aaa gag tgg gat gca 192
 Ile Gln Lys Phe Gly Leu Ala Phe Leu Trp Thr Lys Glu Trp Asp Ala
 50 55 60

ccg aac gat atc tac ggg gcg ctg gtg ccg atc tac ggt acg ttg gtg 240
 Pro Asn Asp Ile Tyr Gly Ala Leu Val Pro Ile Tyr Gly Thr Leu Val
 65 70 75 80

act tcg ttt atc gcg ctg ctg atc gcc gtc ccg gtg agt ttc ggt atc 288
 Thr Ser Phe Ile Ala Leu Leu Ile Ala Val Pro Val Ser Phe Gly Ile
 85 90 95

gcc ctg ttc ctg act gag ctt gcg cct ggc tgg ctg aaa cgc ccg ctg 336
 Ala Leu Phe Leu Thr Glu Leu Ala Pro Gly Trp Leu Lys Arg Pro Leu
 100 105 110

ggt atc gcc att gag ctg ctg gca gcc att cca agt atc gtt tac ggc 384
 Gly Ile Ala Ile Glu Leu Leu Ala Ala Ile Pro Ser Ile Val Tyr Gly
 115 120 125

atg tgg ggc ctg ttt atc ttt gcg ccg ctg ttc gcc gtt tac ttt cag 432
 Met Trp Gly Leu Phe Ile Phe Ala Pro Leu Phe Ala Val Tyr Phe Gln
 130 135 140

gag ccg gtc ggc aat atc atg tcg aat atc ccg att gtt ggc gcg ctg 480
 Glu Pro Val Gly Asn Ile Met Ser Asn Ile Pro Ile Val Gly Ala Leu
 145 150 155 160

ttc tct ggc ccc gca ttt ggt atc ggt atc ctc gcg gca ggc gtg atc 528
 Phe Ser Gly Pro Ala Phe Gly Ile Gly Ile Leu Ala Ala Gly Val Ile

165										170					175					
ctc gcc atc atg att att ccg tac att gcg gcg gta atg cgt gat gtg	576																			
Leu Ala Ile Met Ile Ile Pro Tyr Ile Ala Ala Val Met Arg Asp Val																				
180 185 190																				
ttc gaa caa acc ccg gtg atg atg aaa gag tcg gcc tac ggt att ggc	624																			
Phe Glu Gln Thr Pro Val Met Met Lys Glu Ser Ala Tyr Gly Ile Gly																				
195 200 205																				
tgc acc acc tgg gaa gtt atc tgg cgt atc gtt ctt ccg ttc acc aaa	672																			
Cys Thr Thr Trp Glu Val Ile Trp Arg Ile Val Leu Pro Phe Thr Lys																				
210 215 220																				
aat ggt gtt atc ggc ggc atc atg ctg ggg ctg ggc cgc gcg ctc ggt	720																			
Asn Gly Val Ile Gly Gly Ile Met Leu Gly Leu Gly Arg Ala Leu Gly																				
225 230 235 240																				
gaa acc atg gcg gtg acc ttt atc atc ggt aac acc tac cag ctc gac	768																			
Glu Thr Met Ala Val Thr Phe Ile Ile Gly Asn Thr Tyr Gln Leu Asp																				
245 250 255																				
agc gcc tcg ctg tat atg ccg ggc aac agt atc acc tct gcg ctg gcg	816																			
Ser Ala Ser Leu Tyr Met Pro Gly Asn Ser Ile Thr Ser Ala Leu Ala																				
260 265 270																				
aac gaa ttt gcg gaa gcg gaa tcc ggt ctg cac gtt gcc gca ctg atg	864																			
Asn Glu Phe Ala Glu Ala Glu Ser Gly Leu His Val Ala Ala Leu Met																				
275 280 285																				
gaa ctg ggc ctg atc ctg ttt gtg att acc ttc atc gtc ctc gcc gca	912																			
Glu Leu Gly Leu Ile Leu Phe Val Ile Thr Phe Ile Val Leu Ala Ala																				
290 295 300																				
tcg aag ttt atg att atg cgc ctg gct aag aat gag ggg gca cgc taa	960																			
Ser Lys Phe Met Ile Met Arg Leu Ala Lys Asn Glu Gly Ala Arg *																				
305 310 315																				

<210> 187

<211> 1041

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1041)

<400> 187

atg aaa gtt atg cgt acc acc gtc gca act gtt gtc gcc gcg acc tta	48
Met Lys Val Met Arg Thr Thr Val Ala Thr Val Val Ala Ala Thr Leu	
1 5 10 15	
tcg atg agt gct ttc tct gtg ttt gca gaa gca agc ctg aca ggt gca	96
Ser Met Ser Ala Phe Ser Val Phe Ala Glu Ala Ser Leu Thr Gly Ala	
20 25 30	
ggt gca acc ttc cct gcg ccg gtg tat gcc aaa tgg gct gac act tac	144
Gly Ala Thr Phe Pro Ala Pro Val Tyr Ala Lys Trp Ala Asp Thr Tyr	
35 40 45	

cag	aaa	gaa	acc	ggt	aat	aaa	gtt	aac	tac	cag	ggt	atc	ggt	tct	tcc	192
Gln	Lys	Glu	Thr	Gly	Asn	Lys	Val	Asn	Tyr	Gln	Gly	Ile	Gly	Ser	Ser	
	50					55					60					
ggt	ggc	gta	aaa	cag	att	atc	gct	aat	acc	gtt	gat	ttt	ggt	gcc	tct	240
Gly	Gly	Val	Lys	Gln	Ile	Ile	Ala	Asn	Thr	Val	Asp	Phe	Gly	Ala	Ser	
	65				70					75					80	
gac	gcg	cgc	ctg	tct	gac	gaa	aaa	ctg	gct	cag	gaa	ggt	ctg	ttc	cag	288
Asp	Ala	Pro	Leu	Ser	Asp	Glu	Lys	Leu	Ala	Gln	Glu	Gly	Leu	Phe	Gln	
				85					90					95		
ttc	ccg	acc	gtg	att	ggc	ggc	gtg	gtg	ctg	gcg	gtt	aac	att	cca	ggg	336
Phe	Pro	Thr	Val	Ile	Gly	Gly	Val	Val	Leu	Ala	Val	Asn	Ile	Pro	Gly	
			100					105					110			
ctg	aag	tct	ggc	gaa	ctg	gtg	ctg	gat	ggt	aaa	acc	ctc	ggc	gac	atc	384
Leu	Lys	Ser	Gly	Glu	Leu	Val	Leu	Asp	Gly	Lys	Thr	Leu	Gly	Asp	Ile	
		115					120					125				
tac	ctg	ggc	aaa	atc	aag	aag	tgg	gat	gat	gaa	gcc	atc	gcc	aaa	ctg	432
Tyr	Leu	Gly	Lys	Ile	Lys	Lys	Trp	Asp	Asp	Glu	Ala	Ile	Ala	Lys	Leu	
	130					135					140					
aat	ccg	ggt	ctg	aaa	ctg	cct	tca	caa	aac	att	gct	gta	gta	cgc	cgc	480
Asn	Pro	Gly	Leu	Lys	Leu	Pro	Ser	Gln	Asn	Ile	Ala	Val	Val	Arg	Arg	
	145				150					155					160	
gca	gat	ggc	tcc	ggg	act	tcc	ttc	gtc	ttc	acc	agc	tac	ctg	gcg	aaa	528
Ala	Asp	Gly	Ser	Gly	Thr	Ser	Phe	Val	Phe	Thr	Ser	Tyr	Leu	Ala	Lys	
				165				170						175		
gtg	aac	gaa	gag	tgg	aaa	aac	aac	gtt	ggt	act	ggc	tct	acc	gta	aaa	576
Val	Asn	Glu	Glu	Trp	Lys	Asn	Asn	Val	Gly	Thr	Gly	Ser	Thr	Val	Lys	
		180						185					190			
tgg	ccg	atc	ggt	ctg	ggc	ggg	aaa	ggt	aac	gac	ggt	atc	gcc	gcg	ttc	624
Trp	Pro	Ile	Gly	Leu	Gly	Gly	Lys	Gly	Asn	Asp	Gly	Ile	Ala	Ala	Phe	
		195					200					205				
gtt	cag	cgt	ctg	ccg	ggt	gca	att	ggt	tat	gtt	gaa	tat	gct	tac	gcg	672
Val	Gln	Arg	Leu	Pro	Gly	Ala	Ile	Gly	Tyr	Val	Glu	Tyr	Ala	Tyr	Ala	
	210					215					220					
aag	cag	aac	aac	ctg	gcg	tac	acc	aaa	ctg	atc	tcc	gct	gat	ggt	aaa	720
Lys	Gln	Asn	Asn	Leu	Ala	Tyr	Thr	Lys	Leu	Ile	Ser	Ala	Asp	Gly	Lys	
	225				230					235					240	
ccg	gtt	agt	ccg	acc	gaa	gaa	aac	ttc	gct	aat	gca	gca	aaa	ggt	gca	768
Pro	Val	Ser	Pro	Thr	Glu	Glu	Asn	Phe	Ala	Asn	Ala	Ala	Lys	Gly	Ala	
				245					250					255		
gac	tgg	agc	aaa	acc	ttc	gct	cag	gat	ctg	acc	aac	cag	aaa	ggc	gaa	816
Asp	Trp	Ser	Lys	Thr	Phe	Ala	Gln	Asp	Leu	Thr	Asn	Gln	Lys	Gly	Glu	
			260					265				270				
gat	gca	tgg	cct	att	acc	tct	acc	acg	ttc	att	ctg	atc	cac	aaa	gat	864
Asp	Ala	Trp	Pro	Ile	Thr	Ser	Thr	Thr	Phe	Ile	Leu	Ile	His	Lys	Asp	
		275					280					285				

cag aag aaa cca gaa caa ggc aca gaa gtg ctg aaa ttc ttc gac tgg 912
 Gln Lys Lys Pro Glu Gln Gly Thr Glu Val Leu Lys Phe Phe Asp Trp
 290 295 300

gcg tac aaa acc ggg gct aaa cag gcg aac gac ctg gat tac gcc agc 960
 Ala Tyr Lys Thr Gly Ala Lys Gln Ala Asn Asp Leu Asp Tyr Ala Ser
 305 310 315 320

ctg ccg gat agt gta gtt gaa cag gtt cgc gct gcg tgg aag acc aat 1008
 Leu Pro Asp Ser Val Val Glu Gln Val Arg Ala Ala Trp Lys Thr Asn
 325 330 335

att aaa gac agt agc ggt aag ccg ctg tac taa 1041
 Ile Lys Asp Ser Ser Gly Lys Pro Leu Tyr *
 340 345

<210> 188
 <211> 711
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(711)

<400> 188
 atg gga tct gga ctg gtg aac gga ggt gat tat ttt tat aat aac ctt 48
 Met Gly Ser Gly Leu Val Asn Gly Gly Asp Tyr Phe Tyr Asn Asn Leu
 1 5 10 15

tca ttc aca gtc acc agg tac aac ggc atc atg gca act gac tca aca 96
 Ser Phe Thr Val Thr Arg Tyr Asn Gly Ile Met Ala Thr Asp Ser Thr
 20 25 30

caa tgt gta aaa aaa agc cgt ggc cgc cca aaa gtg ttc gac agg gat 144
 Gln Cys Val Lys Lys Ser Arg Gly Arg Pro Lys Val Phe Asp Arg Asp
 35 40 45

gcc gcg ctt gat aag gcc atg aaa ttg ttc tgg caa cac ggt tat gaa 192
 Ala Ala Leu Asp Lys Ala Met Lys Leu Phe Trp Gln His Gly Tyr Glu
 50 55 60

gcg act tct ctt gcg gac ctc gtc gaa gcg acc gga gcc aaa gcg ccc 240
 Ala Thr Ser Leu Ala Asp Leu Val Glu Ala Thr Gly Ala Lys Ala Pro
 65 70 75 80

acg cta tac gcg gaa ttt acc aac aaa gag ggg tta ttt cgt gcc gtt 288
 Thr Leu Tyr Ala Glu Phe Thr Asn Lys Glu Gly Leu Phe Arg Ala Val
 85 90 95

ctc gac cgc tat atc gat cgt ttt gcc gct aag cat gaa gca cag ctg 336
 Leu Asp Arg Tyr Ile Asp Arg Phe Ala Ala Lys His Glu Ala Gln Leu
 100 105 110

ttt tgt gaa gag aaa agc gtg gag tct gcg ctg gct gac tat ttt gct 384
 Phe Cys Glu Glu Lys Ser Val Glu Ser Ala Leu Ala Asp Tyr Phe Ala
 115 120 125

gcc atc gcc aac tgc ttt acc agc aaa gac acc ccg gca ggc tgc ttc 432
 Ala Ile Ala Asn Cys Phe Thr Ser Lys Asp Thr Pro Ala Gly Cys Phe

130	135	140	
atg atc aac aac tgc acc acc ctc tcc cca gat tca gga gat atc gcc			480
Met Ile Asn Asn Cys Thr Thr Leu Ser Pro Asp Ser Gly Asp Ile Ala			
145	150	155	160
aat acg ttg aaa tca cgc cat gcg atg caa gag cgc act ttg cag cag			528
Asn Thr Leu Lys Ser Arg His Ala Met Gln Glu Arg Thr Leu Gln Gln			
	165	170	175
ttt tta tgt caa cga caa gcg cgc ggg gaa atc ccg ccc cac tgt gac			576
Phe Leu Cys Gln Arg Gln Ala Arg Gly Glu Ile Pro Pro His Cys Asp			
	180	185	190
gtg aca cat ctg gca gaa ttc ctt aat tgt att att cag ggg atg tcg			624
Val Thr His Leu Ala Glu Phe Leu Asn Cys Ile Ile Gln Gly Met Ser			
	195	200	205
atc agc gca cgc gaa ggt gca tcg ctg gaa aaa ctg atg cag att gcc			672
Ile Ser Ala Arg Glu Gly Ala Ser Leu Glu Lys Leu Met Gln Ile Ala			
	210	215	220
gga acg act ttg cgt tta tgg ccc gaa ctg gtg aaa taa			711
Gly Thr Thr Leu Arg Leu Trp Pro Glu Leu Val Lys *			
225	230	235	

<210> 189

<211> 546

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(546)

<400> 189

gtg cag gcc aaa att gcg gca tca aat acg ggt gaa ctg gat gcc ctg			48
Met Gln Ala Lys Ile Ala Ala Ser Asn Thr Gly Glu Leu Asp Ala Leu			
1	5	10	15
caa cag ctg gga ttc tcc ctg gta gaa ggt gaa gtt gat ttg gcg cta			96
Gln Gln Leu Gly Phe Ser Leu Val Glu Gly Glu Val Asp Leu Ala Leu			
	20	25	30
ccc gtg aac aat gcc agt gat agc ggt gct gta gtg gca caa gag acc			144
Pro Val Asn Asn Ala Ser Asp Ser Gly Ala Val Val Ala Gln Glu Thr			
	35	40	45
gat att ccc gca tta cgt cag tta gcc agc gcc gca ttt gcg caa agc			192
Asp Ile Pro Ala Leu Arg Gln Leu Ala Ser Ala Ala Phe Ala Gln Ser			
	50	55	60
cgt ttt cgt gcg ccg tgg tat gcg cct gac gcc agc agt cgc ttt tat			240
Arg Phe Arg Ala Pro Trp Tyr Ala Pro Asp Ala Ser Ser Arg Phe Tyr			
	65	70	75
gca cag tgg att gaa aat gcc gtg cgc ggc acc ttt gat cat caa tgt			288
Ala Gln Trp Ile Glu Asn Ala Val Arg Gly Thr Phe Asp His Gln Cys			
	85	90	95

ctg att tta cgt gcg gcg tcc ggc gat att cgc ggc tat gtc tct tta 336
 Leu Ile Leu Arg Ala Ala Ser Gly Asp Ile Arg Gly Tyr Val Ser Leu
 100 105 110

cgg gaa ctc aat gcg aca gat gcg cga att ggc ctg ctg gct gga cgc 384
 Arg Glu Leu Asn Ala Thr Asp Ala Arg Ile Gly Leu Leu Ala Gly Arg
 115 120 125

ggt gca ggt gct gag ctg atg caa acg gcg cta aac tgg gcg tat cgt 432
 Gly Ala Gly Ala Glu Leu Met Gln Thr Ala Leu Asn Trp Ala Tyr Arg
 130 135 140

cgc ggt aaa aca act ttg cgg gtg gcg acc caa atg ggc aac acc gcc 480
 Arg Gly Lys Thr Thr Leu Arg Val Ala Thr Gln Met Gly Asn Thr Ala
 145 150 155 160

gcg ctt aaa cga tac ata caa agt ggt gcg aat gta gaa agc acc gcg 528
 Ala Leu Lys Arg Tyr Ile Gln Ser Gly Ala Asn Val Glu Ser Thr Ala
 165 170 175

tac tgg tta tac agg tga 546
 Tyr Trp Leu Tyr Arg *
 180

<210> 190
 <211> 1131
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1131)

<400> 190
 atg att cca ttt aac gca ccg ccg gtg gtg gga acc gaa ctc gac tat 48
 Met Ile Pro Phe Asn Ala Pro Pro Val Val Gly Thr Glu Leu Asp Tyr
 1 5 10 15

atg cag tcg gca atg ggt agc ggc aaa ctg tgt ggc gat ggc ggt ttt 96
 Met Gln Ser Ala Met Gly Ser Gly Lys Leu Cys Gly Asp Gly Gly Phe
 20 25 30

acc cgt cgc tgc cag cag tgg ctg gag caa cgt ttt ggc agc gcc aaa 144
 Thr Arg Arg Cys Gln Gln Trp Leu Glu Gln Arg Phe Gly Ser Ala Lys
 35 40 45

gtg tta ctg acg ccg tcc tgc acc gct tcg ctg gag atg gcg gcg ctg 192
 Val Leu Leu Thr Pro Ser Cys Thr Ala Ser Leu Glu Met Ala Ala Leu
 50 55 60

ctg ctc gat atc cag cct ggc gat gaa gtg atc atg ccg agc tac acc 240
 Leu Leu Asp Ile Gln Pro Gly Asp Glu Val Ile Met Pro Ser Tyr Thr
 65 70 75 80

ttt gtc tcc acc gcc aat gcc ttt gtg ctg cgt ggc gca aaa atc gtt 288
 Phe Val Ser Thr Ala Asn Ala Phe Val Leu Arg Gly Ala Lys Ile Val
 85 90 95

ttt gtg gat gtt cgc ccg gac acc atg aac atc gac gaa acg ctg att 336
 Phe Val Asp Val Arg Pro Asp Thr Met Asn Ile Asp Glu Thr Leu Ile

100	105	110	
gaa gcg gcg atc acc gac aaa acg cgc gtt atc gtg ccg gtc cat tac			384
Glu Ala Ala Ile Thr Asp Lys Thr Arg Val Ile Val Pro Val His Tyr			
115	120	125	
gcg ggt gtg gcc tgc gaa atg gac acc att atg gcg ttg gcg aaa aag			432
Ala Gly Val Ala Cys Glu Met Asp Thr Ile Met Ala Leu Ala Lys Lys			
130	135	140	
cat aat ttg ttt gtg gta gaa gat gcc gct cag ggc gtg atg tcc act			480
His Asn Leu Phe Val Glu Asp Ala Ala Gln Gly Val Met Ser Thr			
145	150	155	160
tac aaa ggg cgt gca ctg gga acc att ggt cat att ggc tgc ttt agc			528
Tyr Lys Gly Arg Ala Leu Gly Thr Ile Gly His Ile Gly Cys Phe Ser			
165	170	175	
ttc cat gaa acc aaa aac tac acg gcg ggc ggt gaa ggc ggc gcg acg			576
Phe His Glu Thr Lys Asn Tyr Thr Ala Gly Gly Glu Gly Gly Ala Thr			
180	185	190	
ctg att aac gat aaa gcg tta atc gaa cga gcc gag atc atc cgt gaa			624
Leu Ile Asn Asp Lys Ala Leu Ile Glu Arg Ala Glu Ile Ile Arg Glu			
195	200	205	
aag ggc act aac cgc agc cag ttc ttc cgt ggt cag gtc gat aaa tat			672
Lys Gly Thr Asn Arg Ser Gln Phe Phe Arg Gly Gln Val Asp Lys Tyr			
210	215	220	
acc tgg cgc gat att ggc tcc agc tat ttg atg tcc gat ctg caa gct			720
Thr Trp Arg Asp Ile Gly Ser Ser Tyr Leu Met Ser Asp Leu Gln Ala			
225	230	235	240
gca tac ctg tgg gcg caa ctg gaa gca gcg gat cgt atc aac cag caa			768
Ala Tyr Leu Trp Ala Gln Leu Glu Ala Ala Asp Arg Ile Asn Gln Gln			
245	250	255	
cgt ctg gcg ctg tgg caa aac tac tac gat gcg tta gcg cct ctg gcg			816
Arg Leu Ala Leu Trp Gln Asn Tyr Tyr Asp Ala Leu Ala Pro Leu Ala			
260	265	270	
aaa gcc ggg cgt atc gag ctg ccg tgc att ccc gat ggc tgc gtg cag			864
Lys Ala Gly Arg Ile Glu Leu Pro Ser Ile Pro Asp Gly Cys Val Gln			
275	280	285	
aac gcg cat atg ttc tac att aaa ctg cgg gat att gat gac cgg agc			912
Asn Ala His Met Phe Tyr Ile Lys Leu Arg Asp Ile Asp Asp Arg Ser			
290	295	300	
gcg ttg att aac ttt ctg aaa gaa gcg gaa atc atg gcg gtg ttt cat			960
Ala Leu Ile Asn Phe Leu Lys Glu Ala Glu Ile Met Ala Val Phe His			
305	310	315	320
tac att cgc ctg cac ggt tgc cct gcg ggg gaa cac ttt ggt gag ttc			1008
Tyr Ile Pro Leu His Gly Cys Pro Ala Gly Glu His Phe Gly Glu Phe			
325	330	335	
cac ggt gaa gat cgc tac acc acc aaa gag agc gag cgc ctg ctg cgc			1056
His Gly Glu Asp Arg Tyr Thr Thr Lys Glu Ser Glu Arg Leu Leu Arg			
340	345	350	

ctg ccg ctg ttc tac aac ctg tcg ccc gtc aat cag cgt acg gta att 1104
 Leu Pro Leu Phe Tyr Asn Leu Ser Pro Val Asn Gln Arg Thr Val Ile
 355 360 365

gcg act ttg ttg aac tac ttt tcc tga 1131
 Ala Thr Leu Leu Asn Tyr Phe Ser *
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<211> 1251

<212> DNA

<213> Escherichia coli

<220>

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<400> 191

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 1 5 10 15

aag att ggt gcc ggg tta ctg gtc ggt aag ttg ctg gcg gtg tca ttt 96
 Lys Ile Gly Ala Gly Leu Leu Val Gly Lys Leu Leu Ala Val Ser Phe
 20 25 30

ggt ccg gcg ggg ctt ggg ctg gcg gca aat ttc cgc cag ttg att acc 144
 Gly Pro Ala Gly Leu Gly Leu Ala Ala Asn Phe Arg Gln Leu Ile Thr
 35 40 45

gtg ctc ggc gtg ctt gcc ggg gct ggc atc ttt aac ggt gta acc aaa 192
 Val Leu Gly Val Leu Ala Gly Ala Gly Ile Phe Asn Gly Val Thr Lys
 50 55 60

tac gtt gcc cag tac cat gat aat ccg caa cag ctg cgc cgc gtg gtc 240
 Tyr Val Ala Gln Tyr His Asp Asn Pro Gln Gln Leu Arg Arg Val Val
 65 70 75 80

ggc act tca tca gcg atg gta ctt ggt ttc tct acg ctg atg gcg ctg 288
 Gly Thr Ser Ser Ala Met Val Leu Gly Phe Ser Thr Leu Met Ala Leu
 85 90 95

gtt ttt gtg ctg gca gct gcg cca atc agc cag gga ttg ttt ggt aat 336
 Val Phe Val Leu Ala Ala Ala Pro Ile Ser Gln Gly Leu Phe Gly Asn
 100 105 110

acc gac tat cag ggg ctg gtg cgt tta gtg gcg ctg gtg caa atg ggg 384
 Thr Asp Tyr Gln Gly Leu Val Arg Leu Val Ala Leu Val Gln Met Gly
 115 120 125

atc gcc tgg ggc aac ctg tta ctg gcg ctg atg aaa ggc ttt cgc gat 432
 Ile Ala Trp Gly Asn Leu Leu Leu Ala Leu Met Lys Gly Phe Arg Asp
 130 135 140

gcc gca ggt aat gcg tta tcg ctg att gtc ggc agc ttg att ggc gtt 480
 Ala Ala Gly Asn Ala Leu Ser Leu Ile Val Gly Ser Leu Ile Gly Val
 145 150 155 160

ctc gcg tac tac gtc agt tac cgt ttg ggc ggt tat gaa ggg gcg ttg 528

Leu	Ala	Tyr	Tyr	Val	Ser	Tyr	Arg	Leu	Gly	Gly	Tyr	Glu	Gly	Ala	Leu		
				165					170					175			
ctg	ggt	ctg	gcg	ctg	att	ccc	gcg	ctg	gtg	gta	att	cct	gcc	gcc	atc	576	
Leu	Gly	Leu	Ala	Leu	Ile	Pro	Ala	Leu	Val	Val	Ile	Pro	Ala	Ala	Ile		
			180					185					190				
atg	ttg	atc	aaa	cgt	ggt	gtc	atc	cgc	tta	agc	tat	ctg	aaa	ccc	agc	624	
Met	Leu	Ile	Lys	Arg	Gly	Val	Ile	Pro	Leu	Ser	Tyr	Leu	Lys	Pro	Ser		
		195					200					205					
tgg	gat	aac	ggt	ctg	gca	ggg	cag	ttg	agc	aaa	ttt	acg	ctc	atg	gcg	672	
Trp	Asp	Asn	Gly	Leu	Ala	Gly	Gln	Leu	Ser	Lys	Phe	Thr	Leu	Met	Ala		
	210					215					220						
ttg	att	acg	tcg	gtg	acc	ttg	cct	gtt	gct	tac	atc	atg	atg	cgt	aaa	720	
Leu	Ile	Thr	Ser	Val	Thr	Leu	Pro	Val	Ala	Tyr	Ile	Met	Met	Arg	Lys		
225					230					235					240		
ctg	ctg	gcg	gcg	cag	tat	agc	tgg	gat	gag	gtg	ggg	atc	tgg	caa	ggg	768	
Leu	Leu	Ala	Ala	Gln	Tyr	Ser	Trp	Asp	Glu	Val	Gly	Ile	Trp	Gln	Gly		
				245					250					255			
gtg	agc	agt	att	tcc	gat	gcc	tac	ctg	caa	ttt	att	acg	gca	tcg	ttc	816	
Val	Ser	Ser	Ile	Ser	Asp	Ala	Tyr	Leu	Gln	Phe	Ile	Thr	Ala	Ser	Phe		
			260					265					270				
agc	gta	tat	ttg	ctg	ccc	acg	ttg	tcg	cgg	cta	acg	gaa	aag	cgc	gat	864	
Ser	Val	Tyr	Leu	Leu	Pro	Thr	Leu	Ser	Arg	Leu	Thr	Glu	Lys	Arg	Asp		
		275					280					285					
atc	acc	cgg	gaa	gtg	gtt	aaa	tcg	ctg	aaa	ttc	gtc	tta	ccg	gca	gtg	912	
Ile	Thr	Arg	Glu	Val	Val	Lys	Ser	Leu	Lys	Phe	Val	Leu	Pro	Ala	Val		
	290					295					300						
gcg	gcg	gcg	agt	ttt	acc	gtc	tgg	ctg	ctg	cgt	gat	ttt	gct	atc	tgg	960	
Ala	Ala	Ala	Ser	Phe	Thr	Val	Trp	Leu	Leu	Arg	Asp	Phe	Ala	Ile	Trp		
305					310					315					320		
ctg	ctg	ttg	tcg	aat	aaa	ttt	acc	gct	atg	cgc	gat	ctc	ttt	gcc	tgg	1008	
Leu	Leu	Leu	Ser	Asn	Lys	Phe	Thr	Ala	Met	Arg	Asp	Leu	Phe	Ala	Trp		
				325					330					335			
cag	tta	gtg	ggt	gat	gtg	tta	aaa	gtg	ggc	gct	tat	gtc	ttt	ggt	tat	1056	
Gln	Leu	Val	Gly	Asp	Val	Leu	Lys	Val	Gly	Ala	Tyr	Val	Phe	Gly	Tyr		
			340					345					350				
ctg	gtg	atc	gcc	aaa	gcg	tca	ctg	cgg	ttt	tat	att	ctg	gcg	gaa	gtc	1104	
Leu	Val	Ile	Ala	Lys	Ala	Ser	Leu	Arg	Phe	Tyr	Ile	Leu	Ala	Glu	Val		
		355					360					365					
agc	cag	ttc	act	tta	ttg	atg	gta	ttt	gcc	cac	tgg	cta	atc	cct	gcg	1152	
Ser	Gln	Phe	Thr	Leu	Leu	Met	Val	Phe	Ala	His	Trp	Leu	Ile	Pro	Ala		
	370					375					380						
cat	ggt	gca	ctg	ggc	gcg	gcg	cag	gca	tat	atg	gca	act	tat	atc	gtc	1200	
His	Gly	Ala	Leu	Gly	Ala	Ala	Gln	Ala	Tyr	Met	Ala	Thr	Tyr	Ile	Val		
385				390					395					400			
tat	ttt	tct	ctt	tgt	tgt	ggc	gtg	ttt	tta	ctc	tgg	cgt	agg	cgg	gca	1248	
Tyr	Phe	Ser	Leu	Cys	Cys	Gly	Val	Phe	Leu	Leu	Trp	Arg	Arg	Arg	Ala		

405 410 415

tga 1251
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<210> 192
<211> 1353
<212> DNA
<213> Escherichia coli

<220>
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<400> 192

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Met Ser Leu Leu Gln Phe Ser Gly Leu Phe Val Val Trp Leu Leu Cys	
1 5 10 15	
acg ctg ttt att gcc acg ctg acc tgg ttt gag ttt cgc cgt gtg cgc	96
Thr Leu Phe Ile Ala Thr Leu Thr Trp Phe Glu Phe Arg Arg Val Arg	
20 25 30	
ttt aac ttc aat gtc ttc ttt tca ttg ctg ttt ttg ctc acc ttt ttc	144
Phe Asn Phe Asn Val Phe Phe Ser Leu Leu Phe Leu Thr Phe Phe	
35 40 45	
ttc ggc ttc ccg ctg acc agc gtg ctg gta ttt cgc ttt gat gtt ggt	192
Phe Gly Phe Pro Leu Thr Ser Val Leu Val Phe Arg Phe Asp Val Gly	
50 55 60	
gtc gcg ccg cca gaa atc ttg ttg cag gcg ttg ctt tct gcg ggc tgc	240
Val Ala Pro Pro Glu Ile Leu Leu Gln Ala Leu Leu Ser Ala Gly Cys	
65 70 75 80	
ttc tac gcg gtt tac tat gtc acc tac aaa acc cgc cta cgc aaa cgc	288
Phe Tyr Ala Val Tyr Tyr Val Thr Tyr Lys Thr Arg Leu Arg Lys Arg	
85 90 95	
gtt gct gat gta ccg cgc cgt ccg ctg ttt acc atg aac cgc gtg gag	336
Val Ala Asp Val Pro Arg Arg Pro Leu Phe Thr Met Asn Arg Val Glu	
100 105 110	
acc aat ctt acg tgg gtg atc ctg atg ggt atc gcg ctg gta agc gtc	384
Thr Asn Leu Thr Trp Val Ile Leu Met Gly Ile Ala Leu Val Ser Val	
115 120 125	
ggc atc ttc ttc atg cac aac ggc ttt ttg ctg ttc cgg ctt aac tcc	432
Gly Ile Phe Phe Met His Asn Gly Phe Leu Leu Phe Arg Leu Asn Ser	
130 135 140	
tac agt cag atc ttt tcc agt gaa gtc tcc ggc gtg gcg tta aaa cgc	480
Tyr Ser Gln Ile Phe Ser Ser Glu Val Ser Gly Val Ala Leu Lys Arg	
145 150 155 160	
ttc ttt tac ttt ttc atc ccg gcg atg ctg gtg gtc tac ttt ctg cgc	528
Phe Phe Tyr Phe Phe Ile Pro Ala Met Leu Val Val Tyr Phe Leu Arg	
165 170 175	

cag gac agc aaa gcg tgg ctg ttt ttc ctc gtc agc acg gtc gcc ttt	576
Gln Asp Ser Lys Ala Trp Leu Phe Phe Leu Val Ser Thr Val Ala Phe	
180 185 190	
ggc ttg ctg act tat atg att gtc ggc ggc act cgc gcc aat atc atc	624
Gly Leu Leu Thr Tyr Met Ile Val Gly Gly Thr Arg Ala Asn Ile Ile	
195 200 205	
atc gca ttc gct atc ttc ctg ttt att ggc att att cgc ggc tgg att	672
Ile Ala Phe Ala Ile Phe Leu Phe Ile Gly Ile Ile Arg Gly Trp Ile	
210 215 220	
tcg ttg tgg atg ctg gcg gcg gcg ggc gtg ctg ggg att gtt ggc atg	720
Ser Leu Trp Met Leu Ala Ala Ala Gly Val Leu Gly Ile Val Gly Met	
225 230 235 240	
ttc tgg ctg gca cta aaa cgc tat gga atg aat gtg agc ggc gat gaa	768
Phe Trp Leu Ala Leu Lys Arg Tyr Gly Met Asn Val Ser Gly Asp Glu	
245 250 255	
gcg ttc tat acg ttt ctc tat ctc act cgc gac acc ttc tcg ccg tgg	816
Ala Phe Tyr Thr Phe Leu Tyr Leu Thr Arg Asp Thr Phe Ser Pro Trp	
260 265 270	
gag aat ctg gcg ttg ctg ttg cag aac tac gac aac atc gac ttc cag	864
Glu Asn Leu Ala Leu Leu Leu Gln Asn Tyr Asp Asn Ile Asp Phe Gln	
275 280 285	
ggc ctg gct cca att gtc cgc gat ttc tat gtc ttt atc cct tcc tgg	912
Gly Leu Ala Pro Ile Val Arg Asp Phe Tyr Val Phe Ile Pro Ser Trp	
290 295 300	
ctg tgg ccg ggt cgc ccg agt atg gtg ctg aac tca gcc aac tac ttt	960
Leu Trp Pro Gly Arg Pro Ser Met Val Leu Asn Ser Ala Asn Tyr Phe	
305 310 315 320	
acc tgg gaa gtg ctg aat aac cac tcc gga ctg gcg atc tcg cct acg	1008
Thr Trp Glu Val Leu Asn Asn His Ser Gly Leu Ala Ile Ser Pro Thr	
325 330 335	
ctt ata ggc tca ctg gtg gtg atg ggc ggc gcg ttg ttc atc ccg ctc	1056
Leu Ile Gly Ser Leu Val Val Met Gly Gly Ala Leu Phe Ile Pro Leu	
340 345 350	
ggg gcg atc gtg gtt ggt ctg atc atc aaa tgg ttc gac tgg ctg tat	1104
Gly Ala Ile Val Val Gly Leu Ile Ile Lys Trp Phe Asp Trp Leu Tyr	
355 360 365	
gag ctg ggc aac cgc gag cct aat cgc tat aaa gct gcg ata ttg cac	1152
Glu Leu Gly Asn Arg Glu Pro Asn Arg Tyr Lys Ala Ala Ile Leu His	
370 375 380	
agt ttc tgc ttt ggg gcg atc ttc aat atg atc gtg ctg gcg cgt gaa	1200
Ser Phe Cys Phe Gly Ala Ile Phe Asn Met Ile Val Leu Ala Arg Glu	
385 390 395 400	
ggg ctg gat tcg ttt gtc tca cgc gtg gtc ttt ttt atc gtg gtc ttc	1248
Gly Leu Asp Ser Phe Val Ser Arg Val Val Phe Phe Ile Val Val Phe	
405 410 415	
ggc gca tgt ctg atg atc gca aaa ctg ttg tac tgg ctt ttt gaa agc	1296

Gly Ala Cys Leu Met Ile Ala Lys Leu Leu Tyr Trp Leu Phe Glu Ser
 420 425 430
 gcc gga ctc att cat aaa cgt aca aaa tca tgc ctc cgg acg cag gtt 1344
 Ala Gly Leu Ile His Lys Arg Thr Lys Ser Ser Leu Arg Thr Gln Val
 435 440 445
 gaa gga taa 1353
 Glu Gly *
 450
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 <211> 741
 <212> DNA
 <213> Escherichia coli
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 Met Asn Asn Asn Thr Thr Ala Pro Thr Tyr Thr Leu Arg Gly Leu Gln
 1 5 10 15
 ttg att ggt tgg cgt gat atg cag cac gcc ctc gat tat ctg ttt gct 96
 Leu Ile Gly Trp Arg Asp Met Gln His Ala Leu Asp Tyr Leu Phe Ala
 20 25 30
 gac ggg cag ctt aag cag gga acg ctg gtt gcc att aat gct gaa aaa 144
 Asp Gly Gln Leu Lys Gln Gly Thr Leu Val Ala Ile Asn Ala Glu Lys
 35 40 45
 atg ctg act att gaa gat aac gcc gag gtc agg gag tta att aac gct 192
 Met Leu Thr Ile Glu Asp Asn Ala Glu Val Arg Glu Leu Ile Asn Ala
 50 55 60
 gcc gaa ttt aaa tat gcg gat ggc atc agc gtt gta cgt tca gta cgt 240
 Ala Glu Phe Lys Tyr Ala Asp Gly Ile Ser Val Val Arg Ser Val Arg
 65 70 75 80
 aaa aag tac ccg cag gcg cag gtt tcc cgc gtt gcc ggt gcc gat ctc 288
 Lys Lys Tyr Pro Gln Ala Gln Val Ser Arg Val Ala Gly Ala Asp Leu
 85 90 95
 tgg gaa gag ctg atg gcg cgc gca ggc aaa gaa ggg acg ccg gta ttt 336
 Trp Glu Glu Leu Met Ala Arg Ala Gly Lys Glu Gly Thr Pro Val Phe
 100 105 110
 ctt gtg ggc ggt aaa cct gaa gtg ctg gcg caa act gaa gct aaa ctg 384
 Leu Val Gly Gly Lys Pro Glu Val Leu Ala Gln Thr Glu Ala Lys Leu
 115 120 125
 cgc aac cag tgg aat gtg aat atc gtt ggc agt cag gat ggt tat ttt 432
 Arg Asn Gln Trp Asn Val Asn Ile Val Gly Ser Gln Asp Gly Tyr Phe
 130 135 140
 aaa ccc gag cag cgt cag gcg ctg ttt gaa cgc att cat gcc agc ggt 480
 Lys Pro Glu Gln Arg Gln Ala Leu Phe Glu Arg Ile His Ala Ser Gly
 145 150 155 160

gcg caa atc gtc acc gtt gcg atg gga tcg cca aag cag gag atc atc 528
 Ala Gln Ile Val Thr Val Ala Met Gly Ser Pro Lys Gln Glu Ile Ile
 165 170 175

atg cgc gac tgc cgt ctg gta cat cca gat gcg ctg tat atg ggc gtt 576
 Met Arg Asp Cys Arg Leu Val His Pro Asp Ala Leu Tyr Met Gly Val
 180 185 190

ggc ggg act tac gat gtt ttc acc ggt cac gta aaa cgc gca ccg aaa 624
 Gly Gly Thr Tyr Asp Val Phe Thr Gly His Val Lys Arg Ala Pro Lys
 195 200 205

atc tgg caa acg ctg ggg ctg gag tgg ctc tac cgc ctg ctt tcg cag 672
 Ile Trp Gln Thr Leu Gly Leu Glu Trp Leu Tyr Arg Leu Leu Ser Gln
 210 215 220

ccg agc cgc att aag cgt cag ctt cgt ttg ctg cgt tat tta cgc tgg 720
 Pro Ser Arg Ile Lys Arg Gln Leu Arg Leu Leu Arg Tyr Leu Arg Trp
 225 230 235 240

cac tac acc ggc aac cta tga 741
 His Tyr Thr Gly Asn Leu *
 245

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 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
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<400> 194
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 Met Thr Val Leu Ile His Val Leu Gly Ser Asp Ile Pro His His Asn
 1 5 10 15

cga acc gtt ttg cgg ttt ttc aat gac gcg ctg gcc gcg acg agc gag 96
 Arg Thr Val Leu Arg Phe Phe Asn Asp Ala Leu Ala Ala Thr Ser Glu
 20 25 30

cac gcg cgc gag ttt atg gtt gtt ggc aag gac gac ggc tta agt gat 144
 His Ala Arg Glu Phe Met Val Val Gly Lys Asp Asp Gly Leu Ser Asp
 35 40 45

agc tgt ccg gcg ctt tct gtg caa ttt ttc ccc tgg gaa aaa atc gct 192
 Ser Cys Pro Ala Leu Ser Val Gln Phe Phe Pro Trp Glu Lys Ile Ala
 50 55 60

ggc gga agc ggt cat cgc gaa agc aaa agc taa 225
 Gly Gly Ser Gly His Arg Glu Ser Lys Ser *
 65 70

<210> 195
 <211> 615
 <212> DNA
 <213> Escherichia coli

<220>

<221> CDS

<222> (1)...(615)

<400> 195

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1 5 10 15

aat acg atg gcg aac gat cgg caa cgt gaa ggg aaa atg acc att ctg 96
Asn Thr Met Ala Asn Asp Arg Gln Arg Glu Gly Lys Met Thr Ile Leu
20 25 30

gtg ggg aac tcc ggc gac cgc agc aat gag cat att gct gcc ttg cgc 144
Val Gly Asn Ser Gly Asp Arg Ser Asn Glu His Ile Ala Ala Leu Arg
35 40 45

gcc gtt cat cag caa ttt ggc gat acg gta aaa gtg gtg gtg ccg atg 192
Ala Val His Gln Gln Phe Gly Asp Thr Val Lys Val Val Val Pro Met
50 55 60

gga tat ccg cct aat aac gaa gcg tac att gag gaa gtt cgt cag gcg 240
Gly Tyr Pro Pro Asn Asn Glu Ala Tyr Ile Glu Glu Val Arg Gln Ala
65 70 75 80

ggg ctg gag tta ttc agc gaa gaa aat cta caa att ctg agc gaa aaa 288
Gly Leu Glu Leu Phe Ser Glu Glu Asn Leu Gln Ile Leu Ser Glu Lys
85 90 95

ctg gaa ttt gac gcc tat ctg gcg cta ctt cgt cag tgc gat ctt ggt 336
Leu Glu Phe Asp Ala Tyr Leu Ala Leu Leu Arg Gln Cys Asp Leu Gly
100 105 110

tac ttt att ttt gcc cgc cag cag ggc att ggt acg ctg tgc tta ctg 384
Tyr Phe Ile Phe Ala Arg Gln Gln Gly Ile Gly Thr Leu Cys Leu Leu
115 120 125

att cag gcg ggc att cct tgt gtg ctt aac cgg gaa aat ccg ttc tgg 432
Ile Gln Ala Gly Ile Pro Cys Val Leu Asn Arg Glu Asn Pro Phe Trp
130 135 140

cag gat atg acg gaa caa cat ttg ccg gtg ctg ttt act acc gac gat 480
Gln Asp Met Thr Glu Gln His Leu Pro Val Leu Phe Thr Thr Asp Asp
145 150 155 160

ctc aac gag gat att gtg cgt gaa gcg cag cgc cag ttg gcg tcg gtg 528
Leu Asn Glu Asp Ile Val Arg Glu Ala Gln Arg Gln Leu Ala Ser Val
165 170 175

gat aaa aac acc att gcc ttc ttt agc cct aac tat cta caa ggc tgg 576
Asp Lys Asn Thr Ile Ala Phe Phe Ser Pro Asn Tyr Leu Gln Gly Trp
180 185 190

cag cgg gcg ttg gcg att gcc gcc agg gag gtc gca tga 615
Gln Arg Ala Leu Ala Ile Ala Ala Arg Glu Val Ala *
195 200

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<210> 196

<211> 549

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(549)

<400> 196

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1 5 10 15

atg ggt caa caa gcc gct acc cgg atg atg act tat ccc ccg gtg gtg 96
Met Gly Gln Gln Ala Ala Thr Arg Met Met Thr Tyr Pro Pro Val Val
20 25 30

atg gca cat acg gtc gct gta ttc ctc tct ttt gat ggc gaa ctc gac 144
Met Ala His Thr Val Ala Val Phe Leu Ser Phe Asp Gly Glu Leu Asp
35 40 45

acc cag cca ctc ata gaa caa ctc tgg cgc gcc ggt aag cgc gta tat 192
Thr Gln Pro Leu Ile Glu Gln Leu Trp Arg Ala Gly Lys Arg Val Tyr
50 55 60

ctt cca gtt ttg cat ccc ttt agt gcc ggt aat ttg ctg ttc ctg aat 240
Leu Pro Val Leu His Pro Phe Ser Ala Gly Asn Leu Leu Phe Leu Asn
65 70 75 80

tac cat ccg caa agc gaa ctg gtg atg aac agg ttg aag atc cat gag 288
Tyr His Pro Gln Ser Glu Leu Val Met Asn Arg Leu Lys Ile His Glu
85 90 95

cca aaa ttg gat gtg cgt gac gtg cta ccc ctt tcc cga tta gac gtg 336
Pro Lys Leu Asp Val Arg Asp Val Leu Pro Leu Ser Arg Leu Asp Val
100 105 110

ctg atc aca ccg ctg gtc gcc ttt gat gag tac ggt cag cgc ctg gga 384
Leu Ile Thr Pro Leu Val Ala Phe Asp Glu Tyr Gly Gln Arg Leu Gly
115 120 125

atg ggc ggt ggt ttt tat gat cgg acc tta caa aac tgg cag cac tat 432
Met Gly Gly Gly Phe Tyr Asp Arg Thr Leu Gln Asn Trp Gln His Tyr
130 135 140

aaa acg caa ccg gtg ggt tat gcg cat gat tgt cag ttg gtg gaa aaa 480
Lys Thr Gln Pro Val Gly Tyr Ala His Asp Cys Gln Leu Val Glu Lys
145 150 155 160

ctc ccc gtt gaa gag tgg gat atc cct ctt cct gcg gtg gtt aca ccg 528
Leu Pro Val Glu Glu Trp Asp Ile Pro Leu Pro Ala Val Val Thr Pro
165 170 175

tcg aaa gtc tgg gag tgg taa 549
Ser Lys Val Trp Glu Trp *
180

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<210> 197

<211> 276

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(276)

<400> 197

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atg gca cgc gta act gtt cag gac gct gta gag aaa att ggt aac cgt 48
Met Ala Arg Val Thr Val Gln Asp Ala Val Glu Lys Ile Gly Asn Arg
1 5 10 15

ttt gac ctg gta ctg gtc gcc ggc cgt cgc gct cgt cag atg cag gta 96
Phe Asp Leu Val Leu Val Ala Ala Arg Arg Ala Arg Gln Met Gln Val
20 25 30

ggc gga aag gat ccg ctg gta ccg gaa gaa aac gat aaa acc act gta 144
Gly Gly Lys Asp Pro Leu Val Pro Glu Glu Asn Asp Lys Thr Thr Val
35 40 45

atc gcg ctg cgc gaa atc gaa gaa ggt ctg atc aac aac cag atc ctc 192
Ile Ala Leu Arg Glu Ile Glu Glu Gly Leu Ile Asn Asn Gln Ile Leu
50 55 60

gac gtt cgc gaa cgc cag gaa cag caa gag cag gaa gcc gct gaa tta 240
Asp Val Arg Glu Arg Gln Glu Gln Gln Glu Gln Glu Ala Ala Glu Leu
65 70 75 80

caa gcc gtt acc gct att gct gaa ggt cgt cgt taa 276
Gln Ala Val Thr Ala Ile Ala Glu Gly Arg Arg *
85 90

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<210> 198

<211> 2109

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(2109)

<400> 198

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ttg tat ctg ttt gaa agc ctg aat caa ctg att caa acc tac ctg ccg 48
Met Tyr Leu Phe Glu Ser Leu Asn Gln Leu Ile Gln Thr Tyr Leu Pro
1 5 10 15

gaa gac caa atc aag cgt ctg cgg cag gcg tat ctc gtt gca cgt gat 96
Glu Asp Gln Ile Lys Arg Leu Arg Gln Ala Tyr Leu Val Ala Arg Asp
20 25 30

gct cac gag ggg caa aca cgt tca agc ggt gaa ccc tat atc acg cac 144
Ala His Glu Gly Gln Thr Arg Ser Ser Gly Glu Pro Tyr Ile Thr His
35 40 45

ccg gta gcg gtt gcc tgc att ctg gcc gag atg aaa ctc gac tat gaa 192
Pro Val Ala Val Ala Cys Ile Leu Ala Glu Met Lys Leu Asp Tyr Glu
50 55 60

acg ctg atg gcg gcg ctg ctg cat gac gtg att gaa gat act ccc gcc 240
Thr Leu Met Ala Ala Leu Leu His Asp Val Ile Glu Asp Thr Pro Ala
65 70 75 80

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acc tac cag gat atg gaa cag ctt ttt ggt aaa agc gtc gcc gag ctg	288
Thr Tyr Gln Asp Met Glu Gln Leu Phe Gly Lys Ser Val Ala Glu Leu	
85 90 95	
gta gag ggg gtg tcg aaa ctt gat aaa ctc aag ttc cgc gat aag aaa	336
Val Glu Gly Val Ser Lys Leu Asp Lys Leu Lys Phe Arg Asp Lys Lys	
100 105 110	
gag gcg cag gcc gaa aac ttt cgc aag atg att atg gcg atg gtg cag	384
Glu Ala Gln Ala Glu Asn Phe Arg Lys Met Ile Met Ala Met Val Gln	
115 120 125	
gat atc cgc gtc atc ctc atc aaa ctt gcc gac cgt acc cac aac atg	432
Asp Ile Arg Val Ile Leu Ile Lys Leu Ala Asp Arg Thr His Asn Met	
130 135 140	
cgc acg ctg ggc tca ctt cgc ccg gac aaa cgt cgc cgc atc gcc cgt	480
Arg Thr Leu Gly Ser Leu Arg Pro Asp Lys Arg Arg Arg Ile Ala Arg	
145 150 155 160	
gaa act ctc gaa att tat agc ccg ctg gcg cac cgt tta ggt atc cac	528
Glu Thr Leu Glu Ile Tyr Ser Pro Leu Ala His Arg Leu Gly Ile His	
165 170 175	
cac att aaa acc gaa ctc gaa gag ctg ggt ttt gag gcg ctg tat ccc	576
His Ile Lys Thr Glu Leu Glu Glu Leu Gly Phe Glu Ala Leu Tyr Pro	
180 185 190	
aac cgt tat cgc gta atc aaa gaa gtg gtg aaa gcc gcg cgc ggc aac	624
Asn Arg Tyr Arg Val Ile Lys Glu Val Val Lys Ala Ala Arg Gly Asn	
195 200 205	
cgt aaa gag atg atc cag aag att ctt tct gaa atc gaa ggg cgt ttg	672
Arg Lys Glu Met Ile Gln Lys Ile Leu Ser Glu Ile Glu Gly Arg Leu	
210 215 220	
cag gaa gcg gga ata ccg tgc cgc gtc agt ggt cgc gag aag cat ctt	720
Gln Glu Ala Gly Ile Pro Cys Arg Val Ser Gly Arg Glu Lys His Leu	
225 230 235 240	
tat tcg att tac tgc aaa atg gtg ctc aaa gag cag cgt ttt cac tcg	768
Tyr Ser Ile Tyr Cys Lys Met Val Leu Lys Glu Gln Arg Phe His Ser	
245 250 255	
atc atg gac atc tac gct ttc cgc gtg atc gtc aat gat tct gac acc	816
Ile Met Asp Ile Tyr Ala Phe Arg Val Ile Val Asn Asp Ser Asp Thr	
260 265 270	
tgt tat cgc gtg ctg ggc cag atg cac agc ctg tac aag ccg cgt ccg	864
Cys Tyr Arg Val Leu Gly Gln Met His Ser Leu Tyr Lys Pro Arg Pro	
275 280 285	
ggc cgc gtg aaa gac tat atc gcc att cca aaa gcg aac ggc tat cag	912
Gly Arg Val Lys Asp Tyr Ile Ala Ile Pro Lys Ala Asn Gly Tyr Gln	
290 295 300	
tct ttg cac acc tcg atg atc ggc ccg cac ggt gtg ccg gtt gag gtc	960
Ser Leu His Thr Ser Met Ile Gly Pro His Gly Val Pro Val Glu Val	
305 310 315 320	
cag atc cgt acc gaa gat atg gac cag atg gcg gag atg ggt gtt gcc	1008

Gln Ile Arg Thr Glu Asp Met Asp Gln Met Ala Glu Met Gly Val Ala	
325 330 335	
gcg cac tgg gct tat aaa gag cac ggc gaa acc agt act acc gca caa	1056
Ala His Trp Ala Tyr Lys Glu His Gly Glu Thr Ser Thr Thr Ala Gln	
340 345 350	
atc cgc gcc cag cgc tgg atg caa agc ctg ctg gag ctg caa cag agc	1104
Ile Arg Ala Gln Arg Trp Met Gln Ser Leu Leu Glu Leu Gln Gln Ser	
355 360 365	
gcc ggt agt tgc ttt gaa ttt atc gag agc gtt aaa tcc gat ctc ttc	1152
Ala Gly Ser Ser Phe Glu Phe Ile Glu Ser Val Lys Ser Asp Leu Phe	
370 375 380	
ccg gat gag att tac gtt ttc aca ccg gaa ggg cgc att gtc gag ctg	1200
Pro Asp Glu Ile Tyr Val Phe Thr Pro Glu Gly Arg Ile Val Glu Leu	
385 390 395 400	
cct gcc ggt gca acg ccc gtc gac ttc gct tat gca gtg cat acc gat	1248
Pro Ala Gly Ala Thr Pro Val Asp Phe Ala Tyr Ala Val His Thr Asp	
405 410 415	
atc ggt cat gcc tgc gtg ggc gca cgc gtt gac cgc cag cct tac ccg	1296
Ile Gly His Ala Cys Val Gly Ala Arg Val Asp Arg Gln Pro Tyr Pro	
420 425 430	
ctg tgc cag ccg ctt acc agc ggt caa acc gtt gaa atc att acc gct	1344
Leu Ser Gln Pro Leu Thr Ser Gly Gln Thr Val Glu Ile Ile Thr Ala	
435 440 445	
ccg ggc gct cgc ccg aat gcc gct tgg ctg aac ttt gtc gtt agc tgc	1392
Pro Gly Ala Arg Pro Asn Ala Ala Trp Leu Asn Phe Val Val Ser Ser	
450 455 460	
aaa gcg cgc gcc aaa att cgt cag ttg ctg aaa aac ctc aag cgt gat	1440
Lys Ala Arg Ala Lys Ile Arg Gln Leu Leu Lys Asn Leu Lys Arg Asp	
465 470 475 480	
gat tct gta agc ctg ggc cgt cgt ctg ctc aac cat gct ttg ggt ggt	1488
Asp Ser Val Ser Leu Gly Arg Arg Leu Leu Asn His Ala Leu Gly Gly	
485 490 495	
agc cgt aag ctg aat gaa atc ccg cag gaa aat att cag cgc gag ctg	1536
Ser Arg Lys Leu Asn Glu Ile Pro Gln Glu Asn Ile Gln Arg Glu Leu	
500 505 510	
gat cgc atg aag ctg gca acg ctt gac gat ctg ctg gca gaa atc gga	1584
Asp Arg Met Lys Leu Ala Thr Leu Asp Asp Leu Leu Ala Glu Ile Gly	
515 520 525	
ctt ggt aac gca atg agc gtg gtg gtc gcg aaa aat ctg caa cat ggg	1632
Leu Gly Asn Ala Met Ser Val Val Val Ala Lys Asn Leu Gln His Gly	
530 535 540	
gac gcc tcc att cca ccg gca acc caa agc cac gga cat ctg ccc att	1680
Asp Ala Ser Ile Pro Pro Ala Thr Gln Ser His Gly His Leu Pro Ile	
545 550 555 560	
aaa ggt gcc gat ggc gtg ctg atc acc ttt gcg aaa tgc tgc cgc cct	1728
Lys Gly Ala Asp Gly Val Leu Ile Thr Phe Ala Lys Cys Cys Arg Pro	

565										570										575										
att cct ggc gac	ccg att atc gcc	cac gtc agc ccc	ggg aaa ggt	ctg	1776	Ile Pro Gly Asp	Pro Ile Ile Ala	His Val Ser	Pro Gly Lys	Gly Leu																				
						580					585					590														
gtg atc cac cat	gaa tcc tgc	cgt aat atc	cgt ggc tac	cag aaa gag	1824	Val Ile His His	Glu Ser Cys	Arg Asn Ile	Arg Gly Tyr	Gln Lys Glu																				
						595					600					605														
cca gag aag ttt	atg gct gtg	gaa tgg gat	aaa gag acg	gcg cag gag	1872	Pro Glu Lys Phe	Met Ala Val	Glu Trp Asp	Lys Glu Thr	Ala Gln Glu																				
						610					615					620														
ttc atc acc gaa	atc aag gtg	gag atg ttc	aat cat cag	ggg gcg ctg	1920	Phe Ile Thr Glu	Ile Lys Val	Glu Met Phe	Asn His Gln	Gly Ala Leu																				
						625					630					635					640									
gca aac ctg acg	gcg gca att	aac acc acg	act tcg aat	att caa agt	1968	Ala Asn Leu Thr	Ala Ala Ile	Asn Thr Thr	Thr Ser Asn	Ile Gln Ser																				
						645					650					655														
ttg aat acg gaa	gag aaa gat	ggg cgc gtc	tac agc gcc	ttt att cgt	2016	Leu Asn Thr Glu	Glu Lys Asp	Gly Arg Val	Tyr Ser Ala	Phe Ile Arg																				
						660					665					670														
ctg acc gct cgt	gac cgt gtg	cat ctg gcg	aat atc atg	cgc aaa atc	2064	Leu Thr Ala Arg	Asp Arg Val	His Leu Ala	Asn Ile Met	Arg Lys Ile																				
						675					680					685														
cgc gtg atg cca	gac gtg att	aaa gtc acc	cga aac cga	aat taa	2109	Arg Val Met Pro	Asp Val Ile	Lys Val Thr	Arg Asn Arg	Asn *																				
						690					695					700														

<210> 199

<211> 690

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(690)

<400> 199

atg aac cca aca	cgt tat gca	cgc atc tgc	gaa atg ctc	gcc agg cgg	48	Met Asn Pro Thr	Arg Tyr Ala	Arg Ile Cys	Glu Met Leu	Ala Arg Arg	
						1	5	10	15		
cag cct gat ctg	acc gtc tgc	atg gag cag	gtc cac aaa	cct cat aac	96	Gln Pro Asp Leu	Thr Val Cys	Met Glu Gln	Val His Lys	Pro His Asn	
						20	25	30			
gtt tct gcg att	att cgt acc	gca gat gcc	gtt ggc gta	cat gaa gtt	144	Val Ser Ala Ile	Ile Arg Thr	Ala Asp Ala	Val Gly Val	His Glu Val	
						35	40	45			
cac gcc gtc tgg	cct ggt agc	cgc atg cgc	acc atg gct	tcg gca gcg	192	His Ala Val Trp	Pro Gly Ser	Arg Met Arg	Thr Met Ala	Ser Ala Ala	
						50	55	60			

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gcg ggt agt aac agc tgg gta cag gtg aaa aca cac cgc acc att ggc 240
Ala Gly Ser Asn Ser Trp Val Gln Val Lys Thr His Arg Thr Ile Gly
65          70          75          80

gat gcc gtc gct cat ctc aaa ggc cag ggc atg cag att ctg gca acc 288
Asp Ala Val Ala His Leu Lys Gly Gln Gly Met Gln Ile Leu Ala Thr
85          90          95

cat ctt tct gat aac gct gtc gat ttc cgc gaa att gat tac act cgc 336
His Leu Ser Asp Asn Ala Val Asp Phe Arg Glu Ile Asp Tyr Thr Arg
100         105         110

ccg acc tgc att ttg atg gga cag gag aaa acg ggc atc acg cag gaa 384
Pro Thr Cys Ile Leu Met Gly Gln Glu Lys Thr Gly Ile Thr Gln Glu
115         120         125

gca ttg gcc ctg gcg gat cag gac atc atc att ccg atg atc ggc atg 432
Ala Leu Ala Leu Ala Asp Gln Asp Ile Ile Ile Pro Met Ile Gly Met
130         135         140

gtg cag tcg ctg aat gtt tcc gtt gcc tca gcc ctc att ctt tac gaa 480
Val Gln Ser Leu Asn Val Ser Val Ala Ser Ala Leu Ile Leu Tyr Glu
145         150         155         160

gcc cag cgt cag cgg caa aat gca ggc atg tac ctg cgt gaa aac agc 528
Ala Gln Arg Gln Arg Gln Asn Ala Gly Met Tyr Leu Arg Glu Asn Ser
165         170         175

atg ttg ccg gaa gca gag caa caa cgc ctg ttg ttt gaa ggc ggc tat 576
Met Leu Pro Glu Ala Glu Gln Gln Arg Leu Leu Phe Glu Gly Gly Tyr
180         185         190

ccg gtg ctg gcg aaa gtc gca aaa cgc aaa ggc ctg cct tat ccc cac 624
Pro Val Leu Ala Lys Val Ala Lys Arg Lys Gly Leu Pro Tyr Pro His
195         200         205

gtc aat cag caa ggc gag atc gaa gct gat gcc gac tgg tgg gct act 672
Val Asn Gln Gln Gly Glu Ile Glu Ala Asp Ala Asp Trp Trp Ala Thr
210         215         220

atg cag gct gca ggg taa 690
Met Gln Ala Ala Gly *
225

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<210> 200

<211> 2082

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(2082)

<400> 200

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atg aaa ggt cgc ctg tta gat gct gtc cca ctc agt tcc cta acg ggc 48
Met Lys Gly Arg Leu Leu Asp Ala Val Pro Leu Ser Ser Leu Thr Gly
1          5          10          15

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gtt ggc gca gca ctt agt aac aaa ctg gcg aaa atc aac ctg cat acc 96

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Val	Gly	Ala	Ala	Leu	Ser	Asn	Lys	Leu	Ala	Lys	Ile	Asn	Leu	His	Thr	
			20					25					30			
gtg	cag	gat	cta	ctc	tta	cac	ctt	ccc	ctg	cgc	tac	gaa	gat	cgc	acc	144
Val	Gln	Asp	Leu	Leu	Leu	His	Leu	Pro	Leu	Arg	Tyr	Glu	Asp	Arg	Thr	
		35					40					45				
cat	ctc	tac	ccc	atc	gga	gaa	cta	ctg	ccg	ggc	gtt	tat	gcc	acg	gtg	192
His	Leu	Tyr	Pro	Ile	Gly	Glu	Leu	Leu	Pro	Gly	Val	Tyr	Ala	Thr	Val	
		50				55					60					
gaa	ggc	gaa	gtg	ctg	aac	tgc	aat	atc	tcc	ttc	ggc	ggg	cgg	cgg	atg	240
Glu	Gly	Glu	Val	Leu	Asn	Cys	Asn	Ile	Ser	Phe	Gly	Gly	Arg	Arg	Met	
	65				70				75						80	
atg	acc	tgc	cag	atc	agc	gac	ggg	tcc	ggc	atc	ctc	acc	atg	cgc	ttt	288
Met	Thr	Cys	Gln	Ile	Ser	Asp	Gly	Ser	Gly	Ile	Leu	Thr	Met	Arg	Phe	
				85				90						95		
ttc	aat	ttc	agc	gcg	gca	atg	aaa	aat	agc	ctg	gcg	gcg	ggc	cgc	cgt	336
Phe	Asn	Phe	Ser	Ala	Ala	Met	Lys	Asn	Ser	Leu	Ala	Ala	Gly	Arg	Arg	
			100					105					110			
gta	ctg	gct	tat	ggc	gaa	gca	aag	cgc	ggg	aaa	tat	ggg	gcg	gag	atg	384
Val	Leu		Tyr	Gly	Glu	Ala	Lys	Arg	Gly	Lys	Tyr	Gly	Ala	Glu	Met	
		115					120					125				
atc	cac	ccg	gaa	tac	cgc	gtg	cag	ggc	gat	ctc	agc	acg	cca	gaa	tta	432
Ile	His	Pro	Glu	Tyr	Arg	Val	Gln	Gly	Asp	Leu	Ser	Thr	Pro	Glu	Leu	
						135					140					
cag	gaa	acg	ctc	acg	ccg	gtt	tat	cca	aca	acg	gaa	ggc	gta	aag	cag	480
Gln	Glu	Thr	Leu	Thr	Pro	Val	Tyr	Pro	Thr	Thr	Glu	Gly	Val	Lys	Gln	
	145					150				155					160	
gcc	acg	ctg	cgt	aaa	tta	acc	gac	cag	gcg	ctg	gat	ctg	ctc	gac	acc	528
Ala	Thr	Leu	Arg	Lys	Leu	Thr	Asp	Gln	Ala	Leu	Asp	Leu	Leu	Asp	Thr	
				165					170					175		
tgc	gcc	att	gaa	gaa	ctc	ctg	ccg	ccg	gaa	ctg	tca	caa	gga	atg	atg	576
Cys	Ala	Ile	Glu	Glu	Leu	Leu	Pro	Pro	Glu	Leu	Ser	Gln	Gly	Met	Met	
			180					185					190			
acg	cta	ccg	gaa	gcg	ttg	cgc	act	ttg	cac	cgc	ccg	cca	ccg	acg	cta	624
Thr	Leu	Pro	Glu	Ala	Leu	Arg	Thr	Leu	His	Arg	Pro	Pro	Pro	Thr	Leu	
			195				200					205				
cag	ctt	agc	gat	ctg	gaa	acc	ggg	cag	cat	ccg	gcg	caa	cgt	cgt	ctg	672
Gln	Leu	Ser	Asp	Leu	Glu	Thr	Gly	Gln	His	Pro	Ala	Gln	Arg	Arg	Leu	
		210					215				220					
att	ctg	gaa	gaa	ctg	ctg	gcg	cac	aac	ctc	agc	atg	tta	gcc	tta	cgt	720
Ile	Leu	Glu	Glu	Leu	Leu	Ala	His	Asn	Leu	Ser	Met	Leu	Ala	Leu	Arg	
	225					230				235					240	
gcc	gga	gca	cag	cgt	ttt	cat	gcc	cag	ccg	ctg	agc	gcc	aat	gac	acg	768
Ala	Gly	Ala	Gln	Arg	Phe	His	Ala	Gln	Pro	Leu	Ser	Ala	Asn	Asp	Thr	
			245						250					255		
ctg	aaa	aat	aaa	ctc	ctc	gcc	gcc	tta	ccg	ttc	aag	cca	acg	ggc	gca	816
Leu	Lys	Asn	Lys	Leu	Leu	Ala	Ala	Leu	Pro	Phe	Lys	Pro	Thr	Gly	Ala	

260	265	270	
cag gca cgc gta gtg gcg gag atc gag cgc gat atg gcg ctg gat gtg Gln Ala Arg Val Val Ala Glu Ile Glu Arg Asp Met Ala Leu Asp Val	275	280	285
ccg atg atg cgt ctg gtg cag ggc gat gta ggt tcc ggt aaa acg ctg Pro Met Met Arg Leu Val Gln Gly Asp Val Gly Ser Gly Lys Thr Leu	290	295	300
gtc gcc gcc ctc gcc gcg ttg cgt gcg att gcc cac ggc aaa cag gta Val Ala Ala Leu Ala Ala Leu Arg Ala Ile Ala His Gly Lys Gln Val	305	310	315
gca ttg atg gca cca acc gaa tta ctc gcc gag cag cac gcc aat aac Ala Leu Met Ala Pro Thr Glu Leu Leu Ala Glu Gln His Ala Asn Asn	325	330	335
ttc cgc aac tgg ttt gca ccg ctc ggt atc gaa gtg ggc tgg ctc gcc Phe Arg Asn Trp Phe Ala Pro Leu Gly Ile Glu Val Gly Trp Leu Ala	340	345	350
ggt aag cag aaa ggt aaa gca cgg ctg gca cag cag gaa gcc atc gcc Gly Lys Gln Lys Gly Lys Ala Arg Leu Ala Gln Gln Glu Ala Ile Ala	355	360	365
agc ggt cag gtg cag atg att gtc ggt aca cac gcc atc ttc cag gaa Ser Gly Gln Val Gln Met Ile Val Gly Thr His Ala Ile Phe Gln Glu	370	375	380
cag gtg cag ttt aac ggc ctg gcg ctg gtg att atc gac gaa cag cat Gln Val Gln Phe Asn Gly Leu Ala Leu Val Ile Ile Asp Glu Gln His	385	390	395
cgt ttt ggc gtg cat cag cgt ctg gca ttg tgg gag aaa ggc cag cag Arg Phe Gly Val His Gln Arg Leu Ala Leu Trp Glu Lys Gly Gln Gln	405	410	415
cag ggc ttc cat ccg cat cag ttg atc atg acc gcc acg ccg atc ccc Gln Gly Phe His Pro His Gln Leu Ile Met Thr Ala Thr Pro Ile Pro	420	425	430
cgc acg ctg gca atg act gcg tat gcc gat ctc gat acc tcg gtg ata Arg Thr Leu Ala Met Thr Ala Tyr Ala Asp Leu Asp Thr Ser Val Ile	435	440	445
gat gag ctg ccg cca ggc cgc acg cca gtg act acg gtc gct att cct Asp Glu Leu Pro Pro Gly Arg Thr Pro Val Thr Thr Val Ala Ile Pro	450	455	460
gat acc cgc cgt acc gac atc att gac cgc gtg cac cac gcc tgc ata Asp Thr Arg Arg Thr Asp Ile Ile Asp Arg Val His His Ala Cys Ile	465	470	475
act gaa ggt cgt cag gca tac tgg gtt tgt acg ttg att gaa gag tcg Thr Glu Gly Arg Gln Ala Tyr Trp Val Cys Thr Leu Ile Glu Glu Ser	485	490	495
gaa ttg ctg gaa gcg cag gcg gcg gaa gct acc tgg gaa gag ttg aaa Glu Leu Leu Glu Ala Gln Ala Ala Glu Ala Thr Trp Glu Glu Leu Lys	500	505	510


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ctg gcg cta cca gag ttg aac gtt ggc ctg gta cac ggg cgg atg aaa 1584
Leu Ala Leu Pro Glu Leu Asn Val Gly Leu Val His Gly Arg Met Lys
      515                      520                      525

cct gcc gag aaa cag gcg gtg atg gcg tcg ttt aaa caa ggt gag cta 1632
Pro Ala Glu Lys Gln Ala Val Met Ala Ser Phe Lys Gln Gly Glu Leu
      530                      535                      540

cac ctg ctg gtt gcc aca acc gtt att gaa gtc ggc gtt gat gtg cct 1680
His Leu Leu Val Ala Thr Val Ile Glu Val Gly Val Asp Val Pro
545                      550                      555                      560

aac gcc agt ctg atg att atc gaa aac ccg gag cgt ctg ggt ctg gcg 1728
Asn Ala Ser Leu Met Ile Ile Glu Asn Pro Glu Arg Leu Gly Leu Ala
      565                      570                      575

cag tta cac cag ctg cgc ggg cgc gta ggt cgt ggc gcg gtg gct tct 1776
Gln Leu His Gln Leu Arg Gly Arg Val Gly Arg Gly Ala Val Ala Ser
      580                      585                      590

cac tgc gtg ctg ctc tac aaa acg ccg ctt tct aaa acg gcg caa att 1824
His Cys Val Leu Leu Tyr Lys Thr Pro Leu Ser Lys Thr Ala Gln Ile
      595                      600                      605

cgc ctg caa gtg ctg cgc gac agt aac gac ggt ttt gtg att gcg caa 1872
Arg Leu Gln Val Leu Arg Asp Ser Asn Asp Gly Phe Val Ile Ala Gln
      610                      615                      620

aaa gat ctg gag att cgc ggc cct ggc gaa ttg tta ggc acg cgt cag 1920
Lys Asp Leu Glu Ile Arg Gly Pro Gly Glu Leu Leu Gly Thr Arg Gln
      625                      630                      635                      640

acg ggt aat gct gaa ttt aaa gtg gcg gat tta ctg cgc gat cag gcg 1968
Thr Gly Asn Ala Glu Phe Lys Val Ala Asp Leu Leu Arg Asp Gln Ala
      645                      650                      655

atg atc ccg gaa gtt cag cgc ctg gca cgc cat att cac gaa cgt tac 2016
Met Ile Pro Glu Val Gln Arg Leu Ala Arg His Ile His Glu Arg Tyr
      660                      665                      670

cca caa cag gca aaa gcc ctg ata gaa cgc tgg atg ccg gag acg gaa 2064
Pro Gln Gln Ala Lys Ala Leu Ile Glu Arg Trp Met Pro Glu Thr Glu
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cgt tac tcg aat gcg taa 2082
Arg Tyr Ser Asn Ala *
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<210> 201
<211> 1287
<212> DNA
<213> Escherichia coli

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<220>
<221> CDS
<222> (1)...(1287)

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atg aaa acc tct ctg ttt aaa agc ctt tac ttt cag gtc ctg aca gcg 48

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1				5					10					15			
ata	gcc	att	ggg	att	ctc	ctt	ggc	cat	ttc	tat	cct	gaa	ata	ggc	gag	96	
Ile	Ala	Ile	Gly	Ile	Leu	Leu	Gly	His	Phe	Tyr	Pro	Glu	Ile	Gly	Glu		
			20					25					30				
caa	atg	aaa	ccg	ctt	ggc	gac	ggc	ttc	gtt	aag	ctc	att	aag	atg	atc	144	
Gln	Met	Lys	Pro	Leu	Gly	Asp	Gly	Phe	Val	Lys	Leu	Ile	Lys	Met	Ile		
		35					40					45					
atc	gct	cct	gtc	atc	ttt	tgt	acc	gtc	gta	acg	ggc	att	gcg	ggc	atg	192	
Ile	Ala	Pro	Val	Ile	Phe	Cys	Thr	Val	Val	Thr	Gly	Ile	Ala	Gly	Met		
		50				55					60						
gaa	agc	atg	aag	gcg	gtc	ggg	cgt	acc	ggc	gca	gtc	gca	ctg	ctt	tac	240	
Glu	Ser	Met	Lys	Ala	Val	Gly	Arg	Thr	Gly	Ala	Val	Ala	Leu	Leu	Tyr		
	65				70				75					80			
ttt	gaa	att	gtc	agt	acc	atc	gcg	ctg	att	att	ggg	ctt	atc	atc	gtt	288	
Phe	Glu	Ile	Val	Ser	Thr	Ile	Ala	Leu	Ile	Ile	Gly	Leu	Ile	Ile	Val		
			85					90					95				
aac	gtc	gtg	cag	cct	ggg	gcc	gga	atg	aac	gtc	gat	ccg	gca	acg	ctt	336	
Asn	Val	Val	Gln	Pro	Gly	Ala	Gly	Met	Asn	Val	Asp	Pro	Ala	Thr	Leu		
			100					105					110				
gat	gcg	aaa	gcg	gta	gcg	gtt	tac	gcc	gat	cag	gcg	aaa	gac	cag	ggc	384	
Asp	Ala	Lys	Ala	Val	Ala	Val	Tyr	Ala	Asp	Gln	Ala	Lys	Asp	Gln	Gly		
		115					120					125					
att	gtc	gcc	ttc	att	atg	gat	gtc	atc	ccg	gcg	agc	gtc	att	ggc	gca	432	
Ile	Val	Ala	Phe	Ile	Met	Asp	Val	Ile	Pro	Ala	Ser	Val	Ile	Gly	Ala		
		130				135					140						
ttt	gcc	agc	ggg	aac	att	ctg	cag	gtg	ctg	ctg	ttt	gcc	gta	ctg	ttt	480	
Phe	Ala	Ser	Gly	Asn	Ile	Leu	Gln	Val	Leu	Leu	Phe	Ala	Val	Leu	Phe		
	145				150				155					160			
ggg	ttt	gcg	ctc	cac	cgt	ctg	ggc	agc	aaa	ggc	caa	ctg	att	ttt	aac	528	
Gly	Phe	Ala	Leu	His	Arg	Leu	Gly	Ser	Lys	Gly	Gln	Leu	Ile	Phe	Asn		
				165				170					175				
gtc	atc	gaa	agt	ttc	tcg	cag	gtc	atc	ttc	ggc	atc	atc	aat	atg	atc	576	
Val	Ile	Glu	Ser	Phe	Ser	Gln	Val	Ile	Phe	Gly	Ile	Ile	Asn	Met	Ile		
			180					185					190				
atg	cgt	ctg	gca	cct	att	ggg	gcg	ttc	ggg	gca	atg	gcg	ttt	acc	atc	624	
Met	Arg	Leu	Ala	Pro	Ile	Gly	Ala	Phe	Gly	Ala	Met	Ala	Phe	Thr	Ile		
		195				200						205					
ggg	aaa	tac	ggc	gtc	ggc	aca	ctg	gtg	caa	ctg	ggg	cag	ctg	att	atc	672	
Gly	Lys	Tyr	Gly	Val	Gly	Thr	Leu	Val	Gln	Leu	Gly	Gln	Leu	Ile	Ile		
		210				215					220						
tgt	ttc	tac	att	acc	tgt	atc	ctg	ttt	gtg	gtg	ctg	gta	ttg	ggg	tca	720	
Cys	Phe	Tyr	Ile	Thr	Cys	Ile	Leu	Phe	Val	Val	Leu	Val	Leu	Gly	Ser		
	225				230				235					240			
atc	gct	aaa	gcg	act	ggg	ttc	agt	atc	ttc	aaa	ttt	atc	cgc	tac	atc	768	
Ile	Ala	Lys	Ala	Thr	Gly	Phe	Ser	Ile	Phe	Lys	Phe	Ile	Arg	Tyr	Ile		

245	250	255	
ctg gaa gaa ctg ctg att gta ctg ggg act tca tct tcc gag tcg gcg			816
Arg Glu Glu Leu Leu Ile Val Leu Gly Thr Ser Ser Ser Glu Ser Ala			
260	265	270	
ctg ccg cgt atg ctc gac aag atg gag aaa ctc ggc tgc cgt aaa tcg			864
Leu Pro Arg Met Leu Asp Lys Met Glu Lys Leu Gly Cys Arg Lys Ser			
275	280	285	
gtg gtg ggg ctg gtc atc ccg aca ggc tac tcg ttt aac ctt gat ggc			912
Val Val Gly Leu Val Ile Pro Thr Gly Tyr Ser Phe Asn Leu Asp Gly			
290	295	300	
aca tcg ata tac ctg aca atg gcg gcg gtg ttt atc gcc cag gcc act			960
Thr Ser Ile Tyr Leu Thr Met Ala Ala Val Phe Ile Ala Gln Ala Thr			
305	310	315	320
aac agt cag atg gat atc gtc cac caa atc acg ctg tta atc gtg ttg			1008
Asn Ser Gln Met Asp Ile Val His Gln Ile Thr Leu Leu Ile Val Leu			
325	330	335	
ctg ctt tct tct aaa ggg gcg gca ggg gta acg ggt agt ggc ttt atc			1056
Leu Leu Ser Ser Lys Gly Ala Ala Gly Val Thr Gly Ser Gly Phe Ile			
340	345	350	
gtg ctg gcg gcg acg ctc tct gcg gtg ggc cat ttg ccg gta gcg ggt			1104
Val Leu Ala Ala Thr Leu Ser Ala Val Gly His Leu Pro Val Ala Gly			
355	360	365	
ctg gcg ctg atc ctc ggt atc gac cgc ttt atg tca gaa gct cgt gcg			1152
Leu Ala Leu Ile Leu Gly Ile Asp Arg Phe Met Ser Glu Ala Arg Ala			
370	375	380	
ctg act aac ctg gtc ggt aac ggc gta gcg acc att gtc gtt gct aag			1200
Leu Thr Asn Leu Val Gly Asn Gly Val Ala Thr Ile Val Val Ala Lys			
385	390	395	400
tgg gtg aaa gaa ctg gac cac aaa aaa ctg gac gat gtg ctg aat aat			1248
Trp Val Lys Glu Leu Asp His Lys Lys Leu Asp Asp Val Leu Asn Asn			
405	410	415	
cgt gcg ccg gat ggc aaa acg cac gaa tta tcc tct taa			1287
Arg Ala Pro Asp Gly Lys Thr His Glu Leu Ser Ser *			
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<211> 1191

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<213> Escherichia coli

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<222> (1) ... (1191)

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1	15

ctg ctg gcc atg ttg atg ccg ctg tcg att gat atg tat ctg ccc gcg	96
Leu Leu Ala Met Leu Met Pro Leu Ser Ile Asp Met Tyr Leu Pro Ala	
20 25 30	
cta ccg gta att tca gcg cag ttt ggc gta ccg gcg ggc agt acg cag	144
Leu Pro Val Ile Ser Ala Gln Phe Gly Val Pro Ala Gly Ser Thr Gln	
35 40 45	
atg acc ctc agt act tat att ctg ggc ttt gcg ttg ggg cag tta atc	192
Met Thr Leu Ser Thr Tyr Ile Leu Gly Phe Ala Leu Gly Gln Leu Ile	
50 55 60	
tac ggg ccg atg gca gac agc ttc ggg cgt aag ccg gtg gtg ctc ggc	240
Tyr Gly Pro Met Ala Asp Ser Phe Gly Arg Lys Pro Val Val Leu Gly	
65 70 75 80	
ggg acc ctg gtg ttt gcc gcc gcc gcg gtg gcg tgt gcg ttg gca aac	288
Gly Thr Leu Val Phe Ala Ala Ala Val Ala Cys Ala Leu Ala Asn	
85 90 95	
acc atc gat cag ctg att gtg atg cgt ttc ttc cac ggg ctg gct gcg	336
Thr Ile Asp Gln Leu Ile Val Met Arg Phe Phe His Gly Leu Ala Ala	
100 105 110	
gct gcg gcc agc gtg gtc att aac gcc ctg atg cgc gat att tac ccg	384
Ala Ala Ala Ser Val Val Ile Asn Ala Leu Met Arg Asp Ile Tyr Pro	
115 120 125	
aaa gaa gag ttc tcg ccg atg atg tcg ttt gtc atg ctg gtg aca acc	432
Lys Glu Glu Phe Ser Arg Met Met Ser Phe Val Met Leu Val Thr Thr	
130 135 140	
att gca ccg ctg atg gca ccg ata gtt ggc ggc tgg gtg ctg gtg tgg	480
Ile Ala Pro Leu Met Ala Pro Ile Val Gly Gly Trp Val Leu Val Trp	
145 150 155 160	
ctg agc tgg cat tac atc ttc tgg atc ctg gca tta gcg gcg att ctg	528
Leu Ser Trp His Tyr Ile Phe Trp Ile Leu Ala Leu Ala Ala Ile Leu	
165 170 175	
gct tcg gca atg att ttc ttc ctg att aaa gaa acc tta cca ccg gag	576
Ala Ser Ala Met Ile Phe Phe Leu Ile Lys Glu Thr Leu Pro Pro Glu	
180 185 190	
cgt cgt cag cca ttt cac att cgt acc act att ggt aac ttt gcg gcg	624
Arg Arg Gln Pro Phe His Ile Arg Thr Thr Ile Gly Asn Phe Ala Ala	
195 200 205	
ctg ttc cgc cat aaa cgt gtc ctg agc tac atg ctt gcc agt ggt ttc	672
Leu Phe Arg His Lys Arg Val Leu Ser Tyr Met Leu Ala Ser Gly Phe	
210 215 220	
agc ttt gcc ggg atg ttc tca ttc tta agc gcc gga ccg ttt gtt tat	720
Ser Phe Ala Gly Met Phe Ser Phe Leu Ser Ala Gly Pro Phe Val Tyr	
225 230 235 240	
att gaa att aac cac gtc gcg ccg gaa aac ttt ggt tat tac ttt gcg	768
Ile Glu Ile Asn His Val Ala Pro Glu Asn Phe Gly Tyr Tyr Phe Ala	
245 250 255	
cta aac att gtt ttt ctg ttc gtg atg acc atc ttt aac agc cgc ttc	816

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Leu Asn Ile Val Phe Leu Phe Val Met Thr Ile Phe Asn Ser Arg Phe
      260                      265                      270

gtc cgc cgc att ggc gcg tta aat atg ttc cgc tcg ggg ttg tgg ata 864
Val Arg Arg Ile Gly Ala Leu Asn Met Phe Arg Ser Gly Leu Trp Ile
      275                      280                      285

caa ttt att atg gca gcg tgg atg gtc atc agt gcg ctg ctg ggg ctg 912
Gln Phe Ile Met Ala Ala Trp Met Val Ile Ser Ala Leu Leu Gly Leu
      290                      295                      300

gga ttt tgg tcg ctg gtg gtt ggc gtt gcg gcg ttt gtg ggc tgc gtg 960
Gly Phe Trp Ser Leu Val Val Gly Val Ala Ala Phe Val Gly Cys Val
      305                      310                      315                      320

tcg atg gtg tca tcc aat gcg atg gcg gtc att ctt gat gag ttt ccc 1008
Ser Met Val Ser Ser Asn Ala Met Ala Val Ile Leu Asp Glu Phe Pro
      325                      330                      335

cat atg gcg gga acg gca tct tcg ctg gca gga acc ttc cgt ttt ggc 1056
His Met Ala Gly Thr Ala Ser Ser Leu Ala Gly Thr Phe Arg Phe Gly
      340                      345                      350

ata ggg gca att gtt ggc gca ttg ctt tct ctt gcg acc ttt aac tct 1104
Ile Gly Ala Ile Val Gly Ala Leu Leu Ser Leu Ala Thr Phe Asn Ser
      355                      360                      365

gca tgg ccg atg att tgg tca att gca ttc tgc gca acc agc tcc att 1152
Ala Trp Pro Met Ile Trp Ser Ile Ala Phe Cys Ala Thr Ser Ser Ile
      370                      375                      380

ctc ttc tgt ctg tac gcc agt cgg ccg aaa aaa cgg tga 1191
Leu Phe Cys Leu Tyr Ala Ser Arg Pro Lys Lys Arg *
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<210> 203

<211> 696

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(696)

<400> 203

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      1                      5                      10                      15

att gcc ggg cgt gaa atc cgc ggc aat cgt gtc acc gtc gat ggc gaa 96
Ile Ala Gly Arg Glu Ile Arg Gly Asn Arg Val Thr Val Asp Gly Glu
      20                      25                      30

atc gtc cgt aat gca gcg ttc aaa ctg ctt cct gaa cat gat gtc gct 144
Ile Val Arg Asn Ala Ala Phe Lys Leu Leu Pro Glu His Asp Val Ala
      35                      40                      45

tac gat ggc aac ccg ctg gcg cag caa cac ggt cca cgt tac ttc atg 192
Tyr Asp Gly Asn Pro Leu Ala Gln Gln His Gly Pro Arg Tyr Phe Met
      50                      55                      60

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ctc aat aag cct cag ggc tat gtt tgc tcc acg gac gac cct gat cac 240
Leu Asn Lys Pro Gln Gly Tyr Val Cys Ser Thr Asp Asp Pro Asp His
65 70 75 80

cca acg gtg ctc tat ttt ctt gat gaa ccg gta gcg tgg aaa ctg cat 288
Pro Thr Val Leu Tyr Phe Leu Asp Glu Pro Val Ala Trp Lys Leu His
85 90 95

gcg gcg ggg cgg ttg gat att gat acc acc ggt ctg gtg ctg atg act 336
Ala Ala Gly Arg Leu Asp Ile Asp Thr Thr Gly Leu Val Leu Met Thr
100 105 110

gat gat ggt cag tgg tgc cac cgc att act tct ccg cgc cat cat tgc 384
Asp Asp Gly Gln Trp Ser His Arg Ile Thr Ser Pro Arg His His Cys
115 120 125

gag aag acc tat ctg gtg aca ctg gaa tca cct gta gct gac gat acg 432
Glu Lys Thr Tyr Leu Val Leu Glu Ser Pro Val Ala Asp Asp Thr
130 135 140

gca gag caa ttt gct aaa ggc gtg cag ctg cat aac gaa aaa gat ctc 480
Ala Glu Gln Phe Ala Lys Gly Val Gln Leu His Asn Glu Lys Asp Leu
145 150 155 160

act aag cct gcg gtg ctg gaa gtg att acc cca acg cag gtt cgt ctg 528
Thr Lys Pro Ala Val Leu Glu Val Ile Thr Pro Thr Gln Val Arg Leu
165 170 175

acc atc agc gaa ggg cgt tat cat cag gtg aaa cgc atg ttc gcc gcc 576
Thr Ile Ser Glu Gly Arg Tyr His Gln Val Lys Arg Met Phe Ala Ala
180 185 190

gtg ggt aac cac gtg gtt gag ctg cat cgt gaa cgt att ggc ggt att 624
Val Gly Asn His Val Val Glu Leu His Arg Glu Arg Ile Gly Gly Ile
195 200 205

acg ctg gat gct gat tta gcc ccc ggt gaa tat cgt ccg tta act gaa 672
Thr Leu Asp Ala Asp Leu Ala Pro Gly Glu Tyr Arg Pro Leu Thr Glu
210 215 220

gaa gaa att gcc agc gtc gtc taa 696
Glu Glu Ile Ala Ser Val Val *
225 230

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cag ggg tat atc gac ctg tct gat ttg gat tta aca agt tgt cat ttt 96

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Gln	Gly	Tyr	Ile	Asp	Leu	Ser	Asp	Leu	Asp	Leu	Thr	Ser	Cys	His	Phe	
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Lys	Gly	Asp	Val	Ile	Ser	Lys	Val	Ser	Phe	Leu	Ser	Ser	Asn	Leu	Gln	
		35					40					45				
cat	gta	aca	ttc	gaa	tgt	aaa	gaa	att	ggg	gat	tgc	aat	ttt	act	act	192
His	Val	Thr	Phe	Glu	Cys	Lys	Glu	Ile	Gly	Asp	Cys	Asn	Phe	Thr	Thr	
		50				55				60						
gca	ata	ggt	gat	aat	gtc	ata	ttt	aga	tgt	cga	cgt	tta	cac	aat	gtg	240
Ala	Ile	Val	Asp	Asn	Val	Ile	Phe	Arg	Cys	Arg	Arg	Leu	His	Asn	Val	
	65				70				75						80	
att	ttt	atc	aaa	gcg	agt	ggt	gaa	tgt	gtc	gat	ttc	agc	aaa	aat	att	288
Ile	Phe	Ile	Lys	Ala	Ser	Gly	Glu	Cys	Val	Asp	Phe	Ser	Lys	Asn	Ile	
			85					90						95		
ctt	gat	aca	ggt	gac	ttc	tcg	cag	agt	caa	ctt	ggt	cat	agt	aat	ttt	336
Leu	Asp	Thr	Val	Asp	Phe	Ser	Gln	Ser	Gln	Leu	Gly	His	Ser	Asn	Phe	
			100				105						110			
cgc	gaa	tgt	cag	att	aga	aat	tca	aac	ttc	gat	aat	tgt	tat	ctt	tac	384
Arg	Glu	Cys	Gln	Ile	Arg	Asn	Ser	Asn	Phe	Asp	Asn	Cys	Tyr	Leu	Tyr	
		115					120					125				
gct	tcg	cac	ttc	acc	aga	gca	gag	ttt	ctg	tct	gcc	aaa	gaa	ata	tca	432
Ala	Ser	His	Phe	Thr	Arg	Ala	Glu	Phe	Leu	Ser	Ala	Lys	Glu	Ile	Ser	
		130				135					140					
ttt	att	aaa	tcg	aat	ttg	aca	gct	ggt	atg	ttt	gat	tat	gtg	cga	atg	480
Phe	Ile	Lys	Ser	Asn	Leu	Thr	Ala	Val	Met	Phe	Asp	Tyr	Val	Arg	Met	
	145				150				155						160	
tcg	aca	ggg	aat	ttt	aaa	gat	tgc	att	aca	gaa	caa	ttg	gaa	tta	act	528
Ser	Thr	Gly	Asn	Phe	Lys	Asp	Cys	Ile	Thr	Glu	Gln	Leu	Glu	Leu	Thr	
			165				170						175			
att	gat	tat	tca	gat	ata	ttt	tgg	aat	gaa	gat	ctc	gat	ggt	tat	atc	576
Ile	Asp	Tyr	Ser	Asp	Ile	Phe	Trp	Asn	Glu	Asp	Leu	Asp	Gly	Tyr	Ile	
			180				185						190			
aat	aac	att	ata	aaa	atg	att	gat	aca	ttg	cca	gat	aat	gca	atg	ata	624
Asn	Asn	Ile	Ile	Lys	Met	Ile	Asp	Thr	Leu	Pro	Asp	Asn	Ala	Met	Ile	
		195					200					205				
ttg	aaa	tcc	ggt	ctg	gcc	gta	aaa	ctg	gtg	atg	caa	tta	aaa	ata	ctt	672
Leu	Lys	Ser	Val	Leu	Ala	Val	Lys	Leu	Val	Met	Gln	Leu	Lys	Ile	Leu	
	210					215					220					
aat	att	ggt	aat	aaa	aac	ttt	att	gag	aat	atg	aag	aaa	ata	ttt	agc	720
Asn	Ile	Val	Asn	Lys	Asn	Phe	Ile	Glu	Asn	Met	Lys	Lys	Ile	Phe	Ser	
	225				230				235						240	
cat	tgt	cct	tat	ata	aaa	gat	ccc	att	ata	cgc	agt	tat	atc	cat	tct	768
His	Cys	Pro	Tyr	Ile	Lys	Asp	Pro	Ile	Ile	Arg	Ser	Tyr	Ile	His	Ser	
			245				250						255			
gat	gaa	gat	aac	aag	ttc	gat	gat	ttt	atg	cgt	caa	cat	cga	ttc	agt	816
Asp	Glu	Asp	Asn	Lys	Phe	Asp	Asp	Phe	Met	Arg	Gln	His	Arg	Phe	Ser	

260	265	270	
gag gtg aat ttc gat acc caa cag atg atc gat ttt att aac aga ttt			864
Glu Val Asn Phe Asp Thr Gln Gln Met Ile Asp Phe Ile Asn Arg Phe			
275	280	285	
aat acg aat aaa tgg cta att gat aaa aat aac aat ttt ttt atc caa			912
Asn Thr Asn Lys Trp Leu Ile Asp Lys Asn Asn Asn Phe Phe Ile Gln			
290	295	300	
ctt atc gat cag gcc tta cga tca acg gat gat atg atc aaa gca aat			960
Leu Ile Asp Gln Ala Leu Arg Ser Thr Asp Asp Met Ile Lys Ala Asn			
305	310	315	320
gtt tgg cat ctt tat aaa gag tgg att cgt agt gat gat gtt tca cct			1008
Val Trp His Leu Tyr Lys Glu Trp Ile Arg Ser Asp Asp Val Ser Pro			
325	330	335	
ata ttt ata gaa act gaa gat aat tta aga acc ttt aac acg aat gaa			1056
Ile Phe Ile Glu Thr Glu Asp Asn Leu Arg Thr Phe Asn Thr Asn Glu			
340	345	350	
tta aca cga aac gat aat atc ttt atc ctg ttc tcc tca gtc gat gat			1104
Leu Thr Arg Asn Asp Asn Ile Phe Ile Leu Phe Ser Ser Val Asp Asp			
355	360	365	
ggg cca gtt atg gtg gta agc tcc cag cgc tta cat gat atg ttg aat			1152
Gly Pro Val Met Val Val Ser Ser Gln Arg Leu His Asp Met Leu Asn			
370	375	380	
cct aca aaa gat acc aat tgg aat tcc acg tat atc tac aaa tcc aga			1200
Pro Thr Lys Asp Thr Asn Trp Asn Ser Thr Tyr Ile Tyr Lys Ser Arg			
385	390	395	400
cat gag atg ttg cct gtt aat ctt act cag gaa aca ctt ttc agc tcc			1248
His Glu Met Leu Pro Val Asn Leu Thr Gln Glu Thr Leu Phe Ser Ser			
405	410	415	
aaa tct cat ggt aaa tat gcg ctt ttc ccc att ttt act gcg agt tgg			1296
Lys Ser His Gly Lys Tyr Ala Leu Phe Pro Ile Phe Thr Ala Ser Trp			
420	425	430	
cga gct cat cgt ata atg aat aag ggt gtt taa			1329
Arg Ala His Arg Ile Met Asn Lys Gly Val *			
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Met Gly Arg Lys Trp Ala Asn Ile Val Ala Lys Lys Thr Ala Lys Asp			
1	5	10	15

ggt gca acg tct aaa att tat gca aaa ttc ggt gta gaa atc tat gct	96
Gly Ala Thr Ser Lys Ile Tyr Ala Lys Phe Gly Val Glu Ile Tyr Ala	
20 25 30	
gct gct aaa caa ggt gaa ccc gat cca gaa tta aac aca tct tta aaa	144
Ala Ala Lys Gln Gly Glu Pro Asp Pro Glu Leu Asn Thr Ser Leu Lys	
35 40 45	
ttc gtt att gaa cgt gca aag cag gca caa gtt cca aag cac gtt att	192
Phe Val Ile Glu Arg Ala Lys Gln Ala Gln Val Pro Lys His Val Ile	
50 55 60	
gat aaa gca att gat aaa gcc aaa ggc ggc gga gat gaa acg ttc gtg	240
Asp Lys Ala Ile Asp Lys Ala Lys Gly Gly Gly Asp Glu Thr Phe Val	
65 70 75 80	
cag gga cgt tat gaa ggc ttt ggt cct aat ggc tca atg att atc gcc	288
Gln Gly Arg Tyr Glu Gly Phe Gly Pro Asn Gly Ser Met Ile Ile Ala	
85 90 95	
gag aca ttg act tca aat gtt aac cgt acg att gct aac gtt cgc aca	336
Glu Thr Leu Thr Ser Asn Val Asn Arg Thr Ile Ala Asn Val Arg Thr	
100 105 110	
att ttc aat aaa aaa ggc ggc aat atc gga gcg gca ggt tct gtc agc	384
Ile Phe Asn Lys Lys Gly Gly Asn Ile Gly Ala Ala Gly Ser Val Ser	
115 120 125	
tat atg ttt gac aat acg ggt gtg att gta ttt aaa ggg aca gac cct	432
Tyr Met Phe Asp Asn Thr Gly Val Ile Val Phe Lys Gly Thr Asp Pro	
130 135 140	
gac cat att ttt gaa att tta ctt gaa gct gaa gtt gat gtt cgt gat	480
Asp His Ile Phe Glu Ile Leu Leu Glu Ala Glu Val Asp Val Arg Asp	
145 150 155 160	
gtg act gaa gaa gaa ggt aac att gtt att tat act gaa cct act gac	528
Val Thr Glu Glu Glu Gly Asn Ile Val Ile Tyr Thr Glu Pro Thr Asp	
165 170 175	
ctt cat aaa gga atc gcg gct cta aaa gca gct gga atc act gag ttc	576
Leu His Lys Gly Ile Ala Ala Leu Lys Ala Ala Gly Ile Thr Glu Phe	
180 185 190	
tca aca aca gaa tta gaa atg att gct caa tct gaa gtt gag ctt tcc	624
Ser Thr Thr Glu Leu Glu Met Ile Ala Gln Ser Glu Val Glu Leu Ser	
195 200 205	
cca gaa gat tta gaa atc ttt gaa ggg ctt gtt gat gcc ctt gaa gat	672
Pro Glu Asp Leu Glu Ile Phe Glu Gly Leu Val Asp Ala Leu Glu Asp	
210 215 220	
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aaa gca gca act gaa ccg gcg cac cgc ccg gcc ttt ttc cgt act cta	96
Lys Ala Ala Thr Glu Pro Ala His Arg Pro Ala Phe Phe Arg Thr Leu	
20 25 30	
ctg gaa tcc acc gtc tgg gtg cct ggt acg gcg gcg cag ggc gag gct	144
Leu Glu Ser Thr Val Trp Val Pro Gly Thr Ala Ala Gln Gly Glu Ala	
35 40 45	
gtg gtt gaa gat agc gcg ctt gat tta cag cac tgg gaa aaa gaa gac	192
Val Val Glu Asp Ser Ala Leu Asp Leu Gln His Trp Glu Lys Glu Asp	
50 55 60	
ggc acc agc gtc att cct ttt ttc acc tcg tta gaa gca ctt caa cag	240
Gly Thr Ser Val Ile Pro Phe Phe Thr Ser Leu Glu Ala Leu Gln Gln	
65 70 75 80	
gcg gtt gaa gac gaa cag gca ttt gtc gta atg ccc gtt cgc acg ctg	288
Ala Val Glu Asp Glu Gln Ala Phe Val Val Met Pro Val Arg Thr Leu	
85 90 95	
ttt gag atg aca ctt ggc gaa acg ctc ttc ctt aat gcc aaa ctg cca	336
Phe Glu Met Thr Leu Gly Glu Thr Leu Phe Leu Asn Ala Lys Leu Pro	
100 105 110	
acc ggt aaa gaa ttt atg ccg cgt gaa atc agt ttg ttg att ggt gaa	384
Thr Gly Lys Glu Phe Met Pro Arg Glu Ile Ser Leu Leu Ile Gly Glu	
115 120 125	
gag gga aat ccg ctg agc agc cag gaa atc ctg gaa ggc ggt gaa tcg	432
Glu Gly Asn Pro Leu Ser Ser Gln Glu Ile Leu Glu Gly Gly Glu Ser	
130 135 140	
ctg ata tta tcg gaa gtc gca gag ccg cca gca caa atg att gat tca	480
Leu Ile Leu Ser Glu Val Ala Glu Pro Pro Ala Gln Met Ile Asp Ser	
145 150 155 160	
ctc acc acc tta ttt aaa acc att aag ccg gtg aag cgt gct ttt att	528
Leu Thr Thr Leu Phe Lys Thr Ile Lys Pro Val Lys Arg Ala Phe Ile	
165 170 175	
tgt tca att aaa gag aac gaa gag gca cag cct aat tta ctt att ggc	576
Cys Ser Ile Lys Glu Asn Glu Glu Ala Gln Pro Asn Leu Leu Ile Gly	
180 185 190	
att gaa gcc gat ggt gat atc gaa gaa att att cag gcg acg gga agt	624
Ile Glu Ala Asp Gly Asp Ile Glu Glu Ile Ile Gln Ala Thr Gly Ser	
195 200 205	
gta gcg acc gat aca tta cct ggc gat gaa cca atc gat att tgt cag	672
Val Ala Thr Asp Thr Leu Pro Gly Asp Glu Pro Ile Asp Ile Cys Gln	

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Val Lys Lys Gly Glu Lys Gly Ile Ser His Phe Ile Thr Glu His Ile			
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gcg cca ttc tat gaa cgt cgc tgg ggt ggt ttt ttg cgt gac ttt aaa			768
Ala Pro Phe Tyr Glu Arg Arg Trp Gly Gly Phe Leu Arg Asp Phe Lys			
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ggc ggt aca att tat aaa tta ccg tcg ctg aaa gat gcg ttt tat atc			96
Gly Gly Thr Ile Tyr Lys Leu Pro Ser Leu Lys Asp Ala Phe Tyr Ile			
20	25	30	
ccg atg cag gaa tat ttc cat ttg acc aat ggt caa att ggt aat gct			144
Pro Met Gln Glu Tyr Phe His Leu Thr Asn Gly Gln Ile Gly Asn Ala			
35	40	45	
atg tcg gta aac tca ttt gtc acc aca gtg ggc ttt ttt ctg tct att			192
Met Ser Val Asn Ser Phe Val Thr Thr Val Gly Phe Phe Leu Ser Ile			
50	55	60	
tat ttt gcc gat aaa cta ccg cgc aga tac acc atg tca ttc tca ctc			240
Tyr Phe Ala Asp Lys Leu Pro Arg Arg Tyr Thr Met Ser Phe Ser Leu			
65	70	75	80
att gcg aca gga tta ctg ggt gtt tat ttg acg aca atg ccg ggg tat			288
Ile Ala Thr Gly Leu Leu Gly Val Tyr Leu Thr Thr Met Pro Gly Tyr			
85	90	95	
tgg ggc atc ctc ttt gtc tgg gcg cta ttt ggc gtt act tgc gac atg			336
Trp Gly Ile Leu Phe Val Trp Ala Leu Phe Gly Val Thr Cys Asp Met			
100	105	110	
atg aac tgg ccg gtc ttg ctc aag tcg gta agt cga ttg ggc aat agc			384
Met Asn Trp Pro Val Leu Leu Lys Ser Val Ser Arg Leu Gly Asn Ser			
115	120	125	
gaa caa caa ggt cgg ttg ttt ggc ttc ttc gaa aca ggg cgt ggc att			432
Glu Gln Gln Gly Arg Leu Phe Gly Phe Phe Glu Thr Gly Arg Gly Ile			
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Gly Ser Gly Leu Leu Gly Phe Lys Ala Gly Ile Trp Phe Tyr Ser Leu	
165 170 175	
att gtg att gcc gta ggc att att att ttc ttt gtc ctg aat gac aaa	576
Ile Val Ile Ala Val Gly Ile Ile Ile Phe Phe Val Leu Asn Asp Lys	
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gaa gag gca ccg tcc gtt gag gtg aaa aaa gaa gac gga gca tcg aaa	624
Glu Glu Ala Pro Ser Val Glu Val Lys Lys Glu Asp Gly Ala Ser Lys	
195 200 205	
aac acc agt atg acc tcg gtg ctg aaa gac aaa act atc tgg ctt atc	672
Asn Thr Ser Met Thr Ser Val Leu Lys Asp Lys Thr Ile Trp Leu Ile	
210 215 220	
gct ttt aac gtc ttc ttc gtt tac gcg gtt tac tgt ggc ctg aca ttc	720
Ala Phe Asn Val Phe Phe Val Tyr Ala Val Tyr Cys Gly Leu Thr Phe	
225 230 235 240	
ttc att cca ttc ctg aaa aac atc tat cta ttg ccc gtt gcg ctg gtg	768
Phe Ile Pro Phe Leu Lys Asn Ile Tyr Leu Leu Pro Val Ala Leu Val	
245 250 255	
ggg gct tac ggc atc att aac caa tac tgt ctg aaa atg att ggt gga	816
Gly Ala Tyr Gly Ile Ile Asn Gln Tyr Cys Leu Lys Met Ile Gly Gly	
260 265 270	
cog att ggt ggc atg att tca gat aag atc ctg aaa tcg cca agt aaa	864
Pro Ile Gly Gly Met Ile Ser Asp Lys Ile Leu Lys Ser Pro Ser Lys	
275 280 285	
tat cta tgc tac acc ttt atc att agt acc gct gcg ctc gta ctg ttg	912
Tyr Leu Cys Tyr Thr Phe Ile Ile Ser Thr Ala Ala Leu Val Leu Leu	
290 295 300	
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Ile Met Leu Pro His Glu Ser Met Pro Val Tyr Leu Gly Met Ala Cys	
305 310 315 320	
acg ctg ggc ttt ggc gcg ata gtc ttt aca cag cga gcc gta ttt ttt	1008
Thr Leu Gly Phe Gly Ala Ile Val Phe Thr Gln Arg Ala Val Phe Phe	
325 330 335	
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Ala Pro Ile Gly Glu Ala Lys Ile Ala Glu Asn Lys Thr Gly Ala Ala	
340 345 350	
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Met Ala Leu Gly Ser Phe Ile Gly Tyr Ala Pro Ala Met Phe Cys Phe	
355 360 365	
agt ctg tat ggc tac att ctg gat tta aat ccg ggg att att ggc tac	1152
Ser Leu Tyr Gly Tyr Ile Leu Asp Leu Asn Pro Gly Ile Ile Gly Tyr	
370 375 380	
aaa atc gtg ttt ggc att atg gcc tgc ttc gca ttc agt ggt gcg gtg	1200

Lys Ile Val Phe Gly Ile Met Ala Cys Phe Ala Phe Ser Gly Ala Val
 385 390 395 400
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 Ala Pro Phe Leu Leu Phe Leu Ala Ala Trp Gly Ala Asp Lys Leu Trp
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 cct cta ccg ctg cat gaa gtc aat ccc gca cga gtg gtc gtg gcg cag 144
 Pro Leu Pro Leu His Glu Val Asn Pro Ala Arg Val Val Val Ala Gln
 35 40 45
 gat ggt acg ccg ctc tgg cgc ttc gcc gat gct gac ggc atc tgg cgt 192
 Asp Gly Thr Pro Leu Trp Arg Phe Ala Asp Ala Asp Gly Ile Trp Arg
 50 55 60
 tat ccg gta aca atc gaa gat gtt tct cca cgt tac ctt gaa gcg ctg 240
 Tyr Pro Val Thr Ile Glu Asp Val Ser Pro Arg Tyr Leu Glu Ala Leu
 65 70 75 80
 atc aat tat gaa gat cgc tgg ttc tgg aag cat ccg ggg gtg aat cca 288
 Ile Asn Tyr Glu Asp Arg Trp Phe Trp Lys His Pro Gly Val Asn Pro
 85 90 95
 ttc tcg gtg gcg cgc gca gca tgg caa gat ctc act tcg gga cgg gtt 336
 Phe Ser Val Ala Arg Ala Ala Trp Gln Asp Leu Thr Ser Gly Arg Val
 100 105 110
 att tcc ggt ggc agc acg ctc act atg cag gtt gct cgt ctg ctt gat 384
 Ile Ser Gly Gly Ser Thr Leu Thr Met Gln Val Ala Arg Leu Leu Asp
 115 120 125
 cct cac ccc aaa aca ttt ggc ggc aaa att cgc cag ctc tgg cgc gcg 432
 Pro His Pro Lys Thr Phe Gly Gly Lys Ile Arg Gln Leu Trp Arg Ala
 130 135 140
 ttg caa ctg gaa tgg cat ctg tct aag cgt gaa att ctg acc ttg tat 480
 Leu Gln Leu Glu Trp His Leu Ser Lys Arg Glu Ile Leu Thr Leu Tyr
 145 150 155 160

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Leu Asn Arg Ala Pro Phe Gly Gly Thr Leu Gln Gly Ile Gly Ala Ala	
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Ser Trp Ala Tyr Leu Gly Lys Ser Pro Ala Asn Leu Ser Tyr Ser Glu	
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Ala Ala Met Leu Ala Val Leu Pro Gln Ala Pro Ser Arg Leu Arg Pro	
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gat cgt tgg ccg gag cgt gcc gaa gcc gcg cgt aat aaa gtg ctc gaa	672
Asp Arg Trp Pro Glu Arg Ala Glu Ala Ala Arg Asn Lys Val Leu Glu	
210 215 220	
cgg atg gcc gtg caa ggt gtg tgg tcc cgt gag cag gta aaa gag tca	720
Arg Met Ala Val Gln Gly Val Trp Ser Arg Glu Gln Val Lys Glu Ser	
225 230 235 240	
agg gaa gaa ccc atc tgg ctg gcc ccc cga caa atg ccg caa ctg gca	768
Arg Glu Glu Pro Ile Trp Leu Ala Pro Arg Gln Met Pro Gln Leu Ala	
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Pro Leu Phe Ser Arg Met Met Leu Gly Lys Ser Lys Ser Asp Lys Ile	
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Thr Thr Thr Leu Asp Ala Gly Leu Gln Arg Arg Leu Glu Glu Leu Ala	
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Gln Asn Trp Lys Gly Arg Leu Pro Pro Arg Ser Ser Leu Ala Met Ile	
290 295 300	
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Val Val Asp His Thr Asp Met Arg Val Arg Gly Trp Val Gly Ser Val	
305 310 315 320	
gat ctc aac gat gat tca cgc ttt ggt cat gtt gat atg gtc aat tcg	1008
Asp Leu Asn Asp Asp Ser Arg Phe Gly His Val Asp Met Val Asn Ser	
325 330 335	
atc cga tcg cca gga tca gtg ctc aaa ccg ttt gtt tat ggt ctg gcg	1056
Ile Arg Ser Pro Gly Ser Val Leu Lys Pro Phe Val Tyr Gly Leu Ala	
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Arg Arg Thr Gly Asp Tyr Arg Pro Gly Asn Phe Asp Ser Gly Phe His	
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Gly Pro Ile Ser Met Ser Glu Ala Leu Val Arg Ser Leu Asn Leu Pro	
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Gly Ala Ala Trp Ile Ile Arg Arg Ile Met Ala Asp Glu Ala Gln Pro	
485 490 495	
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Leu Pro Asp Ser Ala Leu Pro Arg Val Ala Pro Leu Ala Trp Lys Thr	
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ggc acc agc tat ggc tat cgt gac gcc tgg gcg att ggg gtt aac gct	1584
Gly Thr Ser Tyr Gly Tyr Arg Asp Ala Trp Ala Ile Gly Val Asn Ala	
515 520 525	
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Arg Tyr Val Ile Gly Ile Trp Thr Gly Arg Pro Asp Gly Thr Pro Val	
530 535 540	
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565 570 575	
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595 600 605	
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Ile Asn Gly Ile Arg Phe Pro Ile Trp Leu Asp Glu Asn Gly Lys Arg	
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gtt gcc gct gat tgc ccg caa gcg cga caa gaa atg ata aat gtc tgg	1968

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Pro	Leu	Pro	Leu	Glu	Pro	Trp	Leu	Pro	Ala	Ser	Glu	Arg	Arg	Ala	Val		
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Gly	Ala	Gly	Glu	Arg	Trp	Trp	Phe	Leu	Asn	Gly	Glu	Pro	Leu	Thr	Glu		
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cgc	ggg	cgc	aac	gtg	acc	ctg	cat	ttg	acg	gat	aaa	ggc	gat	tat	caa	2256	
Arg	Gly	Arg	Asn	Val	Thr	Leu	His	Leu	Thr	Asp	Lys	Gly	Asp	Tyr	Gln		
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 Gly Cys Asp Asn Asn Asp Asn Ala Pro Thr Ala Val Lys Lys Asp Ala
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 cct tct gaa gtt act aaa gcg gcc tct tca gaa aac gcg agt tca gca 144
 Pro Ser Glu Val Thr Lys Ala Ala Ser Ser Glu Asn Ala Ser Ser Ala
 35 40 45
 aaa ctc tcc gtg ccg gag aga caa aaa ctg gcc caa cag agt gcc ggt 192
 Lys Leu Ser Val Pro Glu Arg Gln Lys Leu Ala Gln Gln Ser Ala Gly
 50 55 60

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Lys Val Leu Thr Leu Leu Asp Leu Ser Glu Val Gln Leu Asp Gly Ala	
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Ala Thr Leu Val Leu Thr Phe Ser Ile Pro Leu Asp Pro Asp Gln Asp	
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Phe Ser Arg Val Ile His Val Val Asp Lys Lys Ser Gly Lys Val Asp	
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Leu Glu Pro Lys Arg Asp Leu Ile Val Thr Ile Gly Lys Glu Val Lys	
130 135 140	
gca ctc aac aac gca acc ttc agt aaa gat tac gaa aaa act ata act	480
Ala Leu Asn Asn Ala Thr Phe Ser Lys Asp Tyr Glu Lys Thr Ile Thr	
145 150 155 160	
acc cgc gac atc caa ccc agc gtc ggt ttt gcc agc cgt ggt tcg ctg	528
Thr Arg Asp Ile Gln Pro Ser Val Gly Phe Ala Ser Arg Gly Ser Leu	
165 170 175	
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Leu Pro Gly Lys Val Val Glu Gly Leu Pro Val Met Ala Leu Asn Val	
180 185 190	
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gca ttc att agc caa tgg gaa tac cgc aat tcg ctg gcg aac tgg cag	672
Ala Phe Ile Ser Gln Trp Glu Tyr Arg Asn Ser Leu Ala Asn Trp Gln	
210 215 220	
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Ser Asp Lys Leu Leu Gln Met Ala Asp Leu Val Tyr Thr Gly Arg Phe	
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Asp Leu Asn Pro Ala Arg Asn Thr Arg Glu Lys Leu Leu Leu Pro Leu	
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Gly Asp Ile Lys Pro Leu Gln Gln Ala Gly Val Tyr Leu Ala Val Met	
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Ile Thr Arg His Ser Pro Ser Phe Glu Met His Met Ala Ser Asp Thr				
260	265	270		
ctg aat ttt atg ccg ttt gag aaa gga aca ttg ctg gcg cag gac gga	864			
Leu Asn Phe Met Pro Phe Glu Lys Gly Thr Leu Leu Ala Gln Asp Gly				
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Glu Glu Arg Phe Thr Val Thr His Asp Val Glu Tyr Val Leu Phe Pro				
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cat tac gcg ggc ctg tcg ttt ggt aat gaa gcc tct acc cgt cac cgt	96
His Tyr Ala Gly Leu Ser Phe Gly Asn Glu Ala Ser Thr Arg His Arg	
20 25 30	
ttt cag gtg tct aac ccg cga ctg gcg gcg aag cag ggc tta ctg aaa	144
Phe Gln Val Ser Asn Pro Arg Leu Ala Ala Lys Gln Gly Leu Leu Lys	
35 40 45	
atg aaa gcc ctt gcc gat gcg gga ttc ccc cag gcc gtg atc ccg ccg	192
Met Lys Ala Leu Ala Asp Ala Gly Phe Pro Gln Ala Val Ile Pro Pro	
50 55 60	
cac gag cgt ccg ttt att ccg gtg ctg cgt cag ttg gga ttc agt ggt	240
His Glu Arg Pro Phe Ile Pro Val Leu Arg Gln Leu Gly Phe Ser Gly	
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Ser Asp Glu Gln Val Leu Glu Lys Val Ala Arg Gln Ala Pro His Trp	
85 90 95	

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Leu Ser Ser Val Ser Ser Ala Ser Pro Met Trp Val Ala Asn Ala Ala	
100 105 110	
acg atc gcg cca tct gcc gat acg ctg gat ggc aaa gtg cat ctc acc	384
Thr Ile Ala Pro Ser Ala Asp Thr Leu Asp Gly Lys Val His Leu Thr	
115 120 125	
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Val Ala Asn Leu Asn Asn Lys Phe His Arg Ser Leu Glu Ala Pro Val	
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Thr Glu Ser Leu Leu Lys Ala Ile Phe Asn Asp Glu Glu Lys Phe Ser	
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Val His Ser Ala Leu Pro Gln Val Ala Leu Leu Gly Asp Glu Gly Ala	
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Ala Asn His Asn Arg Leu Gly Gly His Tyr Gly Glu Pro Gly Met Gln	
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Tyr Pro Ala Arg Gln Thr Arg Glu Ala Ser Glu Ala Val Ala Arg Leu	
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Asn Gln Val Asn Pro Gln Gln Val Ile Phe Ala Gln Gln Asn Pro Asp	
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gtt atc gac cag ggc gtt ttt cat aat gac gtg att gcc gtg agt aac	768
Val Ile Asp Gln Gly Val Phe His Asn Asp Val Ile Ala Val Ser Asn	
245 250 255	
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Arg Gln Val Leu Phe Cys His Gln Gln Ala Phe Ala Arg Gln Ser Gln	
260 265 270	
tta ctg gca aac ctg cgt gcg cgg gtc aat ggt ttt atg gcg ata gaa	864
Leu Leu Ala Asn Leu Arg Ala Arg Val Asn Gly Phe Met Ala Ile Glu	
275 280 285	
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Val Pro Ala Thr Gln Val Ser Val Ser Asp Thr Val Ser Thr Tyr Leu	
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Phe Asn Ser Gln Leu Leu Ser Arg Asp Asp Gly Ser Met Met Leu Val	
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ctg cct cag gag tgt cgg gaa cac gcc gga gta tgg ggt tat ctc aat	1008
Leu Pro Gln Glu Cys Arg Glu His Ala Gly Val Trp Gly Tyr Leu Asn	
325 330 335	
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Leu	Arg	Glu	Ser	Met	Ala	Asn	Gly	Gly	Gly	Pro	Ala	Cys	Leu	Arg	Leu		
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cgg	gtg	gta	ttg	aca	gaa	gaa	gaa	cgc	cgg	gcg	gtg	aat	ccg	gcg	gtg	1152	
Arg	Val	Val	Leu	Thr	Glu	Glu	Glu	Arg	Arg	Ala	Val	Asn	Pro	Ala	Val		
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Met	Met	Asn	Asp	Thr	Leu	Phe	Asn	Ala	Leu	Asn	Asp	Trp	Val	Asp	Arg		
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Tyr	Tyr	Arg	Asp	Arg	Leu	Thr	Ala	Ala	Asp	Leu	Ala	Asp	Pro	Gln	Leu		
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Leu	Arg	Glu	Gly	Arg	Glu	Ala	Leu	Asp	Val	Leu	Ser	Gln	Leu	Leu	Asn		
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Arg	Val	Lys	Arg	Asn	Pro	Val	Ser	Gly	Glu	Val	Leu	Trp	Gln	Gly	Asn		
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gat	gcc	gat	gcc	gct	cag	gtc	gag	cag	gct	tgt	cgg	gca	gcc	cgt	gcg	144	
Asp	Ala	Asp	Ala	Ala	Gln	Val	Glu	Gln	Ala	Cys	Arg	Ala	Ala	Arg	Ala		
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gcg	ttt	ccg	cgc	tgg	gcg	cgg	ctt	tca	ttt	gct	gaa	cgt	cat	gcc	gtt	192	
Ala	Phe	Pro	Arg	Trp	Ala	Arg	Leu	Ser	Phe	Ala	Glu	Arg	His	Ala	Val		
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Val	Glu	Arg	Phe	Ala	Ala	Leu	Leu	Glu	Ser	Asn	Lys	Ala	Glu	Leu	Thr		
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Ala	Ile	Ile	Ala	Arg	Glu	Thr	Gly	Lys	Pro	Arg	Trp	Glu	Ala	Ala	Thr		

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290					295					300																				
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305					310					315					320															
ctg	att	tct	gaa	cag	gcc	gca	cag	cag	gtg	gtt	act	gca	tgg	cag	caa	1008														
Leu	Ile	Ser	Glu	Gln	Ala	Ala	Gln	Gln	Val	Val	Thr	Ala	Trp	Gln	Gln															
325					330					335																				

ctg gaa gcg atg ggc gga cga ccc	ctg ctt gcg ccg cgc tta tta caa	1056
Leu Glu Ala Met Gly Gly Arg Pro	Leu Leu Ala Pro Arg Leu Leu Gln	
340	345 350	
gca ggg aca tcg ttg ctg acg ccg ggg atc att	gaa atg aca ggc gtt	1104
Ala Gly Thr Ser Leu Leu Thr Pro Gly Ile Ile	Glu Met Thr Gly Val	
355	360 365	
gct ggc gta cca gat gaa gag gtg ttc gga ccg	tta ttg cgc gtc tgg	1152
Ala Gly Val Pro Asp Glu Glu Val Phe Gly Pro	Leu Leu Arg Val Trp	
370	375 380	
cgt tat gat act ttc gat gaa gcg att cga atg	gcg aat aac act cgc	1200
Arg Tyr Asp Thr Phe Asp Glu Ala Ile Arg Met	Ala Asn Asn Thr Arg	
385	390 395 400	
ttc gga ctc tct tgc ggt ctg gtt tcc ccc gag	ccg gaa aag ttc gat	1248
Phe Gly Leu Ser Cys Gly Leu Val Ser Pro Glu Arg	Glu Lys Phe Asp	
405	410 415	
caa ctg ttg ctg gag gcg ccg gcg ggg att gtt	aac tgg aac aaa ccg	1296
Gln Leu Leu Leu Glu Ala Arg Ala Gly Ile Val	Asn Trp Asn Lys Pro	
420	425 430	
ctt acc ggt gct gcc agt acc gcg cca ttc ggc	ggc att ggt gct tcc	1344
Leu Thr Gly Ala Ala Ser Thr Ala Pro Phe Gly	Gly Ile Gly Ala Ser	
435	440 445	
ggt aac cat cgc ccc agc gcc tgg tat gcc gca	gat tac tgc gca tgg	1392
Gly Asn His Arg Pro Ser Ala Trp Tyr Ala Ala	Asp Tyr Cys Ala Trp	
450	455 460	
ccg atg gcg agc ctg gag tcg gac tcg tta aca	ttg ccc gcc acg ctt	1440
Pro Met Ala Ser Leu Glu Ser Asp Ser Leu Thr	Leu Pro Ala Thr Leu	
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Gln Leu Ala Ser Lys Thr Gly Gly Gly Leu Thr	Ser Leu Pro Ala Asn	
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gaa gcc acg ctt tcg gcg cgt atc gaa agg gca	atc aaa acc tgg caa	144

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Gly	Glu	Leu	Pro	Lys	Ser	Glu	Gln	Gly	Tyr	Val	Phe	Val	Leu	Glu	Asp		
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Ser	Glu	Thr	Gly	Thr	Val	Ala	Gly	Ile	Cys	Ala	Ile	Glu	Val	Ala	Val		
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ggg	ctg	aac	gat	ccc	tgg	tac	aac	tat	cgc	gtc	ggc	acg	ttg	gtt	cac	288	
Gly	Leu	Asn	Asp	Pro	Trp	Tyr	Asn	Tyr	Arg	Val	Gly	Thr	Leu	Val	His		
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gcc	tca	aaa	gag	ctg	aat	gtc	tat	aac	gca	ttg	ccg	acg	ctg	ttt	ctc	336	
Ala	Ser	Lys	Glu	Leu	Asn	Val	Tyr	Asn	Ala	Leu	Pro	Thr	Leu	Phe	Leu		
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Ser	Asn	Asp	His	Thr	Gly	Ser	Ser	Glu	Leu	Cys	Thr	Leu	Phe	Leu	Asp		
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ccg	gac	tgg	cgc	aaa	gag	ggc	aac	ggc	tat	ttg	ctg	tcg	aaa	tcg	cgc	432	
Pro	Asp	Trp	Arg	Lys	Glu	Gly	Asn	Gly	Tyr	Leu	Leu	Ser	Lys	Ser	Arg		
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Phe	Met	Phe	Met	Ala	Ala	Phe	Arg	Asp	Lys	Phe	Asn	Asp	Lys	Val	Val		
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gct	gaa	atg	cgc	ggg	gtg	att	gac	gaa	cac	ggc	tat	tca	ccg	ttc	tgg	528	
Ala	Glu	Met	Arg	Gly	Val	Ile	Asp	Glu	His	Gly	Tyr	Ser	Pro	Phe	Trp		
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caa	agc	ctc	ggt	aaa	cgc	ttc	ttt	tcg	atg	gat	ttt	agc	cgc	gcc	gat	576	
Gln	Ser	Leu	Gly	Lys	Arg	Phe	Phe	Ser	Met	Asp	Phe	Ser	Arg	Ala	Asp		
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Lys	His	Pro	Ile	Tyr	Thr	His	Phe	Leu	Ser	Gln	Glu	Ala	Gln	Asp	Val		
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Ile	Gly	Gln	Val	His	Pro	Gln	Thr	Ala	Pro	Ala	Arg	Ala	Val	Leu	Glu		
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Lys	Glu	Gly	Phe	Arg	Tyr	Arg	Asn	Tyr	Ile	Asp	Ile	Phe	Asp	Gly	Gly		
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Pro	Thr	Leu	Glu	Cys	Asp	Ile	Asp	Arg	Val	Arg	Ala	Ile	Arg	Lys	Ser		
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Ala Cys Leu Val Ala Asn Glu Asn Tyr His His Phe Arg Val Val Leu			
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gtg cgt acc gat ccg gca acc gag cgt ttg att tta acc gcc gca caa			960
Val Arg Thr Asp Pro Ala Thr Glu Arg Leu Ile Leu Thr Ala Ala Gln			
305	310	315	320
ctg gat gcc ctc aaa tgc cac gcc ggg gat cgc gtt cgt ctg gtg cgc			1008
Leu Asp Ala Leu Lys Cys His Ala Gly Asp Arg Val Arg Leu Val Arg			
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1	5	10	15
gtt tac gct ccg gca ccc ttt ata ccg gta cgt ggc gaa ggt tcg cgc			96
Val Tyr Ala Pro Ala Pro Phe Ile Pro Val Arg Gly Glu Gly Ser Arg			
20	25	30	
ttg tgg gat cag cag ggg aaa gag tat atc gac ttc gcg ggt ggc att			144
Leu Trp Asp Gln Gln Gly Lys Glu Tyr Ile Asp Phe Ala Gly Gly Ile			
35	40	45	
gcg gtg aac gcg ctg ggc cat gcg cat ccg gaa ctg cgt gaa gcg ctg			192
Ala Val Asn Ala Leu Gly His Ala His Pro Glu Leu Arg Glu Ala Leu			
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aac gaa cag gcg agt aag ttc tgg cat acc ggc aac ggt tac acc aac			240
Asn Glu Gln Ala Ser Lys Phe Trp His Thr Gly Asn Gly Tyr Thr Asn			
65	70	75	80
gag ccg gta ctg cga ctg gcg aaa aaa ttg atc gac gcc acg ttt gcc			288
Glu Pro Val Leu Arg Leu Ala Lys Lys Leu Ile Asp Ala Thr Phe Ala			
85	90	95	
gat cgc gtc ttc ttt tgt aac tcc ggt gcg gaa gcc aac gaa gcg gcg			336
Asp Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala			
100	105	110	
cta aaa ctg gcg cgt aaa ttc gct cac gac cgc tac ggc agc cat aag			384
Leu Lys Leu Ala Arg Lys Phe Ala His Asp Arg Tyr Gly Ser His Lys			
115	120	125	

agc ggc atc gtg gcg ttc aaa aat gcg ttt cat ggt cgc acg ctg ttt	432
Ser Gly Ile Val Ala Phe Lys Asn Ala Phe His Gly Arg Thr Leu Phe	
130 135 140	
act gtc agt gcg ggt ggg cag cca gcc tat tca cag gat ttt gcg cca	480
Thr Val Ser Ala Gly Gly Gln Pro Ala Tyr Ser Gln Asp Phe Ala Pro	
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Ser Ala Leu Ile Asp Asp Ser Thr Cys Ala Val Ile Val Glu Pro Ile	
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Gln Gly Glu Gly Gly Val Val Pro Ala Ser Asn Ala Phe Leu Gln Gly	
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Leu Arg Glu Leu Cys Asn Arg His Asn Ala Leu Leu Ile Phe Asp Glu	
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Val Gln Thr Gly Val Gly Arg Thr Gly Glu Leu Tyr Ala Tyr Met His	
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Tyr Gly Val Thr Pro Asp Leu Leu Thr Thr Ala Lys Ala Leu Gly Gly	
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Ser Ala Val Ala Gly Lys Val Leu Glu Leu Ile Asn Thr Pro Glu Met	
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 65 70 75 80
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 Ala Glu Val Glu Phe Glu Val Lys Gly Glu Ala Tyr Arg Ala Phe Trp
 85 90 95
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 Arg Val Glu Leu Ala Arg Cys Ala Asp Gly Lys Ile Leu Ala Asp Lys
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Thr Gly Thr Glu Ile Tyr Gly Gln Ile Ser Ala Met Val Phe Glu Gln	
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His Lys Ser Ala Arg Thr Glu Leu Lys Leu Gln Ala Gln Ala Ser	
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Trp Gln Gln Gln Leu Thr His Ala Glu Gln Lys Leu Asn Ala Leu Ala	
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580 585 590	
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Ile Ala Ala His Asn Gln Gln Ile Ile Gln Tyr Gln Gln Gln Ile Glu	
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865 870 875 880	
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Arg Phe Val Val Asn Leu Gln Gln Thr Gly Cys His Leu Val Val Leu	
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Ala Gly Asn His Asp Ser Val Ala Thr Leu Asn Glu Ser Arg Asp Ile	
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Met Ala Phe Leu Asn Thr Thr Val Val Ala Ser Ala Gly His Ala Pro	
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Ile Pro Phe Leu Arg Pro Arg Asp Ile Ile Thr Ser Gln Ala Gly Leu	
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Asn Gly Ile Glu Lys Gln Gln His Leu Leu Ala Ala Ile Thr Asp Tyr	
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Tyr Gln Gln His Tyr Ala Asp Ala Cys Lys Leu Arg Gly Asp Gln Pro	
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Leu Pro Ile Ile Ala Thr Gly His Leu Thr Thr Val Gly Ala Ser Lys	
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Ser Asp Ala Val Arg Asp Ile Tyr Ile Gly Thr Leu Asp Ala Phe Pro	
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ccc att cca ctg agt ttt gat gaa tgc ggt aag agt aaa tat gtc cat	768
Pro Ile Pro Leu Ser Phe Asp Glu Cys Gly Lys Ser Lys Tyr Val His	
245 250 255	
ctg gtg aca ttt tca aac ggc aaa tta gag agc gtg gaa aac ctg aac	816
Leu Val Thr Phe Ser Asn Gly Lys Leu Glu Ser Val Glu Asn Leu Asn	
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gta ccg gta acg caa ccc atg gca gtg ctg aaa ggc gat ctg gcg tcg	864

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Ile	Thr	Ala	Gln	Leu	Glu	Gln	Trp	Arg	Asp	Val	Ser	Gln	Glu	Pro	Pro	
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Val	Trp	Leu	Asp	Ile	Glu	Ile	Thr	Thr	Asp	Glu	Tyr	Leu	His	Asp	Ile	
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cag	cgc	aaa	atc	cag	gca	tta	acc	gaa	tca	ttg	cct	gtc	gaa	gta	ttg	1008
Gln	Arg	Lys	Ile	Gln	Ala	Leu	Thr	Glu	Ser	Leu	Pro	Val	Glu	Val	Leu	
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Ser	Ala	Gln	Gly	Ile	Gly	Phe	Leu	Leu	Ala	Thr	Gly	Leu	Gly	Lys	Tyr	
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ggc	gca	caa	ata	att	att	aat	gat	att	act	gcc	gaa	cgc	gca	gaa	ctt	144
Gly	Ala	Gln	Ile	Ile	Ile	Asn	Asp	Ile	Thr	Ala	Glu	Arg	Ala	Glu	Leu	
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Ala	Val	Glu	Lys	Leu	His	Gln	Glu	Gly	Ile	Gln	Ala	Val	Ala	Ala	Pro	
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Glu Lys Asp Ile Gly Pro Ile Asp Val Leu Val Asn Asn Ala Gly Ile
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Gln Arg Arg His Pro Phe Thr Glu Phe Pro Glu Gln Glu Trp Asn Asp
100 105 110

gtg atc gca gta aac cag acc gcc gtg ttc ctg gta tcg caa gcg gta 384
Val Ile Ala Val Asn Gln Thr Ala Val Phe Leu Val Ser Gln Ala Val
115 120 125

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Thr Arg His Met Val Glu Arg Lys Ala Gly Lys Val Ile Asn Ile Cys
130 135 140

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145 150 155 160

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165 170 175

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Ala Arg His Asn Ile Gln Val Asn Gly Ile Ala Pro Gly Tyr Phe Lys
180 185 190

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Thr Glu Met Thr Lys Ala Leu Val Glu Asp Glu Ala Phe Thr Ala Trp
195 200 205

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210 215 220

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225 230 235 240

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Gln Ile Thr Arg Gly Gly Ile Cys Gly Ser Asp Leu His Tyr Tyr Gln	
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Glu Gly Lys Val Gly Asn Phe Met Ile Lys Ala Pro Met Val Leu Gly	
50 55 60	
cat gaa gtt atc ggt aaa gtt att cat agc gac tca tca gaa tta cat	240
His Glu Val Ile Gly Lys Val Ile His Ser Asp Ser Ser Glu Leu His	
65 70 75 80	
gaa ggg caa acg gta gcc att aat ccg tct aaa ccg tgc ggt cac tgc	288
Glu Gly Gln Thr Val Ala Ile Asn Pro Ser Lys Pro Cys Gly His Cys	
85 90 95	
aaa tac tgc att gaa cat aac gag aat cag tgt aca gat atg cgt ttt	336
Lys Tyr Cys Ile Glu His Asn Glu Asn Gln Cys Thr Asp Met Arg Phe	
100 105 110	
ttt ggc agt gcc atg tat ttc cct cat gtt gat ggt ggt ttt acc cgt	384
Phe Gly Ser Ala Met Tyr Phe Pro His Val Asp Gly Gly Phe Thr Arg	
115 120 125	
tat aaa atg gtc gaa acg tcg caa tgt gtc cct tat ccg gcc aaa gct	432
Tyr Lys Met Val Glu Thr Ser Gln Cys Val Pro Tyr Pro Ala Lys Ala	
130 135 140	
gac gaa aag gtt atg gct ttt gcc gaa cct tta gcc gtc gcg att cat	480
Asp Glu Lys Val Met Ala Phe Ala Glu Pro Leu Ala Val Ala Ile His	
145 150 155 160	
gcc gca cat cag gcc ggc gag tta cag ggc aag cga gta ttt att tcc	528
Ala Ala His Gln Ala Gly Glu Leu Gln Lys Arg Val Phe Ile Ser	
165 170 175	
ggt gtt gga ccc att ggc tgc ctg att gtc agt gca gtg aaa aca ctg	576
Gly Val Gly Pro Ile Gly Cys Leu Ile Val Ser Ala Val Lys Thr Leu	
180 185 190	
ggg gcc gcg gaa att gtc tgt gct gat gtg agt ccc cgt tcc ctt tcg	624
Gly Ala Ala Glu Ile Val Cys Ala Asp Val Ser Pro Arg Ser Leu Ser	
195 200 205	
ctg ggc aaa gag atg ggg gcg gat gtg ctc gta aac cca caa aac gac	672
Leu Gly Lys Glu Met Gly Ala Asp Val Leu Val Asn Pro Gln Asn Asp	
210 215 220	
gac atg gat cac tgg aaa gcg gaa aaa ggc tat ttc gat gtc agc ttt	720
Asp Met Asp His Trp Lys Ala Glu Lys Gly Tyr Phe Asp Val Ser Phe	
225 230 235 240	
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Glu Val Ser Gly His Pro Ser Ser Val Asn Thr Cys Leu Glu Val Thr	
245 250 255	
cgt gca cgc ggc gta atg gtg cag gta ggt atg gga ggc gcg atg gca	816
Arg Ala Arg Gly Val Met Val Gln Val Gly Met Gly Gly Ala Met Ala	
260 265 270	
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Glu Phe Pro Met Met Thr Leu Ile Gly Lys Glu Ile Ser Leu Arg Gly	
275 280 285	
tct ttc cgt ttt acc agc gaa ttt aat acc gca gtg tca tgg ctg gcg	912
Ser Phe Arg Phe Thr Ser Glu Phe Asn Thr Ala Val Ser Trp Leu Ala	
290 295 300	
aat ggc gtt atc aat cca ctg cct tta ctg agt gct gaa tat ccc ttc	960
Asn Gly Val Ile Asn Pro Leu Pro Leu Leu Ser Ala Glu Tyr Pro Phe	
305 310 315 320	
act gac ctg gaa gag gcg cta cgt ttc gcc ggt gat aaa acc cag gca	1008
Thr Asp Leu Glu Glu Ala Leu Arg Phe Ala Gly Asp Lys Thr Gln Ala	
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ttc atg atc tgg caa gcc tgg gag cag gat aaa aac ccg caa cct cag	96
Phe Met Ile Trp Gln Ala Trp Glu Gln Asp Lys Asn Pro Gln Pro Gln	
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gcc caa cag acc acg cag aca acg acc acc gca gcg ggt agc gcc gcc	144
Ala Gln Gln Thr Thr Gln Thr Thr Thr Ala Ala Gly Ser Ala Ala	
35 40 45	
gac cag ggc gta ccg gcc agt ggc cag ggg aaa ctg atc tcg gtt aag	192
Asp Gln Gly Val Pro Ala Ser Gly Gln Gly Lys Leu Ile Ser Val Lys	
50 55 60	
acc gac gtg ctt gat ctg acc atc aac acc cgt ggt ggt gat gtt gag	240
Thr Asp Val Leu Asp Leu Thr Ile Asn Thr Arg Gly Gly Asp Val Glu	
65 70 75 80	
caa gct ctg ctg cct gct tac ccg aaa gag ctg aac tct acc cag ccg	288
Gln Ala Leu Leu Pro Ala Tyr Pro Lys Glu Leu Asn Ser Thr Gln Pro	
85 90 95	

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Phe Gln Leu Leu Glu Thr Ser Pro Gln Phe Ile Tyr Gln Ala Gln Ser	
100 105 110	
ggt ctg acc ggt cgt gat ggc ccg gat aac ccg gct aac ggc ccg cgt	384
Gly Leu Thr Gly Arg Asp Gly Pro Asp Asn Pro Ala Asn Gly Pro Arg	
115 120 125	
ccg ctg tat aac gtt gaa aaa gac gct tat gtg ctg gct gaa ggt caa	432
Pro Leu Tyr Asn Val Glu Lys Asp Ala Tyr Val Leu Ala Glu Gly Gln	
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aac gaa ctg cag gtg ccg atg acg tat acc gac gcg gca ggc aac acg	480
Asn Glu Leu Gln Val Pro Met Thr Tyr Thr Asp Ala Ala Gly Asn Thr	
145 150 155 160	
ttt acc aaa acg ttt gtc ctg aaa cgt ggt gat tac gct gtc aac gtc	528
Phe Thr Lys Thr Phe Val Leu Lys Arg Gly Asp Tyr Ala Val Asn Val	
165 170 175	
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Asn Tyr Asn Val Gln Asn Ala Gly Glu Lys Pro Leu Glu Ile Ser Ser	
180 185 190	
ttt ggt cag ttg aag caa tcc atc act ctg cca ccg cat ctc gat acc	624
Phe Gly Gln Leu Lys Gln Ser Ile Thr Leu Pro Pro His Leu Asp Thr	
195 200 205	
gga agc agc aac ttc gca ctg cac acc ttc cgt ggc gcg gcg tac tcc	672
Gly Ser Ser Asn Phe Ala Leu His Thr Phe Arg Gly Ala Ala Tyr Ser	
210 215 220	
acg cct gac gag aag tat gag aaa tac aag ttc gat acc att gcc gat	720
Thr Pro Asp Glu Lys Tyr Glu Lys Tyr Lys Phe Asp Thr Ile Ala Asp	
225 230 235 240	
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Asn Glu Asn Leu Asn Ile Ser Ser Lys Gly Gly Trp Val Ala Met Leu	
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caa cag tat ttc gcg acg gcg tgg atc ccg cat aac gac ggt acc aac	816
Gln Gln Tyr Phe Ala Thr Ala Trp Ile Pro His Asn Asp Gly Thr Asn	
260 265 270	
aac ttc tat acc gct aat ctg ggt aac ggc atc gcc gct atc ggc tat	864
Asn Phe Tyr Thr Ala Asn Leu Gly Asn Gly Ile Ala Ala Ile Gly Tyr	
275 280 285	
aaa tct cag ccg gta ctg gtt cag cct ggt cag act ggc gcg atg aac	912
Lys Ser Gln Pro Val Leu Val Gln Pro Gly Gln Thr Gly Ala Met Asn	
290 295 300	
agc acc ctg tgg gtt ggc ccg gaa atc cag gac aaa atg gca gct gtt	960
Ser Thr Leu Trp Val Gly Pro Glu Ile Gln Asp Lys Met Ala Ala Val	
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Ala Pro His Leu Asp Leu Thr Val Asp Tyr Gly Trp Leu Trp Phe Ile	
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Ser Gln Pro Leu Phe Lys Leu Leu Lys Trp Ile His Ser Phe Val Gly	
340 345 350	
aac tgg ggc ttc tcc att atc atc atc acc ttt atc gtt cgt ggc atc	1104
Asn Trp Gly Phe Ser Ile Ile Ile Ile Thr Phe Ile Val Arg Gly Ile	
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atg tac ccg ctg acc aaa gcg cag tac acc tcc atg gcg aag atg cgt	1152
Met Tyr Pro Leu Thr Lys Ala Gln Tyr Thr Ser Met Ala Lys Met Arg	
370 375 380	
atg ttg cag ccg aag att cag gca atg cgt gag cgt ctg ggc gat gac	1200
Met Leu Gln Pro Lys Ile Gln Ala Met Arg Glu Arg Leu Gly Asp Asp	
385 390 395 400	
aaa cag cgt atc agc cag gaa atg atg gcg ctg tac aaa gct gag aag	1248
Lys Gln Arg Ile Ser Gln Glu Met Met Ala Leu Tyr Lys Ala Glu Lys	
405 410 415	
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Val Asn Pro Leu Gly Gly Cys Phe Pro Leu Leu Ile Gln Met Pro Ile	
420 425 430	
ttc ctg gcg ttg tac tac atg ctg atg ggt tcc gtt gaa ctg cgt cag	1344
Phe Leu Ala Leu Tyr Tyr Met Leu Met Gly Ser Val Glu Leu Arg Gln	
435 440 445	
gca ccg ttt gca ctg tgg atc cac gac ctg tgc gca cag gac ccg tac	1392
Ala Pro Phe Ala Leu Trp Ile His Asp Leu Ser Ala Gln Asp Pro Tyr	
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tac atc ctg ccg atc ctg atg ggc gta acg atg ttc ttc att cag aag	1440
Tyr Ile Leu Pro Ile Leu Met Gly Val Thr Met Phe Phe Ile Gln Lys	
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atg tgc ccg acc aca gtg acc gac ccg atg cag cag aag atc atg acc	1488
Met Ser Pro Thr Thr Val Thr Asp Pro Met Gln Gln Lys Ile Met Thr	
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ttt atg ccg gtc atc ttc acc gtg ttc ttc ctg tgg ttc ccg tca ggt	1536
Phe Met Pro Val Ile Phe Thr Val Phe Phe Leu Trp Phe Pro Ser Gly	
500 505 510	
ctg gtg ctg tac tat atc gtc agc aac ctg gta acc att att cag cag	1584
Leu Val Leu Tyr Tyr Ile Val Ser Asn Leu Val Thr Ile Ile Gln Gln	
515 520 525	
cag ctg att tac cgt ggt ctg gaa aaa cgt ggc ctg cat agc cgc gag	1632
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Gly Ala Thr Gly Ala Gly Ile Ala Arg Asp Cys Ala Leu Arg Gly Leu	
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cgc gtg att ttg gtt gag cgc cac gac atc gca acc ggt gcc acc ggg	144
Arg Val Ile Leu Val Glu Arg His Asp Ile Ala Thr Gly Ala Thr Gly	
35 40 45	
cgt aac cac ggc ctg ctg cac agc ggt gcg cgc tat gcg gta acc gat	192
Arg Asn His Gly Leu Leu His Ser Gly Ala Arg Tyr Ala Val Thr Asp	
50 55 60	
gcg gaa tcg gcc cgc gaa tgc att agt gaa aac cag atc ctg aaa cgc	240
Ala Glu Ser Ala Arg Glu Cys Ile Ser Glu Asn Gln Ile Leu Lys Arg	
65 70 75 80	
att gca cgt cac tgc gtt gaa cca acc aac ggc ctg ttt atc acc ctg	288
Ile Ala Arg His Cys Val Glu Pro Thr Asn Gly Leu Phe Ile Thr Leu	
85 90 95	
ccg gaa gat gac ctc tcc ttc cag gcc act ttt att cgc gcc tgc gaa	336
Pro Glu Asp Asp Leu Ser Phe Gln Ala Thr Phe Ile Arg Ala Cys Glu	
100 105 110	
gaa gca ggg atc agc gca gaa gct ata gac ccg cag caa gcg cgc att	384
Glu Ala Gly Ile Ser Ala Glu Ala Ile Asp Pro Gln Gln Ala Arg Ile	
115 120 125	
atc gaa cct gcc gtt aac ccg gca ctg att ggc gcg gtg aaa gtt ccg	432
Ile Glu Pro Ala Val Asn Pro Ala Leu Ile Gly Ala Val Lys Val Pro	
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Asp Gly Thr Val Asp Pro Phe Arg Leu Thr Ala Ala Asn Met Leu Asp	
145 150 155 160	
gcc aaa gaa cac ggt gcc gtt atc ctt acc gct cat gaa gtc acg ggg	528
Ala Lys Glu His Gly Ala Val Ile Leu Thr Ala His Glu Val Thr Gly	
165 170 175	
ctg att cgt gaa ggc gcg acg gtg tgc ggt gtt cgt gta cgt aac cat	576
Leu Ile Arg Glu Gly Ala Thr Val Cys Gly Val Arg Val Arg Asn His	
180 185 190	
ctc acc ggc gaa act cag gcc ctt cat gca cct gtc gtg gtt aat gcc	624
Leu Thr Gly Glu Thr Gln Ala Leu His Ala Pro Val Val Val Asn Ala	
195 200 205	
gct ggg atc tgg ggg caa cac att gcc gaa tat gcc gat ctg cgc att	672
Ala Gly Ile Trp Gly Gln His Ile Ala Glu Tyr Ala Asp Leu Arg Ile	
210 215 220	

cgc atg ttc ccg gcg aaa gga tcg ctg ctg atc atg gat cac cgc att	720
Arg Met Phe Pro Ala Lys Gly Ser Leu Leu Ile Met Asp His Arg Ile	
225 230 235 240	
aac cag cat gtg atc aac cgc tgc cgt aaa cct tcc gac gcc gat att	768
Asn Gln His Val Ile Asn Arg Cys Arg Lys Pro Ser Asp Ala Asp Ile	
245 250 255	
ctg gtg cct ggc gat acc att tcg ctg att ggt acc acc tct tta cgt	816
Leu Val Pro Gly Asp Thr Ile Ser Leu Ile Gly Thr Thr Ser Leu Arg	
260 265 270	
att gat tac aac gag att gac gat aat cga gtg acg gca gaa gag gtt	864
Ile Asp Tyr Asn Glu Ile Asp Asp Asn Arg Val Thr Ala Glu Glu Val	
275 280 285	
gat att ctg ctg cgt gaa ggg gaa aaa ctg gcc ccc gtg atg gcg aaa	912
Asp Ile Leu Leu Arg Glu Gly Glu Lys Leu Ala Pro Val Met Ala Lys	
290 295 300	
acg cgc att ttg cgg gcc tat tct ggc gtg cgc ccg ctg gtt gcc agc	960
Thr Arg Ile Leu Arg Ala Tyr Ser Gly Val Arg Pro Leu Val Ala Ser	
305 310 315 320	
gat gac gac ccg agc gga cgt aac gtc agc cgt ggc atc gtg ctg ctc	1008
Asp Asp Asp Pro Ser Gly Arg Asn Val Ser Arg Gly Ile Val Leu Leu	
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Asp His Ala Glu Arg Asp Gly Leu Asp Gly Phe Ile Thr Ile Thr Gly	
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ggc aaa ctg atg acc tat cgg ctg atg gct gaa tgg gct acc gac gcg	1104
Gly Lys Leu Met Thr Tyr Arg Leu Met Ala Glu Trp Ala Thr Asp Ala	
355 360 365	
gta tgc cgc aaa ctg ggc aac acg cgc ccc tgt acg act gcc gat ctg	1152
Val Cys Arg Lys Leu Gly Asn Thr Arg Pro Cys Thr Thr Ala Asp Leu	
370 375 380	
gca ctg cct ggt tca caa gaa ccc gct gaa gtt acc ttg cgt aaa gtc	1200
Ala Leu Pro Gly Ser Gln Glu Pro Ala Glu Val Thr Leu Arg Lys Val	
385 390 395 400	
atc tcc ctg cct gcc ccg ctg cgc ggt tct gcg gtt tat cgt cat ggc	1248
Ile Ser Leu Pro Ala Pro Leu Arg Gly Ser Ala Val Tyr Arg His Gly	
405 410 415	
gat cgc acg cct gcc tgg ctg agc gaa ggc cgt ctg cac cgt agc ctg	1296
Asp Arg Thr Pro Ala Trp Leu Ser Glu Gly Arg Leu His Arg Ser Leu	
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gta tgt gag tgc gaa gcg gta act gcg ggt gaa gtg cag tac gcg gta	1344
Val Cys Glu Cys Glu Ala Val Thr Ala Gly Glu Val Gln Tyr Ala Val	
435 440 445	
gaa aat tta aac gtt aat agc ctg ctg gat tta cgc cgt cgt acc cgt	1392
Glu Asn Leu Asn Val Asn Ser Leu Leu Asp Leu Arg Arg Arg Thr Arg	
450 455 460	

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gga ctg ctg caa cgt ttt aac gtc acg acg tcc gcg caa tct atc gag 1488
Gly Leu Leu Gln Arg Phe Asn Val Thr Thr Ser Ala Gln Ser Ile Glu
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caa ctt tcc acc ttc ctt aac gaa cgc tgg aaa ggc gtg caa ccc atc 1536
Gln Leu Ser Thr Phe Leu Asn Glu Arg Trp Lys Gly Val Gln Pro Ile
          500          505          510

gcc tgg gga gat gca ctg cgc gaa agc gaa ttt acc cgc tgg gtt tat 1584
Ala Trp Gly Asp Ala Leu Arg Glu Ser Glu Phe Thr Arg Trp Val Tyr
          515          520          525

cag gga ttg tgt ggt ctg gag aag gag cag aaa gat gcg ctt tga 1629
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Cys Gly Leu Gln Leu Gln Lys His Gly Leu Arg Cys Ala Ile Val Thr
          20          25          30

cgt ggt caa agc gca ctg cat ttc tca tcc gga tcg ctg gat ttg ctg 144
Arg Gly Gln Ser Ala Leu His Phe Ser Ser Gly Ser Leu Asp Leu Leu
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agc cat ctg cca gat ggt caa ccg gtg aca gac att cac agt gga ctg 192
Ser His Leu Pro Asp Gly Gln Pro Val Thr Asp Ile His Ser Gly Leu
          50          55          60

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Glu Ser Leu Arg Gln Gln Ala Pro Ala His Pro Tyr Ser Leu Leu Glu
          65          70          75          80

cca caa cgc gtg ctc gat ctc gct tgc cag gcg cag gca tta atc gct 288
Pro Gln Arg Val Leu Asp Leu Ala Cys Gln Ala Gln Ala Leu Ile Ala
          85          90          95

gaa agc ggt gcg caa ttg cag ggc agc gta gaa ctt gct cac cag cgg 336
Glu Ser Gly Ala Gln Leu Gln Gly Ser Val Glu Leu Ala His Gln Arg
          100          105          110

gtt acg ccg ctc ggc act ctg cgc tct acc tgg cta agt tcg cca gaa 384

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Val Thr Pro Leu Gly Thr Leu Arg Ser Thr Trp Leu Ser Ser Pro Glu	
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Val Pro Val Trp Pro Leu Pro Ala Lys Lys Ile Cys Val Val Gly Ile	
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Ser Gly Leu Met Asp Phe Gln Ala His Leu Ala Ala Ala Ser Leu Arg	
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gaa ctc ggc ctt gcc gtt gaa acc gca gaa ata gag ctg ccg gaa ctg	528
Glu Leu Gly Leu Ala Val Glu Thr Ala Glu Ile Glu Leu Pro Glu Leu	
165 170 175	
gat gtg ctg cgc aat aac gcc acc gaa ttt cgc gcg gtg aat atc gcc	576
Asp Val Leu Arg Asn Asn Ala Thr Glu Phe Arg Ala Val Asn Ile Ala	
180 185 190	
cgt ttc ctt gat aat gaa gaa aac tgg ccg ctg tta ctt gat gcg ctt	624
Arg Phe Leu Asp Asn Glu Glu Asn Trp Pro Leu Leu Leu Asp Ala Leu	
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att cct gtc gcc aat acc tgc gaa atg atc ctg atg ccc gcc tgc ttc	672
Ile Pro Val Ala Asn Thr Cys Glu Met Ile Leu Met Pro Ala Cys Phe	
210 215 220	
ggc ctg gcc gat gac aaa ctg tgg cgt tgg ttg aat gaa aaa cta cct	720
Gly Leu Ala Asp Asp Lys Leu Trp Arg Trp Leu Asn Glu Lys Leu Pro	
225 230 235 240	
tgt tca ctg atg ctt ttg cca acg ctg ccg cct tcc gtg ctg ggc att	768
Cys Ser Leu Met Leu Leu Pro Thr Leu Pro Pro Ser Val Leu Gly Ile	
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cgt ctg caa aac cag tta cag cgc cag ttt gtg cgc cag ggt ggc gtg	816
Arg Leu Gln Asn Gln Leu Gln Arg Gln Phe Val Arg Gln Gly Gly Val	
260 265 270	
tgg atg ccg ggc gat gaa gtg aaa aaa gtg acc tgt aaa aat ggc gta	864
Trp Met Pro Gly Asp Glu Val Lys Lys Val Thr Cys Lys Asn Gly Val	
275 280 285	
gtg aac gaa atc tgg acc cgc aat cac gcc gat att ccg cta cgt cca	912
Val Asn Glu Ile Trp Thr Arg Asn His Ala Asp Ile Pro Leu Arg Pro	
290 295 300	
cgt ttc gcg gtt ctc gcc agc ggc agt ttc ttt agt ggc gga ctg gta	960
Arg Phe Ala Val Leu Ala Ser Gly Ser Phe Phe Ser Gly Gly Leu Val	
305 310 315 320	
gcg gaa cgt aac ggc att cga gag ccg att ctc ggc ctt gat gtg cta	1008
Ala Glu Arg Asn Gly Ile Arg Glu Pro Ile Leu Gly Leu Asp Val Leu	
325 330 335	
caa acc gcc acg cgg ggt gaa tgg tat aag gga gat ttt ttt gcg ccg	1056
Gln Thr Ala Thr Arg Gly Glu Trp Tyr Lys Gly Asp Phe Phe Ala Pro	
340 345 350	
caa ccg tgg cag cag ttc ggt gta acc act gat gag acg cta cgc ccg	1104
Gln Pro Trp Gln Gln Phe Gly Val Thr Thr Asp Glu Thr Leu Arg Pro	

355	360	365	
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Leu Gly Gly Phe Asp Pro Ile Ala Gln Gly Cys Gly Gly Gly Val Cys			
385	390	395	400
gcc gtc agt gct tta cat gcc gct caa cag att gcc caa cgc gca gga			1248
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Thr Ala Cys Pro Val Ser Arg Val Asn Pro Gly Tyr Pro Gly Pro Lys	
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caa gcc ggg ccg gat ggc gag cgt ctg cgt ttg aaa gat ggc gca ctg	144
Gln Ala Gly Pro Asp Gly Glu Arg Leu Arg Leu Lys Asp Gly Ala Leu	
35 40 45	
tat gac gag gcg ctg aaa tat tgc atc aac tgc aaa cgt tgt gaa gtc	192
Tyr Asp Glu Ala Leu Lys Tyr Cys Ile Asn Cys Lys Arg Cys Glu Val	
50 55 60	
gcc tgc ccg tcc gat gtg aag att ggc gat att atc cag cgc gcg cgg	240
Ala Cys Pro Ser Asp Val Lys Ile Gly Asp Ile Ile Gln Arg Ala Arg	
65 70 75 80	
gcg aaa tat gac acc acg cgc ccg tcg ctg cgt aat ttt gtg ttg agt	288
Ala Lys Tyr Asp Thr Thr Arg Pro Ser Leu Arg Asn Phe Val Leu Ser	
85 90 95	
cat acc gac ctg atg ggt agc gtt tcc acg ccg ttc gca cca atc gtc	336
His Thr Asp Leu Met Gly Ser Val Ser Thr Pro Phe Ala Pro Ile Val	
100 105 110	
aac acc gct acc tcg ctg aaa ccg gtg cgg cag ctg ctt gat gcg gcg	384
Asn Thr Ala Thr Ser Leu Lys Pro Val Arg Gln Leu Leu Asp Ala Ala	
115 120 125	

tta aaa atc gat cat cgc cgc acg cta ccg aaa tac tcc ttc ggc acg	432
Leu Lys Ile Asp His Arg Arg Thr Leu Pro Lys Tyr Ser Phe Gly Thr	
130 135 140	
ttc cgt cgc tgg tat cgc agc gtg gcg gct cag caa gca caa tat aaa	480
Phe Arg Arg Trp Tyr Arg Ser Val Ala Ala Gln Gln Ala Gln Tyr Lys	
145 150 155 160	
gac cag gtc gct ttc ttt cac ggc tgc ttc gtt aac tac aac cat ccg	528
Asp Gln Val Ala Phe Phe His Gly Cys Phe Val Asn Tyr Asn His Pro	
165 170 175	
cag tta ggt aaa gat tta att aaa gtg ctc aac gca atg ggt acc ggt	576
Gln Leu Gly Lys Asp Leu Ile Lys Val Leu Asn Ala Met Gly Thr Gly	
180 185 190	
gta caa ctg ctc agc aaa gaa aaa tgc tgc ggc gta ccg cta atc gcc	624
Val Gln Leu Leu Ser Lys Glu Lys Cys Cys Gly Val Pro Leu Ile Ala	
195 200 205	
aac ggc ttt acc gat aaa gca cgc aaa cag gca att acg aat gta gag	672
Asn Gly Phe Thr Asp Lys Ala Arg Lys Gln Ala Ile Thr Asn Val Glu	
210 215 220	
tcg atc cgc gaa gct gtg gga gta aaa ggc att ccg gtg att gcc acc	720
Ser Ile Arg Glu Ala Val Gly Val Lys Gly Ile Pro Val Ile Ala Thr	
225 230 235 240	
tcc tca acc tgt aca ttt gcc ctg cgc gac gaa tac ccg gaa gtg ctg	768
Ser Ser Thr Cys Thr Phe Ala Leu Arg Asp Glu Tyr Pro Glu Val Leu	
245 250 255	
aat gtc gac aac aaa ggc ttg cgc gat cat atc gaa ctg gca acc cgc	816
Asn Val Asp Asn Lys Gly Leu Arg Asp His Ile Glu Leu Ala Thr Arg	
260 265 270	
tgg ctg tgg cgc aag ctg gac gaa ggc aaa acg tta ccg ctg aaa ccg	864
Trp Leu Trp Arg Lys Leu Asp Glu Gly Lys Thr Leu Pro Leu Lys Pro	
275 280 285	
ctg ccg ctg aaa gtg gtt tat cac act ccg tgc cat atg gaa aaa atg	912
Leu Pro Leu Lys Val Val Tyr His Thr Pro Cys His Met Glu Lys Met	
290 295 300	
ggc tgg acg ctc tac acc ctg gag ctg ttg cgt aac atc ccg ggg ctt	960
Gly Trp Thr Leu Tyr Thr Leu Glu Leu Leu Arg Asn Ile Pro Gly Leu	
305 310 315 320	
gag tta acg gtg ctg gat tcc cag tgc tgc ggt att gcg ggt act tac	1008
Glu Leu Thr Val Leu Asp Ser Gln Cys Cys Gly Ile Ala Gly Thr Tyr	
325 330 335	
ggt ttc aaa aaa gag aac tac ccc acc tca caa gcc atc ggc gca cca	1056
Gly Phe Lys Lys Glu Asn Tyr Pro Thr Ser Gln Ala Ile Gly Ala Pro	
340 345 350	
ctg ttc cgc cag ata gaa gaa agc ggc gca gat ctg gtg gtc acc gac	1104
Leu Phe Arg Gln Ile Glu Glu Ser Gly Ala Asp Leu Val Val Thr Asp	
355 360 365	
tgc gaa acc tgt aaa tgg cag att gag atg tcc aca agt ctt cgc tgc	1152

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Cys Glu Thr Cys Lys Trp Gln Ile Glu Met Ser Thr Ser Leu Arg Cys
 370                               375                               380

gaa cat ccg att acg cta ctg gcc cag gcg ctg gct taa      1191
Glu His Pro Ile Thr Leu Leu Ala Gln Ala Leu Ala *
385                               390                               395

<210> 224
<211> 909
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(909)

<400> 224
atg caa tta cgt aaa cct gcc aca gca atc ctc gcc ctg gcg ctt tcc      48
Met Gln Leu Arg Lys Pro Ala Thr Ala Ile Leu Ala Leu Ala Leu Ser
 1                               5                               10                               15

gca gga ctg gca cag gca gat gac gcc gcc ccg gca gcg ggc agt act      96
Ala Gly Leu Ala Gln Ala Asp Asp Ala Ala Pro Ala Ala Gly Ser Thr
                20                               25                               30

ctg gac aaa atc gcc aaa aac ggt gtg att gtc gtc ggt cac cgt gaa      144
Leu Asp Lys Ile Ala Lys Asn Gly Val Ile Val Val Gly His Arg Glu
                35                               40                               45

tct tca gtg cct ttc tct tat tac gac aat cag caa aaa gtg gtg ggt      192
Ser Ser Val Pro Phe Ser Tyr Tyr Asp Asn Gln Gln Lys Val Val Gly
                50                               55                               60

tac tcg cag gat tac tcc aac gcc att gtt gaa gca gtg aaa aag aaa      240
Tyr Ser Gln Asp Tyr Ser Asn Ala Ile Val Glu Ala Val Lys Lys Lys
        65                               70                               75                               80

ctc aac aaa ccg gac ttg cag gta aaa ctg att ccg att acc tca caa      288
Leu Asn Lys Pro Asp Leu Gln Val Lys Leu Ile Pro Ile Thr Ser Gln
                85                               90                               95

aac cgt att cca ctg ctg caa aac ggc act ttc gat ttt gaa tgt ggt      336
Asn Arg Ile Pro Leu Leu Gln Asn Gly Thr Phe Asp Phe Glu Cys Gly
                100                               105                               110

tct acc acc aac aac gtc gaa cgc caa aaa cag gcg gct ttc tct gac      384
Ser Thr Thr Asn Asn Val Glu Arg Gln Lys Gln Ala Ala Phe Ser Asp
                115                               120                               125

act att ttc gtg gtc ggt acg cgc ctg ttg acc aaa aag ggt ggc gat      432
Thr Ile Phe Val Val Gly Thr Arg Leu Leu Thr Lys Lys Gly Gly Asp
                130                               135                               140

atc aaa gat ttt gcc aac ctg aaa gac aaa gcc gta gtc gtc act tcc      480
Ile Lys Asp Phe Ala Asn Leu Lys Asp Lys Ala Val Val Val Thr Ser
        145                               150                               155                               160

ggc act acc tct gaa gtt ttg ctc aac aaa ctg aat gaa gag caa aaa      528
Gly Thr Thr Ser Glu Val Leu Leu Asn Lys Leu Asn Glu Glu Gln Lys
                165                               170                               175

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atg aat atg cgc atc atc agc gcc aaa gat cac ggt gac tct ttc cgc 576
 Met Asn Met Arg Ile Ile Ser Ala Lys Asp His Gly Asp Ser Phe Arg
 180 185 190

acc ctg gaa agc ggt cgt gcc gtt gcc ttt atg atg gat gac gct ctg 624
 Thr Leu Glu Ser Gly Arg Ala Val Ala Phe Met Met Asp Asp Ala Leu
 195 200 205

ctg gcc ggt gaa cgt gcg aaa gcg aag aaa cca gac aac tgg gaa atc 672
 Leu Ala Gly Glu Arg Ala Lys Ala Lys Lys Pro Asp Asn Trp Glu Ile
 210 215 220

gtc ggc aag ccg cag tct cag gag gcc tac ggt tgt atg ttg cgt aaa 720
 Val Gly Lys Pro Gln Ser Gln Glu Ala Tyr Gly Cys Met Leu Arg Lys
 225 230 235 240

gat gat ccg cag ttc aaa aag ctg atg gat gac acc atc gct cag gtg 768
 Asp Asp Pro Gln Phe Lys Lys Leu Met Asp Asp Thr Ile Ala Gln Val
 245 250 255

cag acc tcc ggt gaa gcg gaa aaa tgg ttt gat aag tgg ttc aaa aat 816
 Gln Thr Ser Gly Glu Ala Glu Lys Trp Phe Asp Lys Trp Phe Lys Asn
 260 265 270

cca att ccg ccg aaa aac ctg aac atg aat ttc gaa ctg tca gac gaa 864
 Pro Ile Pro Pro Lys Asn Leu Asn Met Asn Phe Glu Leu Ser Asp Glu
 275 280 285

atg aaa gca ctg ttc aaa gaa ccg aat gac aag gca ctg aac taa 909
 Met Lys Ala Leu Phe Lys Glu Pro Asn Asp Lys Ala Leu Asn *
 290 295 300

<210> 225

<211> 987

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (987)

<400> 225

atg aat aac agc gct ttt act ttc cag aca cta cac ccg gat acc atc 48
 Met Asn Asn Ser Ala Phe Thr Phe Gln Thr Leu His Pro Asp Thr Ile
 1 5 10 15

atg gac gct ctg ttt gag cat ggg atc cgg gtg gat tcc ggt ctt acc 96
 Met Asp Ala Leu Phe Glu His Gly Ile Arg Val Asp Ser Gly Leu Thr
 20 25 30

ccg ctt aac agc tat gaa aac cgt gtc tat caa ttt cag gac gaa gat 144
 Pro Leu Asn Ser Tyr Glu Asn Arg Val Tyr Gln Phe Gln Asp Glu Asp
 35 40 45

cgt cga cgt ttt gtc gtc aaa ttt tat cgc cct gaa cgt tgg aca gcc 192
 Arg Arg Arg Phe Val Val Lys Phe Tyr Arg Pro Glu Arg Trp Thr Ala
 50 55 60

gat caa atc ctc gaa gaa cat caa ttt gcg ttg cag ctg gta aat gat	240
Asp Gln Ile Leu Glu Glu His Gln Phe Ala Leu Gln Leu Val Asn Asp	
65 70 75 80	
gaa gtt ccg gtc gca gca cct gtg gcc ttt aac ggt cag act tta ttg	288
Glu Val Pro Val Ala Ala Pro Val Ala Phe Asn Gly Gln Thr Leu Leu	
85 90 95	
aat cat cag gga ttt tat ttc gct gtt ttt cca agc gtc ggt ggt cgc	336
Asn His Gln Gly Phe Tyr Phe Ala Val Phe Pro Ser Val Gly Gly Arg	
100 105 110	
cag ttc gaa gct gat aat atc gat cag atg gaa gcg gtt ggg cgt tat	384
Gln Phe Glu Ala Asp Asn Ile Asp Gln Met Glu Ala Val Gly Arg Tyr	
115 120 125	
tta ggg cgt atg cac cag acg ggg cgc aaa cag ctt ttt atc cat cgc	432
Leu Gly Arg Met His Gln Thr Gly Arg Lys Gln Leu Phe Ile His Arg	
130 135 140	
ccg acc atc ggt ttg aac gaa tat ctc att gag cca cgc aag ctg ttt	480
Pro Thr Ile Gly Leu Asn Glu Tyr Leu Ile Glu Pro Arg Lys Leu Phe	
145 150 155 160	
gag gac gct aca ctg ata cct tcc ggg ttg aaa gcg gca ttc ctg aaa	528
Glu Asp Ala Thr Leu Ile Pro Ser Gly Leu Lys Ala Ala Phe Leu Lys	
165 170 175	
gcg aca gat gag ctg att gcc gcc gtt aca gca cac tgg cgg gaa gat	576
Ala Thr Asp Glu Leu Ile Ala Ala Val Thr Ala His Trp Arg Glu Asp	
180 185 190	
ttc acc gtt ctg cgg cta cat gga gac tgc cac gcc ggg aat att ctc	624
Phe Thr Val Leu Arg Leu His Gly Asp Cys His Ala Gly Asn Ile Leu	
195 200 205	
tgg cgc gat ggt cca atg ttt gtt gat ctg gat gat gca cgt aat ggt	672
Trp Arg Asp Gly Pro Met Phe Val Asp Leu Asp Asp Ala Arg Asn Gly	
210 215 220	
cca gcc gtt cag gat ttg tgg atg ttg ctc aat ggc gat aaa gcc gag	720
Pro Ala Val Gln Asp Leu Trp Met Leu Leu Asn Gly Asp Lys Ala Glu	
225 230 235 240	
cag cgg atg caa ctg gaa act att att gaa gct tat gaa gaa ttt agc	768
Gln Arg Met Gln Leu Glu Thr Ile Ile Glu Ala Tyr Glu Glu Phe Ser	
245 250 255	
gag ttc gac acc gct gaa atc gga ctg att gaa cct tta cgc gcc atg	816
Glu Phe Asp Thr Ala Glu Ile Gly Leu Ile Glu Pro Leu Arg Ala Met	
260 265 270	
cgt ttg gtt tat tat ctt gcc tgg cta atg cgg cgt tgg gct gat ccc	864
Arg Leu Val Tyr Tyr Leu Ala Trp Leu Met Arg Arg Trp Ala Asp Pro	
275 280 285	
gcg ttc ccg aaa aat ttc ccg tgg tta acc ggg gaa gat tac tgg ctg	912
Ala Phe Pro Lys Asn Phe Pro Trp Leu Thr Gly Glu Asp Tyr Trp Leu	
290 295 300	
cga cag acg gcg act ttt ata gaa cag gca aaa gtt cta caa gaa ccc	960

Arg Gln Thr Ala Thr Phe Ile Glu Gln Ala Lys Val Leu Gln Glu Pro
 305 310 315 320

cct ttg caa tta aca cct atg tat taa 987
 Pro Leu Gln Leu Thr Pro Met Tyr *
 325

<210> 226

<211> 627

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(627)

<400> 226

atg aaa aag att tgg ctg gcg ctg gct ggt tta gtt tta gcg ttt agc 48
 Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
 1 5 10 15

gca tcg gcg gcg cag tat gaa gat ggt aaa cag tac act acc ctg gaa 96
 Ala Ser Ala Ala Gln Tyr Glu Asp Gly Lys Gln Tyr Thr Thr Leu Glu
 20 25 30

aaa ccg gta gct ggc gcg ccg caa gtg ctg gag ttt ttc tct ttc ttc 144
 Lys Pro Val Ala Gly Ala Pro Gln Val Leu Glu Phe Phe Ser Phe Phe
 35 40 45

tgc ccg cac tgc tat cag ttt gaa gaa gtt ctg cat att tct gat aat 192
 Cys Pro His Cys Tyr Gln Phe Glu Glu Val Leu His Ile Ser Asp Asn
 50 55 60

gtg aag aaa aaa ctg ccg gaa ggc gtg aag atg act aaa tac cac gtc 240
 Val Lys Lys Lys Leu Pro Glu Gly Val Lys Met Thr Lys Tyr His Val
 65 70 75 80

aac ttc atg ggt ggt gac ctg ggc aaa gat ctg act cag gca tgg gct 288
 Asn Phe Met Gly Gly Asp Leu Gly Lys Asp Leu Thr Gln Ala Trp Ala
 85 90 95

gtg gcg atg gcg ctg ggc gtg gaa gac aaa gtg act gtt ccg ctg ttt 336
 Val Ala Met Ala Leu Gly Val Glu Asp Lys Val Thr Val Pro Leu Phe
 100 105 110

gaa ggc gta cag aaa acc cag acc att cgt tct gct tct gat atc cgc 384
 Glu Gly Val Gln Lys Thr Gln Thr Ile Arg Ser Ala Ser Asp Ile Arg
 115 120 125

gat gta ttt atc aac gca ggt att aaa ggt gaa gag tac gac gcg gcg 432
 Asp Val Phe Ile Asn Ala Gly Ile Lys Gly Glu Glu Tyr Asp Ala Ala
 130 135 140

tgg aac agc ttc gtg gtg aaa tct ctg gtc gct cag cag gaa aaa gct 480
 Trp Asn Ser Phe Val Val Lys Ser Leu Val Ala Gln Gln Glu Lys Ala
 145 150 155 160

gca gct gac gtg caa ttg cgt ggc gtt ccg gcg atg ttt gtt aac ggt 528
 Ala Ala Asp Val Gln Leu Arg Gly Val Pro Ala Met Phe Val Asn Gly
 165 170 175

aaa tat cag ctg aat ccg cag ggt atg gat acc agc aat atg gat gtt 576
 Lys Tyr Gln Leu Asn Pro Gln Gly Met Asp Thr Ser Asn Met Asp Val
 180 185 190

ttt gtt cag cag tat gct gat aca gtg aaa tat ctg tcc gag aaa aaa 624
 Phe Val Gln Gln Tyr Ala Asp Thr Val Lys Tyr Leu Ser Glu Lys Lys
 195 200 205

taa 627
 *

<210> 227
 <211> 339
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(339)

<400> 227
 atg acg atg aat tca ttc gag cga agg aat aag atc atc caa tta gtg 48
 Met Thr Met Asn Ser Phe Glu Arg Arg Asn Lys Ile Ile Gln Leu Val
 1 5 10 15

aat gaa cag gga acc gtg ctt gtt cag gat ctg gcg gga gta ttt gct 96
 Asn Glu Gln Gly Thr Val Leu Val Gln Asp Leu Ala Gly Val Phe Ala
 20 25 30

gcc tcg gaa gcg aca atc cgt gcc gat ttg cgc ttt ctc gaa caa aaa 144
 Ala Ser Glu Ala Thr Ile Arg Ala Asp Leu Arg Phe Leu Glu Gln Lys
 35 40 45

ggc gtg gtt acg cgc ttt cat ggc ggt gcg gcg aaa ata atg tct ggt 192
 Gly Val Val Thr Arg Phe His Gly Gly Ala Ala Lys Ile Met Ser Gly
 50 55 60

aat agt gaa acc gag acc cag gaa gtc ggg ttt aaa gag cga ttt cag 240
 Asn Ser Glu Thr Glu Thr Gln Glu Val Gly Phe Lys Glu Arg Phe Gln
 65 70 75 80

ctc gcc agc gcg cca aaa aac aga ata gcg cag gcg gca gtc aaa atg 288
 Leu Ala Ser Ala Pro Lys Asn Arg Ile Ala Gln Ala Ala Val Lys Met
 85 90 95

atc cac gaa ggg atg act gat cct acc cac gta ata tgg aca cag gcc 336
 Ile His Glu Gly Met Thr Asp Pro Thr His Val Ile Trp Thr Gln Ala
 100 105 110

taa 339
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<210> 228
 <211> 1041
 <212> DNA
 <213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (1041)

<400> 228

atg	aaa	tca	gtg	gtg	aat	gat	act	gat	ggg	atc	gtg	cgc	gtt	gca	gaa	48
Met	Lys	Ser	Val	Val	Asn	Asp	Thr	Asp	Gly	Ile	Val	Arg	Val	Ala	Glu	
1				5					10					15		
agc	gtc	att	cct	gaa	att	aaa	cat	cag	gat	gag	gtg	cgg	gta	aaa	att	96
Ser	Val	Ile	Pro	Glu	Ile	Lys	His	Gln	Asp	Glu	Val	Arg	Val	Lys	Ile	
			20					25					30			
gcc	agc	tgc	ggc	tta	tgt	ggg	tcc	gat	tta	ccc	agg	ata	ttt	aaa	aat	144
Ala	Ser	Ser	Gly	Leu	Cys	Gly	Ser	Asp	Leu	Pro	Arg	Ile	Phe	Lys	Asn	
			35				40					45				
ggg	gca	cat	tat	tat	cca	ata	acg	tta	ggc	cat	gaa	ttt	agc	ggc	tat	192
Gly	Ala	His	Tyr	Tyr	Pro	Ile	Thr	Leu	Gly	His	Glu	Phe	Ser	Gly	Tyr	
	50					55					60					
att	gat	gcg	gtg	gga	tcc	ggg	gtt	gat	gat	tta	cac	cct	ggc	gat	gcg	240
Ile	Asp	Ala	Val	Gly	Ser	Gly	Val	Asp	Asp	Leu	His	Pro	Gly	Asp	Ala	
65					70					75				80		
gtt	gcc	tgt	gtg	cgg	tta	tta	ccc	tgt	ttt	act	tgt	cca	gag	tgt	ctg	288
Val	Ala	Cys	Val	Pro	Leu	Leu	Pro	Cys	Phe	Thr	Cys	Pro	Glu	Cys	Leu	
				85				90						95		
aaa	ggg	ttt	tat	tcc	cag	tgc	gca	aaa	tat	gat	ttt	att	ggc	tgc	cgg	336
Lys	Gly	Phe	Tyr	Ser	Gln	Cys	Ala	Lys	Tyr	Asp	Phe	Ile	Gly	Ser	Arg	
			100					105					110			
cgt	gat	ggg	gga	ttt	gct	gaa	tat	att	gtc	gtt	aag	cga	aaa	aat	gtc	384
Arg	Asp	Gly	Gly	Phe	Ala	Glu	Tyr	Ile	Val	Val	Lys	Arg	Lys	Asn	Val	
		115					120					125				
ttt	gct	cta	ccc	acg	gat	atg	cct	att	gag	gat	ggg	gct	ttt	att	gag	432
Phe	Ala	Leu	Pro	Thr	Asp	Met	Pro	Ile	Glu	Asp	Gly	Ala	Phe	Ile	Glu	
	130					135					140					
cgg	att	acc	gtt	ggg	ctg	cat	gct	ttt	cat	tta	gcg	caa	ggg	tgt	gag	480
Pro	Ile	Thr	Val	Gly	Leu	His	Ala	Phe	His	Leu	Ala	Gln	Gly	Cys	Glu	
145					150				155					160		
aat	aaa	aac	gtt	att	att	att	ggg	gcc	gga	acc	att	ggc	ctg	ctg	gcc	528
Asn	Lys	Asn	Val	Ile	Ile	Ile	Gly	Ala	Gly	Thr	Ile	Gly	Leu	Leu	Ala	
				165				170					175			
att	cag	tgc	gct	gtc	gcg	ctg	gga	gca	aag	agt	gtg	acg	gcg	atc	gac	576
Ile	Gln	Cys	Ala	Val	Ala	Leu	Gly	Ala	Lys	Ser	Val	Thr	Ala	Ile	Asp	
			180					185					190			
att	agt	tca	gaa	aaa	ctg	gca	ctg	gca	aaa	tct	ttc	ggg	gcg	atg	caa	624
Ile	Ser	Ser	Glu	Lys	Leu	Ala	Leu	Ala	Lys	Ser	Phe	Gly	Ala	Met	Gln	
			195				200					205				
aca	ttt	aac	agt	agc	gaa	atg	agc	gcg	ccg	caa	atg	cag	agc	gtt	tta	672
Thr	Phe	Asn	Ser	Ser	Glu	Met	Ser	Ala	Pro	Gln	Met	Gln	Ser	Val	Leu	
	210					215				220						

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cgc gaa ctg cgc ttt aat cag ctt atc ctc gag acg gct ggc gta ccg 720
Arg Glu Leu Arg Phe Asn Gln Leu Ile Leu Glu Thr Ala Gly Val Pro
225 230 235 240
/

caa act gtc gaa ctg gcg gta gag att gcc ggt cct cat gcc caa ctg 768
Gln Thr Val Glu Leu Ala Val Glu Ile Ala Gly Pro His Ala Gln Leu
245 250 255

gcg ctg gtg ggc acg ttg cat cag gat ctg cat tta aca tcg gca acg 816
Ala Leu Val Gly Thr Leu His Gln Asp Leu His Leu Thr Ser Ala Thr
260 265 270

ttt ggc aaa ata ttg cgt aaa gag ctg acg gtt atc ggc agt tgg atg 864
Phe Gly Lys Ile Leu Arg Lys Glu Leu Thr Val Ile Gly Ser Trp Met
275 280 285

aac tac tcc agc cct tgg ccg ggg cag gag tgg gaa acg gcg agc cgg 912
Asn Tyr Ser Ser Pro Trp Pro Gly Gln Glu Trp Glu Thr Ala Ser Arg
290 295 300

ttg ctg aca gaa cgt aag tta agc ctg gag cca tta atc gct cac cgt 960
Leu Leu Thr Glu Arg Lys Leu Ser Leu Glu Pro Leu Ile Ala His Arg
305 310 315 320

gga agc ttt gaa agc ttc gcc cag gcg gtg cgt gac atc gct cgt aat 1008
Gly Ser Phe Glu Ser Phe Ala Gln Ala Val Arg Asp Ile Ala Arg Asn
325 330 335

gct atg ccg ggc aaa gtg ttg ctc att ccc tga 1041
Ala Met Pro Gly Lys Val Leu Leu Ile Pro *
340 345

<210> 229
<211> 1356
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1356)

<400> 229
atg ttt tca gaa gtc atg cgt tat att ctc gac ctc ggc cct acg gtg 48
Met Phe Ser Glu Val Met Arg Tyr Ile Leu Asp Leu Gly Pro Thr Val
1 5 10 15

atg ctg ccg att gtc atc att att ttt tct aaa ata tta ggc atg aag 96
Met Leu Pro Ile Val Ile Ile Ile Phe Ser Lys Ile Leu Gly Met Lys
20 25 30

gca ggc gat tgc ttt aaa gcg ggt ctg cat atc ggg att ggc ttt gtt 144
Ala Gly Asp Cys Phe Lys Ala Gly Leu His Ile Gly Ile Gly Phe Val
35 40 45

ggc att ggc ctt gtg att ggc tta atg ctg gat tcc att ggc ccg gcg 192
Gly Ile Gly Leu Val Ile Gly Leu Met Leu Asp Ser Ile Gly Pro Ala
50 55 60

gcg aaa gcg atg gcg gaa aat ttc gac ctg aat ctg cat gtg gtc gat 240

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Ala Lys Ala Met Ala Glu Asn Phe Asp Leu Asn Leu His Val Val Asp	
65 70 75 80	
gtt ggc tgg ccg ggc tct tca cca atg acc tgg gcg tcg caa att gcg	288
Val Gly Trp Pro Gly Ser Ser Pro Met Thr Trp Ala Ser Gln Ile Ala	
85 90 95	
ctg gtg gcg att ccg att gcg att ctg gtt aac gtg gcg atg tta ctg	336
Leu Val Ala Ile Pro Ile Ala Ile Leu Val Asn Val Ala Met Leu Leu	
100 105 110	
acc cgt atg acg ccg gtg gta aat gtt gat atc tgg aat atc tgg cat	384
Thr Arg Met Thr Arg Val Val Asn Val Asp Ile Trp Asn Ile Trp His	
115 120 125	
atg acc ttc acc ggc gcg ttg ctg cat ctg gca acc ggt tca tgg atg	432
Met Thr Phe Thr Gly Ala Leu Leu His Leu Ala Thr Gly Ser Trp Met	
130 135 140	
ata ggg atg gca ggt gtg gta att cac gcg gcg ttt gtt tat aag ctc	480
Ile Gly Met Ala Gly Val Val Ile His Ala Ala Phe Val Tyr Lys Leu	
145 150 155 160	
ggc gac tgg ttt gcc cgc gat acc cga aat ttc ttt gag ctg gaa ggt	528
Gly Asp Trp Phe Ala Arg Asp Thr Arg Asn Phe Phe Glu Leu Glu Gly	
165 170 175	
att gct att ccg cac ggt acg tcg gcg tat atg ggg ccg att gcg gtg	576
Ile Ala Ile Pro His Gly Thr Ser Ala Tyr Met Gly Pro Ile Ala Val	
180 185 190	
ctg gtc gat gct atc atc gag aaa atc cca ggc gtt aac cga att aaa	624
Leu Val Asp Ala Ile Ile Glu Lys Ile Pro Gly Val Asn Arg Ile Lys	
195 200 205	
ttt agc gcc gac gat att cag cgc aaa ttt ggt cca ttt ggc gag cct	672
Phe Ser Ala Asp Asp Ile Gln Arg Lys Phe Gly Pro Phe Gly Glu Pro	
210 215 220	
gtc acc gtg ggt ttt gtg atg ggg ctg att atc ggc atc ctc gcg ggt	720
Val Thr Val Gly Phe Val Met Gly Leu Ile Ile Gly Ile Leu Ala Gly	
225 230 235 240	
tac gat gtc aaa ggt gta ttg cag ctg gcg gta aaa acg gcg gca gtg	768
Tyr Asp Val Lys Gly Val Leu Gln Leu Ala Val Lys Thr Ala Ala Val	
245 250 255	
atg ctg cta atg cca cgg gtg att aaa ccc atc atg gat ggt tta acg	816
Met Leu Leu Met Pro Arg Val Ile Lys Pro Ile Met Asp Gly Leu Thr	
260 265 270	
ccc atc gct aag cag gct cgt agt cgt tta cag gcg aag ttc ggc ggt	864
Pro Ile Ala Lys Gln Ala Arg Ser Arg Leu Gln Ala Lys Phe Gly Gly	
275 280 285	
cag gag ttc ctg att ggc ctt gat ccg gcg ttg ctg ctg gga cat acg	912
Gln Glu Phe Leu Ile Gly Leu Asp Pro Ala Leu Leu Leu Gly His Thr	
290 295 300	
gcg gtg gta tcg gca agc ctg att ttt atc cca ctc acc att tta att	960
Ala Val Val Ser Ala Ser Leu Ile Phe Ile Pro Leu Thr Ile Leu Ile	

305	310	315	320	
gct gtt tgt gtg cgc ggt aat cag gtg ctg ccg ttt ggc gat ctt gcc	1008			
Ala Val Cys Val Pro Gly Asn Gln Val Leu Pro Phe Gly Asp Leu Ala				
325 330 335				
acc atc ggc ttc ttc gtg gcg atg gcg gtc gcc gtg cat cgt gga aat	1056			
Thr Ile Gly Phe Phe Val Ala Met Ala Val Ala Val His Arg Gly Asn				
340 345 350				
ctg ttc cgc acc tta atc tcg ggt gtc atc att atg agc atc acc ctg	1104			
Leu Phe Arg Thr Leu Ile Ser Gly Val Ile Ile Met Ser Ile Thr Leu				
355 360 365				
tgg atc gcg acg caa act att ggt ttg cac acc caa ctg gcg gct aat	1152			
Trp Ile Ala Thr Gln Thr Ile Gly Leu His Thr Gln Leu Ala Ala Asn				
370 375 380				
gct ggg gcg tta aaa gcc ggg ggt atg gtg gct tca atg gat cag ggc	1200			
Ala Gly Ala Leu Lys Ala Gly Gly Met Val Ala Ser Met Asp Gln Gly				
385 390 395 400				
ggg tct ccc att acc tgg tta ctg att cag gtt ttc tcc ccg caa aat	1248			
Gly Ser Pro Ile Thr Trp Leu Leu Ile Gln Val Phe Ser Pro Gln Asn				
405 410 415				
att ccc ggt ttc att att atc ggt gca att tat ctg acc ggt att ttc	1296			
Ile Pro Gly Phe Ile Ile Ile Gly Ala Ile Tyr Leu Thr Gly Ile Phe				
420 425 430				
atg acc tgg cgt aga gcg cgt ggc ttt att aaa caa gag aaa gtc gtt	1344			
Met Thr Trp Arg Arg Ala Arg Gly Phe Ile Lys Gln Glu Lys Val Val				
435 440 445				
ctc gca gaa taa	1356			
Leu Ala Glu *				
450				

<210> 230

<211> 285

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (285)

<400> 230

atg aaa cgc aag att att gtc gct tgc gga ggc gcg gtt gcg acc tct	48
Met Lys Arg Lys Ile Ile Val Ala Cys Gly Gly Ala Val Ala Thr Ser	
1 5 10 15	

acg atg gcg gcg gaa gaa att aaa gag ttg tgt cag aat cat aat att	96
Thr Met Ala Ala Glu Glu Ile Lys Glu Leu Cys Gln Asn His Asn Ile	
20 25 30	

cct gtt gaa tta atc cag tgt cgg gtt aat gaa ata gaa acc tat atg	144
Pro Val Glu Leu Ile Gln Cys Arg Val Asn Glu Ile Glu Thr Tyr Met	
35 40 45	

```

gat ggt gtg cat ttg ata tgc acc act gcc aaa gtg gat cgt agt ttt 192
Asp Gly Val His Leu Ile Cys Thr Thr Ala Lys Val Asp Arg Ser Phe
    50                55                60

ggc gat att ccg tta gtt cac ggc atg cct ttt att tct ggt atc ggt 240
Gly Asp Ile Pro Leu Val His Gly Met Pro Phe Ile Ser Gly Ile Gly
    65                70                75                80

atc gaa gca tta caa aat aaa att ctg act atc tta cag ggg tga 285
Ile Glu Ala Leu Gln Asn Lys Ile Leu Thr Ile Leu Gln Gly *
                85                90

<210> 231
<211> 453
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(453)

<400> 231
atg act aac ctg ttt gtt cgt agc gga att tct ttt gtc gat cgt agc 48
Met Thr Asn Leu Phe Val Arg Ser Gly Ile Ser Phe Val Asp Arg Ser
    1                5                10                15

gaa gtt tta acc cat atc ggt aat gag atg ctc gcc aaa ggt gtg gtt 96
Glu Val Leu Thr His Ile Gly Asn Glu Met Leu Ala Lys Gly Val Val
                20                25                30

cat gat acc tgg cca cag gca tta att gcc aga gaa gca gaa ttc cct 144
His Asp Thr Trp Pro Gln Ala Leu Ile Ala Arg Glu Ala Glu Phe Pro
                35                40                45

acc ggg ata atg ctt gag cag cac gct att gca ata ccg cat tgt gag 192
Thr Gly Ile Met Leu Glu Gln His Ala Ile Ala Ile Pro His Cys Glu
    50                55                60

gcg att cat gct aag tcg tca gcc att tat ctg tta agg cca aca aat 240
Ala Ile His Ala Lys Ser Ser Ala Ile Tyr Leu Leu Arg Pro Thr Asn
    65                70                75                80

aaa gtt cat ttt cag caa gcg gat gat gat aac gac gtg gcg gta tcg 288
Lys Val His Phe Gln Gln Ala Asp Asp Asp Asn Asp Val Ala Val Ser
                85                90                95

ttg gtt att gcg ttg att gtg gaa aat ccg cag cag caa ttg aaa ctt 336
Leu Val Ile Ala Leu Ile Val Glu Asn Pro Gln Gln Gln Leu Lys Leu
                100                105                110

tta cgc tgt tta ttt ggc aag tta caa cag ccc gat atc gtc gag aca 384
Leu Arg Cys Leu Phe Gly Lys Leu Gln Gln Pro Asp Ile Val Glu Thr
                115                120                125

cta atc act ctt cct gaa acc cag tta aag gaa tac ttc aca aag tat 432
Leu Ile Thr Leu Pro Glu Thr Gln Leu Lys Glu Tyr Phe Thr Lys Tyr
                130                135                140

gtt tta gat tca gac gaa taa 453

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Val Leu Asp Ser Asp Glu *
145 150

<210> 232

<211> 1263

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1263)

<400> 232

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atg aaa acg tta att gcc cgg cat aaa gct ggt gaa cat atc ggc ata 48
Met Lys Thr Leu Ile Ala Arg His Lys Ala Gly Glu His Ile Gly Ile
  1           5           10           15

tgt tca gtc tgt tct gcc cat ccg ttg gtt atc gaa gcg gcg ctg gca 96
Cys Ser Val Cys Ser Ala His Pro Leu Val Ile Glu Ala Ala Leu Ala
      20           25           30

ttt gat cgc aac agc acg cgc aaa gtg ctg att gaa gca acg tca aac 144
Phe Asp Arg Asn Ser Thr Arg Lys Val Leu Ile Glu Ala Thr Ser Asn
      35           40           45

cag gtc aat caa ttt ggc ggt tat acc gga atg aca ccg gca gac ttt 192
Gln Val Asn Gln Phe Gly Gly Tyr Thr Gly Met Thr Pro Ala Asp Phe
      50           55           60

cgc gaa ttt gtt ttt acg att gcc gat aaa gtt ggg ttt gca cgc gaa 240
Arg Glu Phe Val Phe Thr Ile Ala Asp Lys Val Gly Phe Ala Arg Glu
      65           70           75           80

cgc att att ctc ggc ggc gat cat ctg ggg cca aac tgc tgg cag caa 288
Arg Ile Ile Leu Gly Gly Asp His Leu Gly Pro Asn Cys Trp Gln Gln
      85           90           95

gaa aat gcg gat gcg gcg atg gaa aaa tcc gtc gag ctg gta aag gaa 336
Glu Asn Ala Asp Ala Ala Met Glu Lys Ser Val Glu Leu Val Lys Glu
      100           105           110

tat gtt cgt gcc ggc ttc agt aaa att cat ctt gat gcg tca atg tcc 384
Tyr Val Arg Ala Gly Phe Ser Lys Ile His Leu Asp Ala Ser Met Ser
      115           120           125

tgc gcg ggg gat ccc ata ccg tta gca cca gaa acg gtt gcg gaa cga 432
Cys Ala Gly Asp Pro Ile Pro Leu Ala Pro Glu Thr Val Ala Glu Arg
      130           135           140

gct gct gtg ctt tgc ttt gct gcg gaa agt gtg gcg aca gat tgc cag 480
Ala Ala Val Leu Cys Phe Ala Ala Glu Ser Val Ala Thr Asp Cys Gln
      145           150           155           160

cgt gag caa ctg agc tat gtc att ggc acc gaa gtt ccg gtt ccg ggc 528
Arg Glu Gln Leu Ser Tyr Val Ile Gly Thr Glu Val Pro Val Pro Gly
      165           170           175

ggt gag gcc agc gcc att cag tca gta cac atc acc cat gtt gaa gat 576
Gly Glu Ala Ser Ala Ile Gln Ser Val His Ile Thr His Val Glu Asp
      180           185           190

```

gcc gcc aat act tta cgt acg cat caa aag gcc ttt att gcc cgt ggg	624
Ala Ala Asn Thr Leu Arg Thr His Gln Lys Ala Phe Ile Ala Arg Gly	
195 200 205	
ctg aca gag gcg tta aca cgt gtg att gcc atc gtg gtg cag ccg ggt	672
Leu Thr Glu Ala Leu Thr Arg Val Ile Ala Ile Val Val Gln Pro Gly	
210 215 220	
gtg gaa ttt gat cac agc aat att atc cat tat cag ccg cag gaa gcg	720
Val Glu Phe Asp His Ser Asn Ile Ile His Tyr Gln Pro Gln Glu Ala	
225 230 235 240	
cag ccg ctg gcg caa tgg ata gaa aac acc cga atg gtt tat gaa gca	768
Gln Pro Leu Ala Gln Trp Ile Glu Asn Thr Arg Met Val Tyr Glu Ala	
245 250 255	
cat tct acc gat tac cag acc cgg acg gct tat tgg gaa tta gtc cgc	816
His Ser Thr Asp Tyr Gln Thr Arg Thr Ala Tyr Trp Glu Leu Val Arg	
260 265 270	
gat cac ttt gca ata ttg aaa gtc ggt ccc gca tta acc ttt gct tta	864
Asp His Phe Ala Ile Leu Lys Val Gly Pro Ala Leu Thr Phe Ala Leu	
275 280 285	
cgc gag gcg ata ttt gca ctg gca caa att gag cag gaa ctt atc gcc	912
Arg Glu Ala Ile Phe Ala Leu Ala Gln Ile Glu Gln Glu Leu Ile Ala	
290 295 300	
cct gaa aat cgc agc ggt tgc ctg gcg gta att gaa gaa gtg atg ctc	960
Pro Glu Asn Arg Ser Gly Cys Leu Ala Val Ile Glu Glu Val Met Leu	
305 310 315 320	
gac gaa ccg caa tac tgg aaa aaa tat tat cgt acg ggt ttt aac gat	1008
Asp Glu Pro Gln Tyr Trp Lys Lys Tyr Tyr Arg Thr Gly Phe Asn Asp	
325 330 335	
tca tta ctg gat att cgt tac agc ctg tgc gat cgt att cgt tat tac	1056
Ser Leu Leu Asp Ile Arg Tyr Ser Leu Ser Asp Arg Ile Arg Tyr Tyr	
340 345 350	
tgg ccg cat agt cgg att aaa aat agc gtc gaa acg atg atg gtg aat	1104
Trp Pro His Ser Arg Ile Lys Asn Ser Val Glu Thr Met Met Val Asn	
355 360 365	
ctt gaa ggc gtg gac atc cca ctg ggc atg att agt cag tat ctt ccc	1152
Leu Glu Gly Val Asp Ile Pro Leu Gly Met Ile Ser Gln Tyr Leu Pro	
370 375 380	
aaa caa ttt gaa cgc att cag tcc ggg gaa tta tca gca ata ccg cat	1200
Lys Gln Phe Glu Arg Ile Gln Ser Gly Glu Leu Ser Ala Ile Pro His	
385 390 395 400	
cag ctg att atg gat aaa att tat gat gtt ttg cgc gcc tat cgc tac	1248
Gln Leu Ile Met Asp Lys Ile Tyr Asp Val Leu Arg Ala Tyr Arg Tyr	
405 410 415	
ggc tgt gcg gaa taa	1263
Gly Cys Ala Glu *	
420	

<210> 233
 <211> 861
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(861)

<400> 233
 atg aaa atg tac gtg gta tcg aca aag cag atg ctg aac aac gca cag 48
 Met Lys Met Tyr Val Val Ser Thr Lys Gln Met Leu Asn Asn Ala Gln
 1 5 10 15
 cgc ggc ggt tat gcg gtt ccg gca ttc aat att cac aat ctc gaa acg 96
 Arg Gly Gly Tyr Ala Val Pro Ala Phe Asn Ile His Asn Leu Glu Thr
 20 25 30
 atg caa gtg gtg gta gaa acc gct gcc aac ctg cat gcg ccg gtc atc 144
 Met Gln Val Val Val Glu Thr Ala Ala Asn Leu His Ala Pro Val Ile
 35 40 45
 atc gcc gga acg cct ggc aca ttt act cat gct ggt aca gaa aat ctg 192
 Ile Ala Gly Thr Pro Gly Thr Phe Thr His Ala Gly Thr Glu Asn Leu
 50 55 60
 ttg gcg ctg gtc agc gcg atg gcg aag caa tat cac cat cca ctg gca 240
 Leu Ala Leu Val Ser Ala Met Ala Lys Gln Tyr His His Pro Leu Ala
 65 70 75 80
 att cat ctc gac cat cac acg aaa ttt gac gat atc gct cag aag gtt 288
 Ile His Leu Asp His His Thr Lys Phe Asp Asp Ile Ala Gln Lys Val
 85 90 95
 cgt tct ggc gtg cgc tca gtc atg att gac gcc tcg cat ttg cct ttt 336
 Arg Ser Gly Val Arg Ser Val Met Ile Asp Ala Ser His Leu Pro Phe
 100 105 110
 gcg caa aat att tca cgg gtc aaa gag gtg gtg gat ttt tgc cat cgc 384
 Ala Gln Asn Ile Ser Arg Val Lys Glu Val Val Asp Phe Cys His Arg
 115 120 125
 ttt gat gtc agc gtc gag gcg gag ctg ggg caa ctt ggc ggc cag gaa 432
 Phe Asp Val Ser Val Glu Ala Glu Leu Gly Gln Leu Gly Gly Gln Glu
 130 135 140
 gat gat gtg caa gtc aat gaa gcc gat gcg ttg tac acc aac ccc gct 480
 Asp Asp Val Gln Val Asn Glu Ala Asp Ala Leu Tyr Thr Asn Pro Ala
 145 150 155 160
 cag gcg cgt gaa ttt gcc gag gca acc gga att gat tcc ctg gcg gtc 528
 Gln Ala Arg Glu Phe Ala Glu Ala Thr Gly Ile Asp Ser Leu Ala Val
 165 170 175
 gcc atc ggc acg gct cat ggg atg tat gcc agc gca ccg gcg ctt gat 576
 Ala Ile Gly Thr Ala His Gly Met Tyr Ala Ser Ala Pro Ala Leu Asp
 180 185 190
 ttt tct aga ctg gag aac att cgc cag tgg gtg aac tta ccg ctg gtg 624
 Phe Ser Arg Leu Glu Asn Ile Arg Gln Trp Val Asn Leu Pro Leu Val

195	200	205	
ctg cat ggc gcg tca ggg tta tgc act aag gat att cag caa acc atc			672
Leu His Gly Ala Ser Gly Leu Ser Thr Lys Asp Ile Gln Gln Thr Ile			
210	215	220	
aaa ctg ggg ata tgc aaa atc aac gtt gca acg gag ctg aaa aat gcc			720
Lys Leu Gly Ile Cys Lys Ile Asn Val Ala Thr Glu Leu Lys Asn Ala			
225	230	235	240
ttc tgc cag gcg tta aaa aat tac ctg acc gag cac cct gaa gcg acc			768
Phe Ser Gln Ala Leu Lys Asn Tyr Leu Thr Glu His Pro Glu Ala Thr			
245	250	255	
gat ccc cgg gat tat ttg cag tgc gct aaa tcc gca atg cgc gat gtg			816
Asp Pro Arg Asp Tyr Leu Gln Ser Ala Lys Ser Ala Met Arg Asp Val			
260	265	270	
gtg agc aaa gtg att gcc gat tgt ggc tgc gag ggc agg gca taa			861
Val Ser Lys Val Ile Ala Asp Cys Gly Cys Glu Gly Arg Ala *			
275	280	285	

<210> 234

<211> 474

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (474)

<400> 234

atg agt caa aac gat atc att atc aga act cat tat aag tct cct cat	48
Met Ser Gln Asn Asp Ile Ile Ile Arg Thr His Tyr Lys Ser Pro His	
1 5 10 15	
aga ttg cac atc gat agc gac ata cca aca cct tca tca gag cct att	96
Arg Leu His Ile Asp Ser Asp Ile Pro Thr Pro Ser Ser Glu Pro Ile	
20 25 30	
aat caa ttt gcg cgc cag ctc atc acc cta ctt gat acc tct gac tta	144
Asn Gln Phe Ala Arg Gln Leu Ile Thr Leu Leu Asp Thr Ser Asp Leu	
35 40 45	
agt tgc atg ctg tca tac tgt gtt act cag gaa ttt acc gca aac tgt	192
Ser Ser Met Leu Ser Tyr Cys Val Thr Gln Glu Phe Thr Ala Asn Cys	
50 55 60	
cga aaa ata tca caa aat tgt tat tcc act gcc ctt ttt acc att aac	240
Arg Lys Ile Ser Gln Asn Cys Tyr Ser Thr Ala Leu Phe Thr Ile Asn	
65 70 75 80	
ttt gcc act tca ccc atc cat aca gaa aat ata ctc att aca tta cac	288
Phe Ala Thr Ser Pro Ile His Thr Glu Asn Ile Leu Ile Thr Leu His	
85 90 95	
tat aaa aaa gaa atc att tcc tta tta ctg gaa acc acg cct att aaa	336
Tyr Lys Lys Glu Ile Ile Ser Leu Leu Leu Glu Thr Thr Pro Ile Lys	
100 105 110	

gct aac cat ttg cga agc ata ctg gat tat att gaa cag gaa cag tta 384
 Ala Asn His Leu Arg Ser Ile Leu Asp Tyr Ile Glu Gln Glu Gln Leu
 115 120 125

act gct gaa gat cgt aac cat tgt atg aaa ctg tct aaa aaa atc cat 432
 Thr Ala Glu Asp Arg Asn His Cys Met Lys Leu Ser Lys Lys Ile His
 130 135 140

aga gaa aaa aac tat aca ccc aac agt aaa tct caa tgg tag 474
 Arg Glu Lys Asn Tyr Thr Pro Asn Ser Lys Ser Gln Trp *
 145 150 155

<210> 235

<211> 1416

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1416)

<400> 235

ttg caa tct cct tct gac gct att ttt tgt cgc cat ctg tca ttg caa 48
 Met Gln Ser Pro Ser Asp Ala Ile Phe Cys Arg His Leu Ser Leu Gln
 1 5 10 15

tac gcc ctt gat tca ttg aga aat gga aaa ggc aaa gtc aac ctg att 96
 Tyr Ala Leu Asp Ser Leu Arg Asn Gly Lys Gly Lys Val Asn Leu Ile
 20 25 30

aaa cat tac tcc tcc gtt gaa tcc ata cag cag cat gtc ccc tta gtc 144
 Lys His Tyr Ser Ser Val Glu Ser Ile Gln Gln His Val Pro Leu Val
 35 40 45

cgg gac gcg gag ttc aga gca tta ctt cgc cat cct cct gca ggg agt 192
 Arg Asp Ala Glu Phe Arg Ala Leu Leu Arg His Pro Pro Ala Gly Ser
 50 55 60

cgc gtt atc gcg agt aag gat ttt ggc ttc gct tta gat att ttc ttt 240
 Arg Val Ile Ala Ser Lys Asp Phe Gly Phe Ala Leu Asp Ile Phe Phe
 65 70 75 80

tgt cga atg atg gca aac aat gtc agt cat atg tcc gcg att tta tat 288
 Cys Arg Met Met Ala Asn Asn Val Ser His Met Ser Ala Ile Leu Tyr
 85 90 95

ata gac aat cat act ttg tca gta agg cta cga ata aag cag tca gtg 336
 Ile Asp Asn His Thr Leu Ser Val Arg Leu Arg Ile Lys Gln Ser Val
 100 105 110

tat gga caa tta aat tat gtt gtg tcc gtt tac gac ccg aac gat acc 384
 Tyr Gly Gln Leu Asn Tyr Val Val Ser Val Tyr Asp Pro Asn Asp Thr
 115 120 125

aac gtt gcc gtc aga gac acc cac agg aca gca cgg ggc ttt ctt tcg 432
 Asn Val Ala Val Arg Asp Thr His Arg Thr Ala Arg Gly Phe Leu Ser
 130 135 140

ctt gat aag ttc atc agt tca ggt ccc gat gct cag acc tgg gct gat	480
Leu Asp Lys Phe Ile Ser Ser Gly Pro Asp Ala Gln Thr Trp Ala Asp	
145 150 155 160	
aga tat gtt cgc aac tgt gca att gct att ctg ccc cta tta cct gtg	528
Arg Tyr Val Arg Asn Cys Ala Ile Ala Ile Leu Pro Leu Leu Pro Val	
165 170 175	
gga gtt cca ggg gct att ttc gcg ggt att gca tca cga atg cca ttt	576
Gly Val Pro Gly Ala Ile Phe Ala Gly Ile Ala Ser Arg Met Pro Phe	
180 185 190	
gcc cct ata cat cca tcg gca atg ttg tta ata atg gct aca ggc cag	624
Ala Pro Ile His Pro Ser Ala Met Leu Leu Ile Met Ala Thr Gly Gln	
195 200 205	
tct caa cag ctt att aca tta ttc aaa cag ttg ccc ata ctc cct gaa	672
Ser Gln Gln Leu Ile Thr Leu Phe Lys Gln Leu Pro Ile Leu Pro Glu	
210 215 220	
aaa gaa atc att gaa ata ata act gcg cag aat agc gtt ggt aca cct	720
Lys Glu Ile Ile Glu Ile Ile Thr Ala Gln Asn Ser Val Gly Thr Pro	
225 230 235 240	
gct tta ttt ttg gct atg atg aac gga cat act gac aac gtg aaa ata	768
Ala Leu Phe Leu Ala Met Met Asn Gly His Thr Asp Asn Val Lys Ile	
245 250 255	
ttt atg caa gaa att cag tca ctg gta gat aat cac atc att cat gaa	816
Phe Met Gln Glu Ile Gln Ser Leu Val Asp Asn His Ile Ile His Glu	
260 265 270	
gat aat ctg gtt aaa tta ctg caa act aaa agt gct aac gaa aca cct	864
Asp Asn Leu Val Lys Leu Leu Thr Lys Ser Ala Asn Glu Thr Pro	
275 280 285	
gga ctt tat atc tcc atg ttg tat gga ttc gat gaa ata atc gat atc	912
Gly Leu Tyr Ile Ser Met Leu Tyr Gly Phe Asp Glu Ile Ile Asp Ile	
290 295 300	
ttt ctg aat gca tta acc act cca ata gca caa gag ctt tta aac aaa	960
Phe Leu Asn Ala Leu Thr Pro Ile Ala Gln Glu Leu Leu Asn Lys	
305 310 315 320	
aaa ctg gtg atg agt att tta gcc atg aaa ata cat gat ggt gag cca	1008
Lys Leu Val Met Ser Ile Leu Ala Met Lys Ile His Asp Gly Glu Pro	
325 330 335	
gga tta tac gcc gca atg gaa aat aat cac cct ttg tgt gtc aca cgg	1056
Gly Leu Tyr Ala Ala Met Glu Asn Asn His Pro Leu Cys Val Thr Arg	
340 345 350	
ttc ctc tct aaa att aat ggc atc gcc ttt aaa tac aag ttg agc aaa	1104
Phe Leu Ser Lys Ile Asn Gly Ile Ala Phe Lys Tyr Lys Leu Ser Lys	
355 360 365	
gct aac atc atg gat tta tta aaa gga gct aca gca cag gga acc cct	1152
Ala Asn Ile Met Asp Leu Leu Lys Gly Ala Thr Ala Gln Gly Thr Pro	
370 375 380	
gca tta tac atc gcc atg agc aag ggt aat gaa gac gtc gtg tta tct	1200

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Ala Leu Tyr Ile Ala Met Ser Lys Gly Asn Glu Asp Val Val Leu Ser
385                      390                      395                      400

tat ata tcg acg ctg ggt gct ttt gca aaa aaa cat tct ttt agt caa 1248
Tyr Ile Ser Thr Leu Gly Ala Phe Ala Lys Lys His Ser Phe Ser Gln
                      405                      410                      415

cat cag tta ttt aca cta ttg gcc gct aaa aat cat gac aac atg tca 1296
His Gln Leu Phe Thr Leu Leu Ala Ala Lys Asn His Asp Asn Met Ser
                      420                      425                      430

gct gtt cat ata gcc att cat cat aag cat tat aaa act gta gaa aca 1344
Ala Val His Ile Ala Ile His His Lys His Tyr Lys Thr Val Glu Thr
                      435                      440                      445

tat tat gct gct att aat gca atc agc caa agc ctg agt ttt agt gct 1392
Tyr Tyr Ala Ala Ile Asn Ala Ile Ser Gln Ser Leu Ser Phe Ser Ala
                      450                      455                      460

gat gaa ata aag acg tat tta taa 1416
Asp Glu Ile Lys Thr Tyr Leu *
465                      470

<210> 236
<211> 387
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(387)

<400> 236
atg cca tct gga tta ttt atg gac tta ttg cct ttt tta ctg gac gcg 48
Met Pro Ser Gly Leu Phe Met Asp Leu Leu Pro Phe Leu Leu Asp Ala
1                      5                      10                      15

aac ctc agc gcg aca aac cca ccc gct att ccg cac tgg tgg aag cgt 96
Asn Leu Ser Ala Thr Asn Pro Pro Ala Ile Pro His Trp Trp Lys Arg
20                      25                      30

caa ccg ctt att ccc aac ctt ctg tca cag gaa ctg aaa aac tat ctg 144
Gln Pro Leu Ile Pro Asn Leu Leu Ser Gln Glu Leu Lys Asn Tyr Leu
35                      40                      45

aag ctt aat gtt aaa gag aaa aat att cag att gca gac cag gta att 192
Lys Leu Asn Val Lys Glu Lys Asn Ile Gln Ile Ala Asp Gln Val Ile
50                      55                      60

att gat gaa act gca ggt gaa gtt gtt atc ggc gcg aat acc cgt att 240
Ile Asp Glu Thr Ala Gly Glu Val Val Ile Gly Ala Asn Thr Arg Ile
65                      70                      75                      80

tgt cat ggt gcc gtt att cag ggt ccg gta gtg att ggc gca aac tgc 288
Cys His Gly Ala Val Ile Gln Gly Pro Val Val Ile Gly Ala Asn Cys
85                      90                      95

ctg ata ggt aat tgg att tgc ccc tat att tcc aga cat ctg tta tca 336
Leu Ile Gly Asn Trp Ile Cys Pro Tyr Ile Ser Arg His Leu Leu Ser
100                      105                      110

```

ctt aac cca tta caa gcc cgc tgc cgc aga tat tcc cgt ggc gag cga 384
 Leu Asn Pro Leu Gln Ala Arg Cys Arg Arg Tyr Ser Arg Gly Glu Arg
 115 120 125

taa 387
 *

<210> 237
 <211> 1197
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1197)

<400> 237
 atg aaa acc tgg ata ttt atc tgt atg tcc ata gca atg ttg cta tgg 48
 Met Lys Thr Trp Ile Phe Ile Cys Met Ser Ile Ala Met Leu Leu Trp
 1 5 10 15
 ttt tta agt acg cta aga cgt aaa ccc agt caa aag aaa ggc tgt att 96
 Phe Leu Ser Thr Leu Arg Arg Lys Pro Ser Gln Lys Lys Gly Cys Ile
 20 25 30
 gac gcc att ata cct gcg tat aac gaa ggc ccg tgt ctg gcg cag tca 144
 Asp Ala Ile Ile Pro Ala Tyr Asn Glu Gly Pro Cys Leu Ala Gln Ser
 35 40 45
 ctg gat aat cta ctg cgt aac cct tat ttt tgc cgg gta att tgc gtt 192
 Leu Asp Asn Leu Leu Arg Asn Pro Tyr Phe Cys Arg Val Ile Cys Val
 50 55 60
 aac gac ggc tcc acg gac aat acc gaa gcg gtc atg gcg gaa gtc aaa 240
 Asn Asp Gly Ser Thr Asp Asn Thr Glu Ala Val Met Ala Glu Val Lys
 65 70 75 80
 cgc aaa tgg ggc gac cgc ttt gtt gcc gtc acg caa aaa aat acc ggt 288
 Arg Lys Trp Gly Asp Arg Phe Val Ala Val Thr Gln Lys Asn Thr Gly
 85 90 95
 aaa ggt ggt gcg ctg atg aat ggc ctc aat tac gcc acc tgc gac cag 336
 Lys Gly Gly Ala Leu Met Asn Gly Leu Asn Tyr Ala Thr Cys Asp Gln
 100 105 110
 gtt ttt tta agt gat gcc gac acc tat gtt ccg ccc gat caa gac gga 384
 Val Phe Leu Ser Asp Ala Asp Thr Tyr Val Pro Pro Asp Gln Asp Gly
 115 120 125
 atg ggc tat atg ctg gca gaa att gag cgc ggt gcc gat gcc gta ggc 432
 Met Gly Tyr Met Leu Ala Glu Ile Glu Arg Gly Ala Asp Ala Val Gly
 130 135 140
 ggc att ccc tct act gcg ttg aaa ggc gcg ggt ctg tta ccg cac atc 480
 Gly Ile Pro Ser Thr Ala Leu Lys Gly Ala Gly Leu Leu Pro His Ile
 145 150 155 160
 cgc gcg acc gta aag ttg ccg atg att gtt atg aag cgc acg cta cag 528

Arg	Ala	Thr	Val	Lys	Leu	Pro	Met	Ile	Val	Met	Lys	Arg	Thr	Leu	Gln	
				165					170					175		
cag	ctc	ctg	ggt	ggc	gca	ccg	ttt	att	atc	agc	ggt	gcc	tgc	ggg	atg	576
Gln	Leu	Leu	Gly	Gly	Ala	Pro	Phe	Ile	Ile	Ser	Gly	Ala	Cys	Gly	Met	
			180					185					190			
ttc	cgt	act	gat	gta	ttg	cgt	aag	ttc	ggt	ttc	tcg	gat	cgt	act	aaa	624
Phe	Arg	Thr	Asp	Val	Leu	Arg	Lys	Phe	Gly	Phe	Ser	Asp	Arg	Thr	Lys	
		195					200					205				
gtc	gaa	gac	ctt	gat	ctc	acc	tgg	aca	ttg	gtg	gca	aac	ggc	tac	cgt	672
Val	Glu	Asp	Leu	Asp	Leu	Thr	Trp	Thr	Leu	Val	Ala	Asn	Gly	Tyr	Arg	
	210					215					220					
att	cgg	cag	gcg	aat	cgc	tgc	atc	gta	tac	cca	cag	gaa	tgc	aac	agc	720
Ile	Arg	Gln	Ala	Asn	Arg	Cys	Ile	Val	Tyr	Pro	Gln	Glu	Cys	Asn	Ser	
225				230						235					240	
ccg	cgt	gag	gag	tgg	cgt	cgc	tgg	cgg	cgt	tgg	att	gtg	gga	tac	gcg	768
Pro	Arg	Glu	Glu	Trp	Arg	Arg	Trp	Arg	Arg	Trp	Ile	Val	Gly	Tyr	Ala	
				245					250					255		
gtc	tgt	atg	cgc	ctg	cat	aaa	aga	ctt	tta	ttt	agc	cgc	ttc	ggt	atc	816
Val	Cys	Met	Arg	Leu	His	Lys	Arg	Leu	Leu	Phe	Ser	Arg	Phe	Gly	Ile	
			260					265					270			
ttc	agt	ata	ttt	cct	atg	ctg	ttg	gtt	gtg	ctt	tat	ggc	gtt	ggg	att	864
Phe	Ser	Ile	Phe	Pro	Met	Leu	Leu	Val	Val	Leu	Tyr	Gly	Val	Gly	Ile	
		275					280					285				
tat	ctc	act	acc	tgg	ttt	aat	gaa	ttc	atc	acc	acc	ggg	ccg	cat	gga	912
Tyr	Leu	Thr	Thr	Trp	Phe	Asn	Glu	Phe	Ile	Thr	Thr	Gly	Pro	His	Gly	
	290					295					300					
gtg	gtg	ttg	gca	atg	ttt	ccg	ctt	atc	tgg	gtc	ggc	gta	gtt	tgt	gtt	960
Val	Val	Leu	Ala	Met	Phe	Pro	Leu	Ile	Trp	Val	Gly	Val	Val	Cys	Val	
305					310					315					320	
att	ggt	gct	ttt	agc	gcc	tgg	ttt	cat	cgt	tgc	tgg	ttg	ttg	gtg	cct	1008
Ile	Gly	Ala	Phe	Ser	Ala	Trp	Phe	His	Arg	Cys	Trp	Leu	Leu	Val	Pro	
				325					330					335		
tta	gcg	ccg	ctt	tcc	gtt	gtg	tat	gta	tta	tta	gct	tat	gcc	atc	tgg	1056
Leu	Ala	Pro	Leu	Ser	Val	Val	Tyr	Val	Leu	Leu	Ala	Tyr	Ala	Ile	Trp	
			340					345					350			
att	att	tat	gga	ctt	att	gcc	ttt	ttt	act	gga	cgc	gaa	cct	cag	cgc	1104
Ile	Ile	Tyr	Gly	Leu	Ile	Ala	Phe	Phe	Thr	Gly	Arg	Glu	Pro	Gln	Arg	
		355				360						365				
gac	aaa	ccc	acc	cgc	tat	tcc	gca	ctg	gtg	gaa	gcg	tca	acc	gct	tat	1152
Asp	Lys	Pro	Thr	Arg	Tyr	Ser	Ala	Leu	Val	Glu	Ala	Ser	Thr	Ala	Tyr	
	370					375					380					
tcc	caa	cct	tct	gtc	aca	gga	act	gaa	aaa	cta	tct	gaa	gct	taa		1197
Ser	Gln	Pro	Ser	Val	Thr	Gly	Thr	Glu	Lys	Leu	Ser	Glu	Ala	*		
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 <211> 1659
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
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 1 5 10 15
 ttg tcg ttg atg ctg gaa caa aac aac gtc ctg att ggg gag aac gcg 96
 Leu Ser Leu Met Leu Glu Gln Asn Asn Val Leu Ile Gly Glu Asn Ala
 20 25 30
 tgg ggt aaa tcc agc ttg ctg gac gcc tta act ctg ctg cta tcg cca 144
 Trp Gly Lys Ser Ser Leu Leu Asp Ala Leu Thr Leu Leu Leu Ser Pro
 35 40 45
 gaa tca gat ctc tac cat ttt gag cgc gac gat ttc tgg ttc ccg ccg 192
 Glu Ser Asp Leu Tyr His Phe Glu Arg Asp Asp Phe Trp Phe Pro Pro
 50 55 60
 gga gat atc aac ggg cga gaa cat cat ctg cat att att ttg acc ttc 240
 Gly Asp Ile Asn Gly Arg Glu His His Leu His Ile Ile Leu Thr Phe
 65 70 75 80
 cgc gaa tcg ctg cca ggc cga cat cgg gtt cgc cgt tat cgg ccg ctg 288
 Arg Glu Ser Leu Pro Gly Arg His Arg Val Arg Arg Tyr Arg Pro Leu
 85 90 95
 gaa gcg tgc tgg acg cca tgc acc gat ggc tat cac cgt att ttt tat 336
 Glu Ala Cys Trp Thr Pro Cys Thr Asp Gly Tyr His Arg Ile Phe Tyr
 100 105 110
 cgt ctg gaa ggg gag agt gcg gaa gac ggc agc gtg atg aca ctg cgc 384
 Arg Leu Glu Gly Glu Ser Ala Glu Asp Gly Ser Val Met Thr Leu Arg
 115 120 125
 agt ttt ctc gat aaa gac gga cat ccg att gat gtc gag gat att aac 432
 Ser Phe Leu Asp Lys Asp Gly His Pro Ile Asp Val Glu Asp Ile Asn
 130 135 140
 gat cag gca cgc cat ctg gtg cgt tta atg ccg gtg ctg cgc ttg cgt 480
 Asp Gln Ala Arg His Leu Val Arg Leu Met Pro Val Leu Arg Leu Arg
 145 150 155 160
 gat gcc cgt ttt atg cgc cgt att cgt aac ggc acg gtg cca aat gtc 528
 Asp Ala Arg Phe Met Arg Arg Ile Arg Asn Gly Thr Val Pro Asn Val
 165 170 175
 cct aat gtg gaa gtc acc gcg cgc cag ctc gat ttc ctc gcc cgt gag 576
 Pro Asn Val Glu Val Thr Ala Arg Gln Leu Asp Phe Leu Ala Arg Glu
 180 185 190
 tta tcc tca cat ccg caa aat ctc tct gat ggg cag att cgt cag gga 624
 Leu Ser Ser His Pro Gln Asn Leu Ser Asp Gly Gln Ile Arg Gln Gly
 195 200 205

ctt tcc gca atg gta cag	ctg ctt gag cat tat ttc tct gag cag ggg	672
Leu Ser Ala Met Val Gln	Leu Leu Glu His Tyr Phe Ser Glu Gln Gly	
210	215 220	
gcc gga cag gcg cga tat	cgt tta atg cgg cgg cga gcc agc aat gag	720
Ala Gly Gln Ala Arg Tyr	Arg Leu Met Arg Arg Arg Ala Ser Asn Glu	
225	230 235 240	
caa cga agc tgg cgc tat	ctg gat atc atc aac cgg atg att gac cga	768
Gln Arg Ser Trp Arg Tyr	Leu Asp Ile Ile Asn Arg Met Ile Asp Arg	
245	250 255	
cct ggt ggg cgc tgc tat	cgg gtt att ttg ctc ggc cta ttt gct act	816
Pro Gly Gly Arg Ser Tyr	Arg Val Ile Leu Leu Gly Leu Phe Ala Thr	
260	265 270	
ttg ttg cag gca aaa ggc	aca ttg cga ctg gat aaa gac gcc cgt cca	864
Leu Leu Gln Ala Lys Gly	Thr Leu Arg Leu Asp Lys Asp Ala Arg Pro	
275	280 285	
ttg ttg ctg atc gaa gat	cca gaa acc cgt tta cac ccc att atg ctt	912
Leu Leu Leu Ile Glu Asp	Pro Glu Thr Arg Leu His Pro Ile Met Leu	
290	295 300	
tca gtt gcc tgg cat ctg	ttg aat ctt ctg cca ttg cag cgc att gcc	960
Ser Val Ala Trp His Leu	Leu Leu Asn Leu Leu Pro Leu Gln Arg Ile Ala	
305	310 315 320	
acc acc aac tgc ggt gag	ttg ctt tgc tta acg ccg gta gag cat gtt	1008
Thr Thr Asn Ser Gly Glu	Leu Leu Ser Leu Thr Pro Val Glu His Val	
325	330 335	
tgc cga ctg gta cgt gag	tcc tgc cgc gtt gcc gcc tgg cgt ctg ggg	1056
Cys Arg Leu Val Arg Glu	Ser Ser Arg Val Ala Ala Trp Arg Leu Gly	
340	345 350	
ccg agt ggc ttg agt acc	gaa gat agc cga cgc ata tcc ttt cac att	1104
Pro Ser Gly Leu Ser Thr	Glu Asp Ser Arg Arg Ile Ser Phe His Ile	
355	360 365	
cgt ttt aac cgt ccg tca	tgc ctg ttt gca cgc tgc tgg ttg ctg gtg	1152
Arg Phe Asn Arg Pro Ser	Ser Ser Leu Phe Ala Arg Cys Trp Leu Leu Val	
370	375 380	
gaa ggg gaa acg gaa acc	tgg gtt atc aat gaa ctg gcg cgt cag tgc	1200
Glu Gly Glu Thr Glu Thr	Trp Val Ile Asn Glu Leu Ala Arg Gln Cys	
385	390 395 400	
gga cat cat ttt gat gcc	gaa ggg atc aag gtc att gag ttt gcc cag	1248
Gly His His Phe Asp Ala	Glu Gly Ile Lys Val Ile Glu Phe Ala Gln	
405	410 415	
tcc ggg cta aag cca ctg	ggt aaa ttt gcc cgc cga atg ggg att gaa	1296
Ser Gly Leu Lys Pro Leu	Val Lys Phe Ala Arg Arg Met Gly Ile Glu	
420	425 430	
tgg cat gta ctg gtc gat	ggc gat gaa gca ggg aag aaa tat gcc gct	1344
Trp His Val Leu Val Asp	Gly Asp Glu Ala Gly Lys Lys Tyr Ala Ala	
435	440 445	


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acg gta cgc agc ctg ttg aat aac gat cgg gaa gcc gaa cga gaa cat 1392
Thr Val Arg Ser Leu Leu Asn Asn Asp Arg Glu Ala Glu Arg Glu His
450 455 460

tta acg gcg tta ccg gcg ctg gat atg gaa cat ttt atg tat cgc cag 1440
Leu Thr Ala Leu Pro Ala Leu Asp Met Glu His Phe Met Tyr Arg Gln
465 470 475 480

gga ttt tcc gat gtg ttc cac cgc atg gcg caa atc ccg gaa aat gta 1488
Gly Phe Ser Asp Val Phe His Arg Met Ala Gln Ile Pro Glu Asn Val
485 490 495

ccg atg aat cta cgc aaa att atc tcg aaa gcg atc cat cgc tct tcc 1536
Pro Met Asn Leu Arg Lys Ile Ile Ser Lys Ala Ile His Arg Ser Ser
500 505 510

aaa ccc gat ctt gcc att gaa gtg gca atg gag gca gga cgt cgt ggt 1584
Lys Pro Asp Leu Ala Ile Glu Val Ala Met Glu Ala Gly Arg Arg Gly
515 520 525

gtg gac tcc gta ccg acg ctg ctg aaa aaa atg ttc tca cgc gtg ctg 1632
Val Asp Ser Val Pro Thr Leu Leu Lys Lys Met Phe Ser Arg Val Leu
530 535 540

tgg ctg gcg cgc ggt cgc gcg gat taa 1659
Trp Leu Ala Arg Gly Arg Ala Asp *
545 550

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<210> 239

<211> 1059

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1059)

<400> 239

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Met Leu Pro Ser Ile Ser Ile Asn Asn Thr Ser Ala Ala Tyr Pro Glu
1 5 10 15

tcc atc aat gaa aat aac aat gat gaa gtt aat gga tta gta caa gag 96
Ser Ile Asn Glu Asn Asn Asn Asp Glu Val Asn Gly Leu Val Gln Glu
20 25 30

ttc aaa aac ctt ttt aat ggt aag gaa gga ata agc acc tgt att aaa 144
Phe Lys Asn Leu Phe Asn Gly Lys Glu Gly Ile Ser Thr Cys Ile Lys
35 40 45

cat cta ctt gag ctt ata aaa aac gcc ata cga gta aac gac gat cct 192
His Leu Leu Glu Leu Ile Lys Asn Ala Ile Arg Val Asn Asp Asp Pro
50 55 60

tat aga ttt aat att aat aat tcc tca gtt act tat att gat att gac 240
Tyr Arg Phe Asn Ile Asn Asn Ser Ser Val Thr Tyr Ile Asp Ile Asp
65 70 75 80

tcc aat gat aca gac cat att act att ggt atc gac aac caa gaa cca 288
Ser Asn Asp Thr Asp His Ile Thr Ile Gly Ile Asp Asn Gln Glu Pro

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85										90										95										
ata gaa tta cct gcg aac tat aaa gac	aaa gaa ctc gtc cgt act atc	336																												
Ile Glu Leu Pro Ala Asn Tyr Lys Asp	Lys Glu Leu Val Arg Thr Ile																													
100	105	110																												
att aat gac aac ata gtt gag aag act	cat gat atc aat aac aag gaa	384																												
Ile Asn Asp Asn Ile Val Glu Lys Thr	His Asp Ile Asn Asn Lys Glu																													
115	120	125																												
atg atc ttc agc gca tta aaa gaa ata	tat gat gga gat cct ggt ttt	432																												
Met Ile Phe Ser Ala Leu Lys Glu Ile	Tyr Asp Gly Asp Pro Gly Phe																													
130	135	140																												
atc ttc gat aag ata tca cac aaa ctc	aga cat acg gta acg gaa ttt	480																												
Ile Phe Asp Lys Ile Ser His Lys Leu	Arg His Thr Val Thr Glu Phe																													
145	150	155																												
gat gag agc ggg aaa agc gaa cca acg	gac tta ttt acc tgg tac ggt	528																												
Asp Glu Ser Gly Lys Ser Glu Pro Thr	Asp Leu Phe Thr Trp Tyr Gly																													
165	170	175																												
aaa gat aaa aaa ggc gac tct ctc gct	att gta att aaa aat aaa aac	576																												
Lys Asp Lys Lys Gly Asp Ser Leu Ala	Ile Val Ile Lys Asn Lys Asn																													
180	185	190																												
gga aat gat tac tta tct ctc ggt tac	tac gat cag gac gac tac cac	624																												
Gly Asn Asp Tyr Leu Ser Leu Gly Tyr	Tyr Asp Gln Asp Asp Tyr His																													
195	200	205																												
att caa aga gga att cgt att aat ggt	gat agt ctc acc caa tat tgt	672																												
Ile Gln Arg Gly Ile Arg Ile Asn Gly	Asp Ser Leu Thr Gln Tyr Cys																													
210	215	220																												
agt gaa aac gcc agg agt gct tca gcg	tgg ttt gaa agc agt aaa gct	720																												
Ser Glu Asn Ala Arg Ser Ala Ser Ala	Trp Phe Glu Ser Ser Lys Ala																													
225	230	235																												
atc atg gca gaa tca ttt gca act ggt	tcc gat cat cag gtt gta aac	768																												
Ile Met Ala Glu Ser Phe Ala Thr Gly	Ser Asp His Gln Val Val Asn																													
245	250	255																												
gag ctc aac ggg gaa aga ctg aga gaa	cca aac gac gtt ttt aaa cgt	816																												
Glu Leu Asn Gly Glu Arg Leu Arg Glu	Pro Asn Asp Val Phe Lys Arg																													
260	265	270																												
tat ggt cga gca ata aga tat gat ttt	caa gtg gac gat gca aaa tat	864																												
Tyr Gly Arg Ala Ile Arg Tyr Asp Phe	Gln Val Asp Asp Ala Lys Tyr																													
275	280	285																												
aaa tgc gac cat cta aaa gaa ata gtt	tct act tta gtc ggt aac aaa	912																												
Lys Cys Asp His Leu Lys Glu Ile Val	Ser Thr Leu Val Gly Asn Lys																													
290	295	300																												
att aac gtt ggc cat tct caa aaa ata	tat aag cat ttt aag gat ctc	960																												
Ile Asn Val Gly His Ser Gln Lys Ile	Tyr Lys His Phe Lys Asp Leu																													
305	310	315																												
gaa ggt aaa att gaa gaa agg ctt caa	aat cgc cag gct gaa tat caa	1008																												
Glu Gly Lys Ile Glu Glu Arg Leu Gln	Asn Arg Gln Ala Glu Tyr Gln																													
325	330	335																												

aat gaa att aat caa cca tct gcg cca ggt gtt aat ttt gat gat att 1056
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 340 345 350

taa 1059
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<210> 240
 <211> 1128
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1128)

<400> 240
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 1 5 10 15

 cgc agt ctg ctg ggt gat aaa gcg atg ctg acg ctg att gtc ttc tcg 96
 Arg Ser Leu Leu Gly Asp Lys Ala Met Leu Thr Leu Ile Val Phe Ser
 20 25 30

 ttt acg gtg tcg gtg tat tcg tca gcg acc gtt acg cca gga tcg ttg 144
 Phe Thr Val Ser Val Tyr Ser Ser Ala Thr Val Thr Pro Gly Ser Leu
 35 40 45

 aac ctc gcg ccg atc gcc att gcc gat atg gat caa tcg cag tta tcg 192
 Asn Leu Ala Pro Ile Ala Ile Ala Asp Met Asp Gln Ser Gln Leu Ser
 50 55 60

 aac cgg atc gtt aac agc ttc tat cgt ccg tgg ttt ttg cca ccg gag 240
 Asn Arg Ile Val Asn Ser Phe Tyr Arg Pro Trp Phe Leu Pro Pro Glu
 65 70 75 80

 atg atc acc gcc gat gag atg gat gcc gga ctg gac gcc gga cgc tat 288
 Met Ile Thr Ala Asp Glu Met Asp Ala Gly Leu Asp Ala Gly Arg Tyr
 85 90 95

 acc ttc gcg ata aat att ccg cct aat ttt cag cgt gat gtc ctc gcc 336
 Thr Phe Ala Ile Asn Ile Pro Pro Asn Phe Gln Arg Asp Val Leu Ala
 100 105 110

 gga cgc cag ccg gat att cag gtg aac gtc gat gcc acg cgc atg agc 384
 Gly Arg Gln Pro Asp Ile Gln Val Asn Val Asp Ala Thr Arg Met Ser
 115 120 125

 cag gca ttt acc ggc aat ggg tat atc cag aat att atc aac ggt gaa 432
 Gln Ala Phe Thr Gly Asn Gly Tyr Ile Gln Asn Ile Ile Asn Gly Glu
 130 135 140

 gtg aac agc ttt gtc gcg cgc tac cgt gat aac agc gaa ccg ttg gta 480
 Val Asn Ser Phe Val Ala Arg Tyr Arg Asp Asn Ser Glu Pro Leu Val
 145 150 155 160

 tcg ctg gaa acc ccg atg cgc ttt aac ccg aac ctc gat ccc gcg tgg 528

Ser	Leu	Glu	Thr	Arg	Met	Arg	Phe	Asn	Pro	Asn	Leu	Asp	Pro	Ala	Trp		
				165					170					175			
ttt	ggc	ggg	gtg	atg	gcg	atc	atc	aac	aac	att	acc	atg	ctg	gcg	att	576	
Phe	Gly	Gly	Val	Met	Ala	Ile	Ile	Asn	Asn	Ile	Thr	Met	Leu	Ala	Ile		
			180					185					190				
gta	ttg	acc	gga	tcg	gcg	ctg	atc	cgc	gag	cgt	gaa	cac	ggc	acg	gtg	624	
Val	Leu	Thr	Gly	Ser	Ala	Leu	Ile	Arg	Glu	Arg	Glu	His	Gly	Thr	Val		
			195				200					205					
gaa	cac	tta	ctg	gtg	atg	ccg	ata	acg	ccg	ttt	gag	atc	atg	atg	gcg	672	
Glu	His	Leu	Leu	Val	Met	Pro	Ile	Thr	Pro	Phe	Glu	Ile	Met	Met	Ala		
	210					215					220						
aag	atc	tgg	tcg	atg	ggg	ctg	gtg	gtg	ctg	gtg	gta	tcg	gga	tta	tcg	720	
Lys	Ile	Trp	Ser	Met	Gly	Leu	Val	Val	Leu	Val	Val	Ser	Gly	Leu	Ser		
225					230				235					240			
ctg	gtg	ctg	atg	gtg	aaa	ggc	gta	ctg	ggc	gta	ccg	att	gaa	ggc	tcg	768	
Leu	Val	Leu	Met	Val	Lys	Gly	Val	Leu	Gly	Val	Pro	Ile	Glu	Gly	Ser		
			245					250					255				
atc	ccg	ctg	ttt	atg	ctg	ggc	gtg	gcg	ctc	agt	ctg	ttt	gcc	acc	acg	816	
Ile	Pro	Leu	Phe	Met	Leu	Gly	Val	Ala	Leu	Ser	Leu	Phe	Ala	Thr	Thr		
			260				265						270				
tca	atc	ggc	att	ttt	atg	ggg	acg	ata	gcg	cgt	tca	atg	ccg	caa	ctg	864	
Ser	Ile	Gly	Ile	Phe	Met	Gly	Thr	Ile	Ala	Arg	Ser	Met	Pro	Gln	Leu		
		275					280					285					
ggg	ctg	ctg	gtg	att	ctg	gtg	ctg	ctg	ccg	ctg	caa	atg	ctt	tcc	ggc	912	
Gly	Leu	Leu	Val	Ile	Leu	Val	Leu	Leu	Pro	Leu	Gln	Met	Leu	Ser	Gly		
	290					295					300						
ggc	tcc	acg	ccg	cgc	gaa	agt	atg	ccg	cag	atg	gtg	cag	gac	att	atg	960	
Gly	Ser	Thr	Pro	Arg	Glu	Ser	Met	Pro	Gln	Met	Val	Gln	Asp	Ile	Met		
305				310				315						320			
ctg	acc	atg	ccg	acg	aca	cac	ttt	gtt	agc	ctc	gcg	cag	gcc	atc	ctc	1008	
Leu	Thr	Met	Pro	Thr	Thr	His	Phe	Val	Ser	Leu	Ala	Gln	Ala	Ile	Leu		
			325					330					335				
tac	cgg	ggc	gcc	gga	ttc	gaa	atc	gtc	tgg	ccg	cag	ttt	ctg	acg	ctg	1056	
Tyr	Arg	Gly	Ala	Gly	Phe	Glu	Ile	Val	Trp	Pro	Gln	Phe	Leu	Thr	Leu		
		340						345				350					
atg	gca	att	ggc	ggc	gca	ttt	ttc	acc	att	gcg	ctg	ctg	cga	ttc	agg	1104	
Met	Ala	Ile	Gly	Gly	Ala	Phe	Phe	Thr	Ile	Ala	Leu	Leu	Arg	Phe	Arg		
		355				360						365					
aag	acg	att	ggg	aca	atg	gcg	taa									1128	
Lys	Thr	Ile	Gly	Thr	Met	Ala	*										
	370					375											

<210> 241

<211> 2685

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(2685)

<400> 241

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gat att ccg gcc cgc tgt atg gtc ggg ctg att ggc ccg gac ggc gtc 96
Asp Ile Pro Ala Arg Cys Met Val Gly Leu Ile Gly Pro Asp Gly Val
20 25 30

ggg aag tcg agc ttg ttg tgc ttg att tcc ggt gcc cgc gtc att gaa 144
Gly Lys Ser Ser Leu Leu Ser Leu Ile Ser Gly Ala Arg Val Ile Glu
35 40 45

cag ggc aat gtg atg gtg ctg ggc ggc gat atg cgc gac ccg aag cat 192
Gln Gly Asn Val Met Val Leu Gly Gly Asp Met Arg Asp Pro Lys His
50 55 60

cgc cgc gac gtc tgc ccg cgc atc gcc tgg atg ccg cag ggg ctg ggc 240
Arg Arg Asp Val Cys Pro Arg Ile Ala Trp Met Pro Gln Gly Leu Gly
65 70 75 80

aaa aac ctc tac cac acc ttg tgc gtg tat gaa aac gtc gat ttt ttc 288
Lys Asn Leu Tyr His Thr Leu Ser Val Tyr Glu Asn Val Asp Phe Phe
85 90 95

gct cgc ctg ttc ggt cac gac aaa gcg gag cgg gaa gtg cga atc aat 336
Ala Arg Leu Phe Gly His Asp Lys Ala Glu Arg Glu Val Arg Ile Asn
100 105 110

gag ctg ctg acc agc acc ggg tta gca ccg ttt cgc gat cgt ccg gca 384
Glu Leu Leu Thr Ser Thr Gly Leu Ala Pro Phe Arg Asp Arg Pro Ala
115 120 125

ggg aaa ctc tcc ggc ggg atg aag caa aaa ctt ggg ctg tgc tgc gcg 432
Gly Lys Leu Ser Gly Gly Met Lys Gln Lys Leu Gly Leu Cys Cys Ala
130 135 140

tta atc cac gac ccg gaa ctg ttg atc ctt gat gag cca aca acg ggg 480
Leu Ile His Asp Pro Glu Leu Leu Ile Leu Asp Glu Pro Thr Thr Gly
145 150 155 160

gtt gac ccg ctc tcc cgc tcc cag ttc tgg gat ctg atc gac agt att 528
Val Asp Pro Leu Ser Arg Ser Gln Phe Trp Asp Leu Ile Asp Ser Ile
165 170 175

cgc cag cgg cag agc aat atg agc gtg ctg gtc gcc acc gcc tat atg 576
Arg Gln Arg Gln Ser Asn Met Ser Val Leu Val Ala Thr Ala Tyr Met
180 185 190

gaa gag gcc gaa cgc ttc gac tgg ctg gta gcg atg aat gcc gga gaa 624
Glu Glu Ala Glu Arg Phe Asp Trp Leu Val Ala Met Asn Ala Gly Glu
195 200 205

gtg ctg gca act ggc agc gcc gaa gag cta cgg cag caa acg caa agc 672
Val Leu Ala Thr Gly Ser Ala Glu Glu Leu Arg Gln Gln Thr Gln Ser
210 215 220

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gct acg ctg gaa gaa gca ttt ata aat ctg tta ccg caa gcg caa cgc	720
Ala Thr Leu Glu Glu Ala Phe Ile Asn Leu Leu Pro Gln Ala Gln Arg	
225 230 235 240	
cag gcg cat cag gcg gta gtg atc cca ccg tat caa cct gaa aac gca	768
Gln Ala His Gln Ala Val Val Ile Pro Pro Tyr Gln Pro Glu Asn Ala	
245 250 255	
gag att gcc atc gaa gcg cgc gat ctg acc atg cgt ttt ggt tcc ttc	816
Glu Ile Ala Ile Glu Ala Arg Asp Leu Thr Met Arg Phe Gly Ser Phe	
260 265 270	
gtt gcc gtt gat cac gtt aat ttc cgc att cca cgc ggg gag att ttt	864
Val Ala Val Asp His Val Asn Phe Arg Ile Pro Arg Gly Glu Ile Phe	
275 280 285	
ggg ttt ctt ggt tgc aac ggc tgc ggt aaa tcc acc acc atg aaa atg	912
Gly Phe Leu Gly Ser Asn Gly Cys Gly Lys Ser Thr Thr Met Lys Met	
290 295 300	
ctc acc gga ctg ctg ccc gcc agc gaa ggt gag gcg tgg ctg ttc ggg	960
Leu Thr Gly Leu Leu Pro Ala Ser Glu Gly Glu Ala Trp Leu Phe Gly	
305 310 315 320	
caa ccg gtt gat cca aaa gat atc gat acc cgc cgt cgg gtg ggc tat	1008
Gln Pro Val Asp Pro Lys Asp Ile Asp Thr Arg Arg Arg Val Gly Tyr	
325 330 335	
atg tgc cag gcg ttt tgc ctc tat aac gaa ctc acc gtg cgg caa aac	1056
Met Ser Gln Ala Phe Ser Leu Tyr Asn Glu Leu Thr Val Arg Gln Asn	
340 345 350	
ctt gag tta cat gcc cgt ttg ttt cac atc ccg gaa gcg gaa att ccc	1104
Leu Glu Leu His Ala Arg Leu Phe His Ile Pro Glu Ala Glu Ile Pro	
355 360 365	
gca aga gtg gct gaa atg agc gag cgt ttt aag ctc aac gac gtt gaa	1152
Ala Arg Val Ala Glu Met Ser Glu Arg Phe Lys Leu Asn Asp Val Glu	
370 375 380	
gat att ctg ccg gag tca ttg ccg ctc ggc att cgc cag cgg ctt tgc	1200
Asp Ile Leu Pro Glu Ser Leu Pro Leu Gly Ile Arg Gln Arg Leu Ser	
385 390 395 400	
ctg gcg gtg gcg gtg att cat cgc ccg gag atg tta atc ctc gat gag	1248
Leu Ala Val Ala Val Ile His Arg Pro Glu Met Leu Ile Leu Asp Glu	
405 410 415	
cct act tct ggt gtc gat ccg gtg gcg agg gat atg ttc tgg cag ttg	1296
Pro Thr Ser Gly Val Asp Pro Val Ala Arg Asp Met Phe Trp Gln Leu	
420 425 430	
atg gtc gat ctc tgc cgc cag gac aaa gtg act atc ttc atc tcc acc	1344
Met Val Asp Leu Ser Arg Gln Asp Lys Val Thr Ile Phe Ile Ser Thr	
435 440 445	
cac ttt atg aac gaa gcg gaa cgt tgc gac cgc atc tca ctg atg cac	1392
His Phe Met Asn Glu Ala Glu Arg Cys Asp Arg Ile Ser Leu Met His	
450 455 460	
gcc gga aaa gtg ctt gcc agc ggt aca ccg cag gaa ctg gtt gag aaa	1440

Ala Gly Lys Val Leu Ala Ser Gly Thr Pro Gln Glu Leu Val Glu Lys	
465 470 475 480	
cgc gga gcc gcc agt ctg gaa gag gca ttt atc gcc tat ttg cag gaa	1488
Arg Gly Ala Ala Ser Leu Glu Glu Ala Phe Ile Ala Tyr Leu Gln Glu	
485 490 495	
gcg gca ggg cag agc aac gaa gcc gaa gcg ccg ccc gtg gta cac gac	1536
Ala Ala Gly Gln Ser Asn Glu Ala Glu Ala Pro Pro Val Val His Asp	
500 505 510	
acc acc cac gcg ccg cgt cag gga ttt agc ctg cgc cgt ctg ttt agc	1584
Thr Thr His Ala Pro Arg Gln Gly Phe Ser Leu Arg Arg Leu Phe Ser	
515 520 525	
tac agc cgc cgc gaa gcg ctg gaa ctg cga cgc gat cca gta cgt tgc	1632
Tyr Ser Arg Arg Glu Ala Leu Glu Leu Arg Arg Asp Pro Val Arg Ser	
530 535 540	
acg ctg gcg ctg atg gga acg gtg atc ctg atg ctg ata atg ggt tac	1680
Thr Leu Ala Leu Met Gly Thr Val Ile Leu Met Leu Ile Met Gly Tyr	
545 550 555 560	
ggc atc agt atg gat gtg gaa aac ctg cgc ttt gcg gtg ctc gac cgc	1728
Gly Ile Ser Met Asp Val Glu Asn Leu Arg Phe Ala Val Leu Asp Arg	
565 570 575	
gac cag acc gtc agt agc cag gcg tgg aca ctc aac ctc tcc ggt tcc	1776
Asp Gln Thr Val Ser Ser Gln Ala Trp Thr Leu Asn Leu Ser Gly Ser	
580 585 590	
cgt tac ttt atc gaa cag ccg ccg ctc acc agt tat gac gag ctt gat	1824
Arg Tyr Phe Ile Glu Gln Pro Leu Thr Ser Tyr Asp Glu Leu Asp	
595 600 605	
cgt cgg atg cgt gcg ggc gat atc acg gtg gcg att gag atc ccg ccc	1872
Arg Arg Met Arg Ala Gly Asp Ile Thr Val Ala Ile Glu Ile Pro Pro	
610 615 620	
aat ttc ggg cgc gat atc gcg cgt ggt acg cct gtg gaa ctc ggc gtc	1920
Asn Phe Gly Arg Asp Ile Ala Arg Gly Thr Pro Val Glu Leu Gly Val	
625 630 635 640	
tgg atc gac gga gcg atg ccg agc cgt gct gaa acg gta aaa ggt tac	1968
Trp Ile Asp Gly Ala Met Pro Ser Arg Ala Glu Thr Val Lys Gly Tyr	
645 650 655	
gtg cag gcc atg cac cag agc tgg tta cag gat gtg gcg agc cga caa	2016
Val Gln Ala Met His Gln Ser Trp Leu Gln Asp Val Ala Ser Arg Gln	
660 665 670	
tcg aca ccc gcc agc caa agc ggg ctg atg aat att gag acg cgc tat	2064
Ser Thr Pro Ala Ser Gln Ser Gly Leu Met Asn Ile Glu Thr Arg Tyr	
675 680 685	
cgc tat aac ccg gac gta aaa agc ctg cca gcg att gtt ccg gcg gtg	2112
Arg Tyr Asn Pro Asp Val Lys Ser Leu Pro Ala Ile Val Pro Ala Val	
690 695 700	
atc ccg ctt ctg ctg atg atg atc ccg tca atg cta agc gcc ctt agc	2160
Ile Pro Leu Leu Leu Met Met Ile Pro Ser Met Leu Ser Ala Leu Ser	

705	710	715	720	
gtg gtg cgg gaa aaa gag ctt ggg tcg att atc aac ctt tac gtg acc				2208
Val Val Arg Glu Lys	Glu Leu Gly Ser	Ile Ile Asn Leu Tyr	Val Thr	
	725	730	735	
ccc acc acg cgt agt gaa ttt ttg ctt ggt aaa cag ttg cca tac atc				2256
Pro Thr Thr Arg Ser	Glu Phe Leu Leu	Gly Lys Gln Leu	Pro Tyr Ile	
	740	745	750	
gcg ctg ggg atg ctg aac ttt ttc ctg ctc tgc ggc ctg tcg gtg ttt				2304
Ala Leu Gly Met Leu	Asn Phe Phe Leu	Leu Cys Gly Leu	Ser Val Phe	
	755	760	765	
gtg ttt ggc gta ccg cat aaa ggc agt ttc ctg acg ctc acc ctg gcg				2352
Val Phe Gly Val Pro	His Lys Gly Ser	Phe Leu Thr	Leu Thr Leu Ala	
	770	775	780	
gcg ctg ctg tat atc atc att gcc acc gga atg ggg ctg ctg atc tcc				2400
Ala Leu Leu Tyr Ile	Ile Ile Ala Thr	Gly Met Gly Leu	Leu Ile Ser	
	785	790	800	
acc ttt atg aaa agc cag att gcc gcc att ttc gga acg gcg att atc				2448
Thr Phe Met Lys Ser	Gln Ile Ala Ala	Ile Phe Gly Thr	Ala Ile Ile	
	805	810	815	
acg ttg atc ccg gcg aca cag ttt tcc ggg atg atc gat ccg gta gct				2496
Thr Leu Ile Pro	Ala Thr Gln Phe	Ser Gly Met Ile	Asp Pro Val Ala	
	820	825	830	
tcg ctg gaa ggg cct gga cgt tgg atc ggc gag gtt tac ccg acc agt				2544
Ser Leu Glu Gly Pro	Gly Arg Trp Ile	Gly Glu Val Tyr	Pro Thr Ser	
	835	840	845	
cat ttt ctg act atc gcc cgc ggg acg ttc tcg aaa gcg ctg gat ctg				2592
His Phe Leu Thr Ile	Ala Arg Gly Thr	Phe Ser Lys Ala	Leu Asp Leu	
	850	855	860	
act gat ttg tgg caa ctt ttt atc ccg tta ctg ata gcc atc ccg ctg				2640
Thr Asp Leu Trp Gln	Leu Phe Ile Pro	Leu Leu Ile Ala	Ile Pro Leu	
	865	870	875	880
gtg atg ggc tta agt atc ctg ctg ctg aaa aaa cag gag gga tga				2685
Val Met Gly Leu Ser	Ile Leu Leu Leu	Lys Lys Gln Glu	Gly *	
	885	890		

<210> 242

<211> 1068

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (1068)

<400> 242

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Met Asp Lys Ser Lys Arg His Leu Ala Trp Trp Val Val Gly Leu Leu	
1 5 10 15	

gcg gtg gcg gct atc gtg gcg tgg tgg ctg ttg cgc ccg gca ggt gtg	96
Ala Val Ala Ala Ile Val Ala Trp Trp Leu Leu Arg Pro Ala Gly Val	
20 25 30	
ccg gaa ggc ttt gct gtc agt aat ggg cgc att gaa gcg acg gaa gtg	144
Pro Glu Gly Phe Ala Val Ser Asn Gly Arg Ile Glu Ala Thr Glu Val	
35 40 45	
gat att gcc agc aaa att gcc ggg cgt atc gac acc att ctg gtg aaa	192
Asp Ile Ala Ser Lys Ile Ala Gly Arg Ile Asp Thr Ile Leu Val Lys	
50 55 60	
gaa ggc aag ttt gtt cgc gaa ggt gaa gtg ctg gcg aag atg gat act	240
Glu Gly Lys Phe Val Arg Glu Gly Glu Val Leu Ala Lys Met Asp Thr	
65 70 75 80	
cgc gtg ttg cag gaa cag cga ctg gaa gcc atc gcg caa atc aaa gag	288
Arg Val Leu Gln Glu Gln Arg Leu Glu Ala Ile Ala Gln Ile Lys Glu	
85 90 95	
gca caa agc gcc gtt gct gcc gcg cag gct ttg ctg gag caa cga caa	336
Ala Gln Ser Ala Val Ala Ala Ala Gln Ala Leu Leu Glu Gln Arg Gln	
100 105 110	
agc gaa act cgt gcc gca cag tgc ctg gtt aat caa cgc cag gca gaa	384
Ser Glu Thr Arg Ala Ala Gln Ser Leu Val Asn Gln Arg Gln Ala Glu	
115 120 125	
ctg gac tcc gta gca aaa cgt cat acg cgt tcc cgt tca ctg gcc caa	432
Leu Asp Ser Val Ala Lys Arg His Thr Arg Ser Arg Ser Leu Ala Gln	
130 135 140	
cga ggg gct att tct gcg caa cag ctg gat gac gat cgc gcc gcc gct	480
Arg Gly Ala Ile Ser Ala Gln Gln Leu Asp Asp Asp Arg Ala Ala Ala	
145 150 155 160	
gag agc gcc cga gct gcg ctg gaa tgc gcg aaa gct cag gta tgc gct	528
Glu Ser Ala Arg Ala Ala Leu Glu Ser Ala Lys Ala Gln Val Ser Ala	
165 170 175	
tct aaa gcg gct ata gaa gcg gca cgc acc aat atc att cag gcg caa	576
Ser Lys Ala Ala Ile Glu Ala Ala Arg Thr Asn Ile Ile Gln Ala Gln	
180 185 190	
acc cgc gtc gaa gcg gca caa gcc act gaa cgg cgc att gcc gca gat	624
Thr Arg Val Glu Ala Ala Gln Ala Thr Glu Arg Arg Ile Ala Ala Asp	
195 200 205	
atc gat gac agc gaa ctg aaa gcc ccg cgt gac gga cgc gtg cag tat	672
Ile Asp Asp Ser Glu Leu Lys Ala Pro Arg Asp Gly Arg Val Gln Tyr	
210 215 220	
cgg gtt gcc gag cca ggc gaa gtg ctg gcg gca ggc ggt cgg gtg ctg	720
Arg Val Ala Glu Pro Gly Glu Val Leu Ala Ala Gly Gly Arg Val Leu	
225 230 235 240	
aat atg gtc gat ctc agc gac gtc tat atg act ttc ttc ctg cca acc	768
Asn Met Val Asp Leu Ser Asp Val Tyr Met Thr Phe Phe Leu Pro Thr	
245 250 255	

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gaa cag gcg ggc acg ctg aaa ctg ggc ggt gaa gcc cgg ctg atc ctc 816
Glu Gln Ala Gly Thr Leu Lys Leu Gly Gly Glu Ala Arg Leu Ile Leu
      260              265              270

gat gcc gcg cca gat ctg cgt att cct gca acc atc agt ttt gtc gcc 864
Asp Ala Ala Pro Asp Leu Arg Ile Pro Ala Thr Ile Ser Phe Val Ala
      275              280              285

agt gtc gcc cag ttc acg cca aaa acc gtc gaa acc agc gat gaa cgg 912
Ser Val Ala Gln Phe Thr Pro Lys Thr Val Glu Thr Ser Asp Glu Arg
      290              295              300

ctg aaa ctg atg ttc cgc gtc aaa gcg cgt atc cca ccg gaa tta ctc 960
Leu Lys Leu Met Phe Arg Val Lys Ala Arg Ile Pro Pro Glu Leu Leu
305              310              315              320

cag cag cat ctg gaa tat gtc aaa acc ggt ttg ccg ggc gta gcg tgg 1008
Gln Gln His Leu Glu Tyr Val Lys Thr Gly Leu Pro Gly Val Ala Trp
      325              330              335

gtg cgg gtg aat gaa gaa ctt ccg tgg cct gac gac ctc gtg gtg agg 1056
Val Arg Val Asn Glu Glu Leu Pro Trp Pro Asp Asp Leu Val Val Arg
      340              345              350

ttg ccg caa tga 1068
Leu Pro Gln *
      355

<210> 243
<211> 708
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(708)

<400> 243
atg tac cgt tat ttg tct att gct gcg gtg gta ctg agc gca gca ttt 48
Met Tyr Arg Tyr Leu Ser Ile Ala Ala Val Val Leu Ser Ala Ala Phe
  1              5              10              15

tcc ggc ccg gcg ttg gcc gaa ggt atc aat agt ttt tct cag gcg aaa 96
Ser Gly Pro Ala Leu Ala Glu Gly Ile Asn Ser Phe Ser Gln Ala Lys
      20              25              30

gcc gcg gcg gta aaa gtc cac gct gac gcg ccc ggt acg ttt tat tgc 144
Ala Ala Ala Val Lys Val His Ala Asp Ala Pro Gly Thr Phe Tyr Cys
      35              40              45

gga tgt aaa att aac tgg cag ggc aaa aaa ggc gtt gtt gat ctg caa 192
Gly Cys Lys Ile Asn Trp Gln Gly Lys Lys Gly Val Val Asp Leu Gln
      50              55              60

tcg tgc ggc tat cag gtg cgc aaa aat gaa aac cgc gcc agc cgc gta 240
Ser Cys Gly Tyr Gln Val Arg Lys Asn Glu Asn Arg Ala Ser Arg Val
      65              70              75              80

gag tgg gaa cat gtc gtt ccc gcc tgg cag ttc ggt cac cag cgc cag 288
Glu Trp Glu His Val Val Pro Ala Trp Gln Phe Gly His Gln Arg Gln

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	85	90	95	
tgc tgg cag gac ggt gga cgt aaa aac tgc gct aaa gat ccg gtc tat				336
Cys Trp Gln Asp Gly Gly Arg Lys Asn Cys Ala Lys Asp Pro Val Tyr				
	100	105	110	
cgc aag atg gaa agc gat atg cat aac ctg cag ccg tca gtc ggt gag				384
Arg Lys Met Glu Ser Asp Met His Asn Leu Gln Pro Ser Val Gly Glu				
	115	120	125	
gtg aat ggc gat cgc ggc aac ttt atg tac agc cag tgg aat ggc ggt				432
Val Asn Gly Asp Arg Gly Asn Phe Met Tyr Ser Gln Trp Asn Gly Gly				
	130	135	140	
gaa ggc cag tac ggt caa tgc gcc atg aag gtc gat ttc aaa gaa aaa				480
Glu Gly Gln Tyr Gly Gln Cys Ala Met Lys Val Asp Phe Lys Glu Lys				
	145	150	155	160
gct gcc gaa cca cca gcg cgt gca cgc ggt gcc att gcg cgc acc tac				528
Ala Ala Glu Pro Pro Ala Arg Ala Arg Gly Ala Ile Ala Arg Thr Tyr				
	165	170	175	
ttc tat atg cgc gac caa tac aac ctg aca ctc tct cgc cag caa acg				576
Phe Tyr Met Arg Asp Gln Tyr Asn Leu Thr Leu Ser Arg Gln Gln Thr				
	180	185	190	
cag ctg ttc aac gca tgg aac aag atg tat ccg gtt acc gac tgg gag				624
Gln Leu Phe Asn Ala Trp Asn Lys Met Tyr Pro Val Thr Asp Trp Glu				
	195	200	205	
tgc gag cgc gat gaa cgc atc gcg aag gtg cag ggc aat cat aac ccg				672
Cys Glu Arg Asp Glu Arg Ile Ala Lys Val Gln Gly Asn His Asn Pro				
	210	215	220	
tat gtg caa cgc gct tgc cag gcg cga aag agc taa				708
Tyr Val Gln Arg Ala Cys Gln Ala Arg Lys Ser *				
	225	230	235	

<210> 244

<211> 1443

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (1443)

<400> 244

atg tcc aga agg ctt cgc aga aca aaa atc gtt acc acg tta ggc cca				48
Met Ser Arg Arg Leu Arg Arg Thr Lys Ile Val Thr Thr Leu Gly Pro				
1	5	10	15	
gca aca gat cgc gat aat aat ctt gaa aaa gtt atc gcg gcg ggt gcc				96
Ala Thr Asp Arg Asp Asn Asn Leu Glu Lys Val Ile Ala Ala Gly Ala				
	20	25	30	
aac gtt gta cgt atg aac ttt tct cac ggc tog cct gaa gat cac aaa				144
Asn Val Val Arg Met Asn Phe Ser His Gly Ser Pro Glu Asp His Lys				
	35	40	45	

atg cgc gcg gat aaa gtt cgt gag att gcc gca aaa ctg ggg cgt cat	192
Met Arg Ala Asp Lys Val Arg Glu Ile Ala Ala Lys Leu Gly Arg His	
50 55 60	
gtg gct att ctg ggt gac ctc cag ggg ccc aaa atc cgt gta tcc acc	240
Val Ala Ile Leu Gly Asp Leu Gln Gly Pro Lys Ile Arg Val Ser Thr	
65 70 75 80	
ttt aaa gaa ggc aaa gtt ttc ctc aat att ggg gat aaa ttc ctg ctc	288
Phe Lys Glu Gly Lys Val Phe Leu Asn Ile Gly Asp Lys Phe Leu Leu	
85 90 95	
gac gcc aac ctg ggt aaa ggt gaa ggc gac aaa gaa aaa gtc ggt atc	336
Asp Ala Asn Leu Gly Lys Gly Glu Gly Asp Lys Glu Lys Val Gly Ile	
100 105 110	
gac tac aaa ggc ctg cct gct gac gtc gtg cct ggt gac atc ctg ctg	384
Asp Tyr Lys Gly Leu Pro Ala Asp Val Val Pro Gly Asp Ile Leu Leu	
115 120 125	
ctg gac gat ggt cgc gtc cag tta aaa gta ctg gaa gtt cag ggc atg	432
Leu Asp Asp Gly Arg Val Gln Leu Lys Val Leu Glu Val Gln Gly Met	
130 135 140	
aaa gtg ttc acc gaa gtc acc gtc ggt ggt ccc ctc tcc aac aat aaa	480
Lys Val Phe Thr Glu Val Thr Val Gly Gly Pro Leu Ser Asn Asn Lys	
145 150 155 160	
ggt atc aac aaa ctt ggc ggc ggt ttg tgc gct gaa gcg ctg acc gaa	528
Gly Ile Asn Lys Leu Gly Gly Gly Leu Ser Ala Glu Ala Leu Thr Glu	
165 170 175	
aaa gac aaa gca gac att aag act gcg gcg ttg att ggc gta gat tac	576
Lys Asp Lys Ala Asp Ile Lys Thr Ala Ala Leu Ile Gly Val Asp Tyr	
180 185 190	
ctg gct gtc tcc ttc cca cgc tgt ggc gaa gat ctg aac tat gcc cgt	624
Leu Ala Val Ser Phe Pro Arg Cys Gly Glu Asp Leu Asn Tyr Ala Arg	
195 200 205	
cgc ctg gca cgc gat gca gga tgt gat gcg aaa att gtt gcc aag gtt	672
Arg Leu Ala Arg Asp Ala Gly Cys Asp Ala Lys Ile Val Ala Lys Val	
210 215 220	
gaa cgt gcg gaa gcc gtt tgc agc cag gat gca atg gat gac atc atc	720
Glu Arg Ala Glu Ala Val Cys Ser Gln Asp Ala Met Asp Asp Ile Ile	
225 230 235 240	
ctc gcc tct gac gtg gta atg gtt gca cgt ggc gac ctc ggt gtg gaa	768
Leu Ala Ser Asp Val Val Met Val Ala Arg Gly Asp Leu Gly Val Glu	
245 250 255	
att ggc gac ccg gaa ctg gtc ggc att cag aaa gcg ttg atc cgt cgt	816
Ile Gly Asp Pro Glu Leu Val Gly Ile Gln Lys Ala Leu Ile Arg Arg	
260 265 270	
gcg cgt cag cta aac cga gcg gta atc acg gcg acc cag atg atg gag	864
Ala Arg Gln Leu Asn Arg Ala Val Ile Thr Ala Thr Gln Met Met Glu	
275 280 285	
cca atg att act aac ccg atg ccg acg cgt gca gaa gtc atg gac gta	912

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Ser Met Ile Thr Asn Pro Met Pro Thr Arg Ala Glu Val Met Asp Val
290                               295                               300

gca aac gcc gtt ctg gat ggt act gac gct gtg atg ctg tct gca gaa 960
Ala Asn Ala Val Leu Asp Gly Thr Asp Ala Val Met Leu Ser Ala Glu
305                               310                               315                               320

act gcc gct ggg cag tat ccg tca gaa acc gtt gca gcc atg gcg cgc 1008
Thr Ala Ala Gly Gln Tyr Pro Ser Glu Thr Val Ala Ala Met Ala Arg
                               325                               330                               335

gtt tgc ctg ggt gcg gaa aaa atc ccg agc atc aac gtt tct aaa cac 1056
Val Cys Leu Gly Ala Glu Lys Ile Pro Ser Ile Asn Val Ser Lys His
                               340                               345                               350

cgt ctg gac gtt cag ttc gac aat gtg gaa gaa gct att gcc atg tca 1104
Arg Leu Asp Val Gln Phe Asp Asn Val Glu Glu Ala Ile Ala Met Ser
                               355                               360                               365

gca atg tac gca gct aac cac ctg aaa ggc gtt acg gcg atc atc acc 1152
Ala Met Tyr Ala Ala Asn His Leu Lys Gly Val Thr Ala Ile Ile Thr
                               370                               375                               380

atg acc gaa tcg ggt cgt acc gcg ctg atg acc tcc cgt atc agc tct 1200
Met Thr Glu Ser Gly Arg Thr Ala Leu Met Thr Ser Arg Ile Ser Ser
385                               390                               395                               400

ggt ctg cca att ttc gcc atg tcg cgc cat gaa cgt acg ctg aac ctg 1248
Gly Leu Pro Ile Phe Ala Met Ser Arg His Glu Arg Thr Leu Asn Leu
                               405                               410                               415

act gct ctc tat cgt ggc gtt acg ccg gtg cac ttt gat agc gct aat 1296
Thr Ala Leu Tyr Arg Gly Val Thr Pro Val His Phe Asp Ser Ala Asn
                               420                               425                               430

gac ggc gta gca gct gcc agc gaa gcg gtt aat ctg ctg cgc gat aaa 1344
Asp Gly Val Ala Ala Ala Ser Glu Ala Val Asn Leu Leu Arg Asp Lys
                               435                               440                               445

ggt tac ttg atg tct ggt gac ctg gtg att gtc acc cag ggc gac gtg 1392
Gly Tyr Leu Met Ser Gly Asp Leu Val Ile Val Thr Gln Gly Asp Val
                               450                               455                               460

atg agt acc gtg ggt tct act aat acc acg cgt att tta acg gta gag 1440
Met Ser Thr Val Gly Ser Thr Asn Thr Thr Arg Ile Leu Thr Val Glu
465                               470                               475                               480

taa
*
1443

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<210> 245

<211> 720

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(720)

<400> 245

atg atc aat gta tta att atc gat gac gac gca atg gtc gcg gag ctg	48
Met Ile Asn Val Leu Ile Ile Asp Asp Ala Met Val Ala Glu Leu	
1 5 10 15	
aat cgc cga tac gta gca caa atc cca ggc ttt caa tgc tgt gga aca	96
Asn Arg Arg Tyr Val Ala Gln Ile Pro Gly Phe Gln Cys Cys Gly Thr	
20 25 30	
gcc tcg acg ctg gag aaa gcc aaa gag att atc ttc aat agc gat acg	144
Ala Ser Thr Leu Glu Lys Ala Lys Glu Ile Ile Phe Asn Ser Asp Thr	
35 40 45	
cct atc gac ctg ata ttg ctc gat atc tat atg caa aaa gag aac ggg	192
Pro Ile Asp Leu Ile Leu Leu Asp Ile Tyr Met Gln Lys Glu Asn Gly	
50 55 60	
ctc gat tta ctg cct gtc ctg cat aac gcg cgt tgc aaa agt gat gtg	240
Leu Asp Leu Leu Pro Val Leu His Asn Ala Arg Cys Lys Ser Asp Val	
65 70 75 80	
att gtc atc tcc tcc gca gcc gat gcg gca acc att aaa gat tcg ctg	288
Ile Val Ile Ser Ser Ala Ala Asp Ala Ala Thr Ile Lys Asp Ser Leu	
85 90 95	
cat tac ggt gtc gtg gat tac ctg atc aaa ccc ttc cag gct tcc cgc	336
His Tyr Gly Val Val Asp Tyr Leu Ile Lys Pro Phe Gln Ala Ser Arg	
100 105 110	
ttt gaa gag gcg ctc acc ggc tgg cgg caa aag aaa atg gcg ctg gaa	384
Phe Glu Glu Ala Leu Thr Gly Trp Arg Gln Lys Lys Met Ala Leu Glu	
115 120 125	
aaa cat cag tat tat gac cag gcc gag ctt gat cag cta atc cac ggc	432
Lys His Gln Tyr Tyr Asp Gln Ala Glu Leu Asp Gln Leu Ile His Gly	
130 135 140	
agc agc tcc aac gaa cag gat cct cgt cgc ttg cca aaa ggc tta acg	480
Ser Ser Ser Asn Glu Gln Asp Pro Arg Arg Leu Pro Lys Gly Leu Thr	
145 150 155 160	
ccg cag acg tta cgc aca ctg tgc cag tgg att gac gcg cat cag gac	528
Pro Gln Thr Leu Arg Thr Leu Cys Gln Trp Ile Asp Ala His Gln Asp	
165 170 175	
tat gaa ttt tca acc gac gag cta gcc aac gag gtt aac att tcg cgt	576
Tyr Glu Phe Ser Thr Asp Glu Leu Ala Asn Glu Val Asn Ile Ser Arg	
180 185 190	
gtt tcc tgc cgt aaa tac ctc atc tgg ctg gtc aac tgc cac atc ttg	624
Val Ser Cys Arg Lys Tyr Leu Ile Trp Leu Val Asn Cys His Ile Leu	
195 200 205	
ttc acc agt atc cat tat ggc gtc acg ggg cgt cca gtt tac cgt tac	672
Phe Thr Ser Ile His Tyr Gly Val Thr Gly Arg Pro Val Tyr Arg Tyr	
210 215 220	
cgt att cag gca gaa cac tac tca cta ctg aaa caa tat tgc caa taa	720
Arg Ile Gln Ala Glu His Tyr Ser Leu Leu Lys Gln Tyr Cys Gln *	
225 230 235	

<210> 246
 <211> 1632
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1632)

<400> 246
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 Met Arg His Ser Leu Pro Tyr Arg Met Leu Arg Lys Arg Pro Met Lys
 1 5 10 15
 ttg agt acc aca gtg atc tta atg gtc agt gcg gta ctg ttc tcg gtg 96
 Leu Ser Thr Thr Val Ile Leu Met Val Ser Ala Val Leu Phe Ser Val
 20 25 30
 cta ttg gtg gtg cat ctg att tac ttc tcg caa atc agt gat atg acg 144
 Leu Leu Val Val His Leu Ile Tyr Phe Ser Gln Ile Ser Asp Met Thr
 35 40 45
 cga gat ggg cta gcc aac aag gca ctg gca gtg gcg cgt acc ctc gcc 192
 Arg Asp Gly Leu Ala Asn Lys Ala Leu Ala Val Ala Arg Thr Leu Ala
 50 55 60
 gac tcg ccg gaa atc cgt cag ggc ttg cag aaa aaa ccg cag gag agt 240
 Asp Ser Pro Glu Ile Arg Gln Gly Leu Gln Lys Lys Pro Gln Glu Ser
 65 70 75 80
 ggc atc cag gcc atc gcg gaa gcc gta cgc aaa cgc aac gat ctg ctg 288
 Gly Ile Gln Ala Ile Ala Glu Ala Val Arg Lys Arg Asn Asp Leu Leu
 85 90 95
 ttt att gtc gtt acc gat atg caa agt ctt cgc tac tcg cat cct gaa 336
 Phe Ile Val Val Thr Asp Met Gln Ser Leu Arg Tyr Ser His Pro Glu
 100 105 110
 gcc cag cgt att ggt cag cca ttt aaa ggt gat gac atc ctt aaa gcg 384
 Ala Gln Arg Ile Gly Gln Pro Phe Lys Gly Asp Asp Ile Leu Lys Ala
 115 120 125
 ctg aat ggc gaa gaa aat gtc gct atc aat cgc ggt ttt ctg gcg cag 432
 Leu Asn Gly Glu Glu Asn Val Ala Ile Asn Arg Gly Phe Leu Ala Gln
 130 135 140
 gct tta cgc gta ttt acc ccc atc tac gat gaa aat cat aaa caa att 480
 Ala Leu Arg Val Phe Thr Pro Ile Tyr Asp Glu Asn His Lys Gln Ile
 145 150 155 160
 ggc gtg gtg gcg atc ggc ctt gag tta agc cgt gtg acc caa cag atc 528
 Gly Val Val Ala Ile Gly Leu Glu Leu Ser Arg Val Thr Gln Gln Ile
 165 170 175
 aat gac agt cgc tgg agc att atc tgg tcg gta tta ttt ggc atg ctg 576
 Asn Asp Ser Arg Trp Ser Ile Ile Trp Ser Val Leu Phe Gly Met Leu
 180 185 190
 gtc gga ctg att ggc acc tgc att ctg gtt aag gta ctg aaa aaa atc 624

Val Gly Leu Ile Gly Thr Cys Ile Leu Val Lys Val Leu Lys Lys Ile	
195 200 205	
ctt ttc ggc ctg gaa ccc tac gaa atc tcc acg ctg ttt gag caa cgc	672
Leu Phe Gly Leu Glu Pro Tyr Glu Ile Ser Thr Leu Phe Glu Gln Arg	
210 215 220	
cag gcc atg ttg cag tct atc aaa gaa ggc gtc gtt gcc gtg gac gat	720
Gln Ala Met Leu Gln Ser Ile Lys Glu Gly Val Val Ala Val Asp Asp	
225 230 235 240	
cgc ggc gag gtc acg ctg atc aac gat gcc gca caa gaa ttg ctg aat	768
Arg Gly Glu Val Thr Leu Ile Asn Asp Ala Ala Gln Glu Leu Leu Asn	
245 250 255	
tac cgt aag tcg cag gac gat gag aaa ctg tcg acg cta agc cac tca	816
Tyr Arg Lys Ser Gln Asp Asp Glu Lys Leu Ser Thr Leu Ser His Ser	
260 265 270	
tgg tca cag gtg gta gat gtc tcg gaa gtg tta cgc gac ggt acc ccg	864
Trp Ser Gln Val Val Asp Val Ser Glu Val Leu Arg Asp Gly Thr Pro	
275 280 285	
cgc cgc gac gaa gag att acg att aaa gac cgg cta tta ctg atc aac	912
Arg Arg Asp Glu Glu Ile Thr Ile Lys Asp Arg Leu Leu Leu Ile Asn	
290 295 300	
acc gtt ccg gtg cgc agt aat ggc gtt atc atc ggt gcc att tca acc	960
Thr Val Pro Val Arg Ser Asn Gly Val Ile Ile Gly Ala Ile Ser Thr	
305 310 315 320	
ttc agg gac aaa act gaa gta cgt aaa ctg atg cag cga ctc gac ggt	1008
Phe Arg Asp Lys Thr Glu Val Arg Lys Leu Met Gln Arg Leu Asp Gly	
325 330 335	
ctg gtc aac tat gct gac gca ctt cgt gaa cga tcc cac gaa ttt atg	1056
Leu Val Asn Tyr Ala Asp Ala Leu Arg Glu Arg Ser His Glu Phe Met	
340 345 350	
aat aaa ttg cat gtg att ctc gga tta ttg cat ctg aag agt tat aag	1104
Asn Lys Leu His Val Ile Leu Gly Leu Leu His Leu Lys Ser Tyr Lys	
355 360 365	
cag ttg gaa gat tac att ctc aaa aca gcc aat aac tat cag gaa gag	1152
Gln Leu Glu Asp Tyr Ile Leu Lys Thr Ala Asn Asn Tyr Gln Glu Glu	
370 375 380	
att ggc tct ctg ctg ggt aag atc aaa tct ccg gtt atc gct ggt ttt	1200
Ile Gly Ser Leu Leu Gly Lys Ile Lys Ser Pro Val Ile Ala Gly Phe	
385 390 395 400	
tta atc agc aag att aac cgc gcg acc gat tta ggc cat acg ctg att	1248
Leu Ile Ser Lys Ile Asn Arg Ala Thr Asp Leu Gly His Thr Leu Ile	
405 410 415	
tta aac agt gaa agc cag ctg cca gac agc ggc agt gag gac cag gtc	1296
Leu Asn Ser Glu Ser Gln Leu Pro Asp Ser Gly Ser Glu Asp Gln Val	
420 425 430	
gcg acg ctg att acc acg ttg gga aat ctg ata gaa aac gcg ctg gag	1344
Ala Thr Leu Ile Thr Thr Leu Gly Asn Leu Ile Glu Asn Ala Leu Glu	

435	440	445	
gca tta ggg ccg gaa ccc gga ggc gaa att agc gta aca ttg cac tac			1392
Ala Leu Gly Pro Glu Pro Gly Gly Glu Ile Ser Val Thr Leu His Tyr			
450	455	460	
cgt cac ggc tgg ctg cac tgt gaa gtt aat gat gat gga ccg ggg atc			1440
Arg His Gly Trp Leu His Cys Glu Val Asn Asp Asp Gly Pro Gly Ile			
465	470	475	480
gca ccc gat aaa atc gat cac att ttt gac aaa ggt gtc tcg aca aaa			1488
Ala Pro Asp Lys Ile Asp His Ile Phe Asp Lys Gly Val Ser Thr Lys			
485	490	495	
gga agc gag cga ggc gtc ggt tta gca ctt gtc aaa caa cag gta gaa			1536
Gly Ser Glu Arg Gly Val Gly Leu Ala Leu Val Lys Gln Gln Val Glu			
500	505	510	
aat ctc ggc ggc agc atc gcc gtg gaa tcg gaa ccc ggg att ttc aca			1584
Asn Leu Gly Gly Ser Ile Ala Val Glu Ser Glu Pro Gly Ile Phe Thr			
515	520	525	
caa ttt ttt gtc cag ata ccc tgg gac ggg gag agg tcg aac aga tga			1632
Gln Phe Phe Val Gln Ile Pro Trp Asp Gly Glu Arg Ser Asn Arg *			
530	535	540	

<210> 247

<211> 987

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(987)

<400> 247

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1 5 10 15	
tat cta cag aag gta act atg ttt cca caa tgc aaa ttt tcc cgc gag	96
Tyr Leu Gln Lys Val Thr Met Phe Pro Gln Cys Lys Phe Ser Arg Glu	
20 25 30	
ttt cta cat cct cgc tac tgg ctc aca tgg ttt ggg ctt ggt gta ctc	144
Phe Leu His Pro Arg Tyr Trp Leu Thr Trp Phe Gly Leu Gly Val Leu	
35 40 45	
tgg ctt tgg gta cag ctt cct tat cct gtt ctc tgc ttt ctc ggc acg	192
Trp Leu Trp Val Gln Leu Pro Tyr Pro Val Leu Cys Phe Leu Gly Thr	
50 55 60	
cgt att ggc gca atg gcg cga cca ttc ctg aaa cgt cgt gaa tct atc	240
Arg Ile Gly Ala Met Ala Arg Pro Phe Leu Lys Arg Arg Glu Ser Ile	
65 70 75 80	
gcc cgt aaa aac ctg gaa ctt tgt ttc ccg cag cat tct gcg gaa gaa	288
Ala Arg Lys Asn Leu Glu Leu Cys Phe Pro Gln His Ser Ala Glu Glu	
85 90 95	

cgc gag aag atg att gcc gaa aac ttt cgt tca ctc ggc atg gcg ctg	336
Arg Glu Lys Met Ile Ala Glu Asn Phe Arg Ser Leu Gly Met Ala Leu	
100 105 110	
gta gaa acc ggc atg gca tgg ttc tgg ccc gac agt cgc gta cgt aaa	384
Val Glu Thr Gly Met Ala Trp Phe Trp Pro Asp Ser Arg Val Arg Lys	
115 120 125	
tgg ttt gat gtt gaa ggg ttg gat aac ctt aaa cgc gca caa atg caa	432
Trp Phe Asp Val Glu Gly Leu Asp Asn Leu Lys Arg Ala Gln Met Gln	
130 135 140	
aat cgc ggc gta atg gtt gtc ggc gtc cat ttt atg tcg ctg gaa ctg	480
Asn Arg Gly Val Met Val Val Gly Val His Phe Met Ser Leu Glu Leu	
145 150 155 160	
ggc ggc cgc gtg atg gga ctg tgc caa cca atg atg gct acc tat cgt	528
Gly Gly Arg Val Met Gly Leu Cys Gln Pro Met Met Ala Thr Tyr Arg	
165 170 175	
cca cat aat aat cag ctg atg gaa tgg gtg cag acc cgt ggg cgc atg	576
Pro His Asn Asn Gln Leu Met Glu Trp Val Gln Thr Arg Gly Arg Met	
180 185 190	
cgc tct aac aaa gcg atg atc ggc aga aat aat ctg cgc ggc att gtc	624
Arg Ser Asn Lys Ala Met Ile Gly Arg Asn Asn Leu Arg Gly Ile Val	
195 200 205	
ggg gca ctg aag aaa ggt gaa gcg gta tgg ttt gct ccc gat cag gat	672
Gly Ala Leu Lys Lys Gly Glu Ala Val Trp Phe Ala Pro Asp Gln Asp	
210 215 220	
tat ggt cgt aaa ggc agc tcc ttc gcg ccg ttc ttt gcg gtg gaa aat	720
Tyr Gly Arg Lys Gly Ser Ser Phe Ala Pro Phe Phe Ala Val Glu Asn	
225 230 235 240	
gtc gcc aca acc aat ggc acc tat gtt ctc tcc cgt ctc tct ggc gca	768
Val Ala Thr Thr Asn Gly Thr Tyr Val Leu Ser Arg Leu Ser Gly Ala	
245 250 255	
gcc atg ttg acc gta acg atg gta aga aaa gcg gat tac agc gga tat	816
Ala Met Leu Thr Val Thr Met Val Arg Lys Ala Asp Tyr Ser Gly Tyr	
260 265 270	
cgt ttg ttc atc acc cca gag atg gaa ggc tac ccg aca gat gaa aat	864
Arg Leu Phe Ile Thr Pro Glu Met Glu Gly Tyr Pro Thr Asp Glu Asn	
275 280 285	
caa gcc gct gcc tat atg aac aag att atc gag aaa gag atc atg cgc	912
Gln Ala Ala Ala Tyr Met Asn Lys Ile Ile Glu Lys Glu Ile Met Arg	
290 295 300	
gca ccg gag cag tac ctc tgg atc cac cgt cgc ttt aaa acg cgc ccg	960
Ala Pro Glu Gln Tyr Leu Trp Ile His Arg Arg Phe Lys Thr Arg Pro	
305 310 315 320	
gtg gga gaa tcg tcg ttg tac att taa	987
Val Gly Glu Ser Ser Leu Tyr Ile *	
325	

<210> 248
 <211> 264
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(264)

<400> 248
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 Met Ala Asn Ile Lys Ser Ala Lys Lys Arg Ala Ile Gln Ser Glu Lys
 1 5 10 15
 gct cgt aag cac aac gca agc cgt cgc tct atg atg cgt act ttc atc 96
 Ala Arg Lys His Asn Ala Ser Arg Arg Ser Met Met Arg Thr Phe Ile
 20 25 30
 aag aaa gta tac gca gct atc gaa gct ggc gac aaa gct gct gca cag 144
 Lys Lys Val Tyr Ala Ala Ile Glu Ala Gly Asp Lys Ala Ala Ala Gln
 35 40 45
 aaa gca ttt aac gaa atg caa ccg atc gtg gac cgt cag gct gct aaa 192
 Lys Ala Phe Asn Glu Met Gln Pro Ile Val Asp Arg Gln Ala Ala Lys
 50 55 60
 ggt ctg atc cac aaa aac aaa gct gca cgt cat aag gct aac ctg act 240
 Gly Leu Ile His Lys Asn Lys Ala Ala Arg His Lys Ala Asn Leu Thr
 65 70 75 80
 gca cag atc aac aaa ctg gct taa 264
 Ala Gln Ile Asn Lys Leu Ala *
 85

<210> 249
 <211> 1293
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1293)

<400> 249
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 Met Arg Tyr Asn Gly Leu Asn Asn Met Phe Phe Pro Leu Cys Leu Ile
 1 5 10 15
 aac gat aac cac tct gtc aca agt cca tca cat aca aag aaa aca aaa 96
 Asn Asp Asn His Ser Val Thr Ser Pro Ser His Thr Lys Lys Thr Lys
 20 25 30
 tca gat aat tac agc aaa cat cat aaa aac acg tta att gac aat aaa 144
 Ser Asp Asn Tyr Ser Lys His His Lys Asn Thr Leu Ile Asp Asn Lys
 35 40 45
 gcc ctc tct ctt ttc aaa atg gat gat cat gaa aaa gtg ata ggc ttg 192
 Ala Leu Ser Leu Phe Lys Met Asp Asp His Glu Lys Val Ile Gly Leu
 50 55 60

att cag aaa atg aaa aga att tat gat agt tta cca tca gga aaa atc	240
Ile Gln Lys Met Lys Arg Ile Tyr Asp Ser Leu Pro Ser Gly Lys Ile	
65 70 75 80	
acg aaa gaa acg gac agg aaa ata cat aaa tat ttt ata gat ata gct	288
Thr Lys Glu Thr Asp Arg Lys Ile His Lys Tyr Phe Ile Asp Ile Ala	
85 90 95	
tca cat gca aat aat aaa tgt gac gat aga att acg aga aga gtt tac	336
Ser His Ala Asn Asn Lys Cys Asp Asp Arg Ile Thr Arg Arg Val Tyr	
100 105 110	
ctt aat aaa gat aag gaa gtg tca att aag gtg gta tat ttt ata aat	384
Leu Asn Lys Asp Lys Glu Val Ser Ile Lys Val Val Tyr Phe Ile Asn	
115 120 125	
aat gtc acc gtc cat aat aat act atc gaa atc cca cag aca gta aat	432
Asn Val Thr Val His Asn Asn Thr Ile Glu Ile Pro Gln Thr Val Asn	
130 135 140	
ggg ggt tac gat ttt tca cac ctt agc ctg aaa ggt atc gtg att aaa	480
Gly Gly Tyr Asp Phe Ser His Leu Ser Leu Lys Gly Ile Val Ile Lys	
145 150 155 160	
gat gaa gat tta tcc aat tcg aat ttt gca ggt tgc aga cta caa aac	528
Asp Glu Asp Leu Ser Asn Ser Asn Phe Ala Gly Cys Arg Leu Gln Asn	
165 170 175	
gct att ttt cag gac tgt aat atg tat aaa acg aat ttt aat ttc gcc	576
Ala Ile Phe Gln Asp Cys Asn Met Tyr Lys Thr Asn Phe Asn Phe Ala	
180 185 190	
ata atg gaa aaa ata ctt ttt gat aat tgt att ctc gat gac tca aat	624
Ile Met Glu Lys Ile Leu Phe Asp Asn Cys Ile Leu Asp Asp Ser Asn	
195 200 205	
ttc gct cag ata aaa atg act gac gga act cta aat tca tgt tcc gct	672
Phe Ala Gln Ile Lys Met Thr Asp Gly Thr Leu Asn Ser Cys Ser Ala	
210 215 220	
atg cat gtt caa ttc tac aat gca aca atg aat aga gcc aat att aaa	720
Met His Val Gln Phe Tyr Asn Ala Thr Met Asn Arg Ala Asn Ile Lys	
225 230 235 240	
aat acc ttc ctt gat tat tca aat ttt tat atg gca tac atg gct gag	768
Asn Thr Phe Leu Asp Tyr Ser Asn Phe Tyr Met Ala Tyr Met Ala Glu	
245 250 255	
gta aat ctt tat aaa gta ata gcg cca tat att aat tta ttt aga gcc	816
Val Asn Leu Tyr Lys Val Ile Ala Pro Tyr Ile Asn Leu Phe Arg Ala	
260 265 270	
gac ctt agc ttc tct aaa ctt gat tta att aac ttt gaa cat gct gat	864
Asp Leu Ser Phe Ser Lys Leu Asp Leu Ile Asn Phe Glu His Ala Asp	
275 280 285	
ctg tct cgt gtc aac ctg aat aaa gca acc ctc cag aat ata aac tta	912
Leu Ser Arg Val Asn Leu Asn Lys Ala Thr Leu Gln Asn Ile Asn Leu	
290 295 300	

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att gat agc aaa ctc ttt ttt acg cgg tta aca aat acg ttc ctc gaa 960
Ile Asp Ser Lys Leu Phe Phe Thr Arg Leu Thr Asn Thr Phe Leu Glu
305          310          315          320

atg gtt ata tgt acc gac tct aat atg gct aat gtt aat ttt aat aat 1008
Met Val Ile Cys Thr Asp Ser Asn Met Ala Asn Val Asn Phe Asn Asn
          325          330          335

gcc aat tta agc aat tgc cat ttc aac tgt tct gtt tta aca aaa gcc 1056
Ala Asn Leu Ser Asn Cys His Phe Asn Cys Ser Val Leu Thr Lys Ala
          340          345          350

tgg atg ttt aat atc cgt ctc tat cgt gtt aat ttc gat gag gct agc 1104
Trp Met Phe Asn Ile Arg Leu Tyr Arg Val Asn Phe Asp Glu Ala Ser
          355          360          365

gtc cag gga atg ggt att acc att ctc cgt ggt gag gaa aat atc tcc 1152
Val Gln Gly Met Gly Ile Thr Ile Leu Arg Gly Glu Glu Asn Ile Ser
          370          375          380

att aat agt gat atc ctg gta aca cta cag aaa ttc ttt gaa gaa gat 1200
Ile Asn Ser Asp Ile Leu Val Thr Leu Gln Lys Phe Phe Glu Glu Asp
385          390          395          400

tgt gcc act cat act ggc atg tca caa act gag gat aat ctt cat gca 1248
Cys Ala Thr His Thr Gly Met Ser Gln Thr Glu Asp Asn Leu His Ala
          405          410          415

gtc gct atg aag att act gca gat att atg caa gat gca gat tga 1293
Val Ala Met Lys Ile Thr Ala Asp Ile Met Gln Asp Ala Asp *
          420          425          430

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<210> 250

<211> 2652

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(2652)

<400> 250

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1          5          10          15

aaa gtg ctg gga gaa acc atc aag gat gcg ttg gga gaa cac att ctt 96
Lys Val Leu Gly Glu Thr Ile Lys Asp Ala Leu Gly Glu His Ile Leu
          20          25          30

gaa cgc gta gaa act atc cgt aag ttg tcg aaa tct tca cgc gct ggc 144
Glu Arg Val Glu Thr Ile Arg Lys Leu Ser Lys Ser Ser Arg Ala Gly
          35          40          45

aat gat gct aac cgc cag gag ttg ctc acc acc tta caa aat ttg tcg 192
Asn Asp Ala Asn Arg Gln Glu Leu Leu Thr Thr Leu Gln Asn Leu Ser
          50          55          60

aac gac gag ctg ctg ccc gtt gcg cgt gcg ttt agt cag ttc ctg aac 240

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Asn	Asp	Glu	Leu	Leu	Pro	Val	Ala	Arg	Ala	Phe	Ser	Gln	Phe	Leu	Asn	
65					70					75					80	
ctg	gcc	aac	acc	gcc	gag	caa	tac	cac	agc	att	tcg	ccg	aaa	ggc	gaa	288
Leu	Ala	Asn	Thr	Ala	Glu	Gln	Tyr	His	Ser	Ile	Ser	Pro	Lys	Gly	Glu	
				85					90					95		
gct	gcc	agc	aac	ccg	gaa	gtg	atc	gcc	cgc	acc	ctg	cgt	aaa	ctg	aaa	336
Ala	Ala	Ser	Asn	Pro	Glu	Val	Ile	Ala	Arg	Thr	Leu	Arg	Lys	Leu	Lys	
			100					105					110			
aac	cag	ccg	gaa	ctg	agc	gaa	gac	acc	atc	aaa	aaa	gca	gtg	gaa	tcg	384
Asn	Gln	Pro	Glu	Leu	Ser	Glu	Asp	Thr	Ile	Lys	Lys	Ala	Val	Glu	Ser	
		115					120					125				
ctg	tcg	ctg	gaa	ctg	gtc	ctc	acg	gct	cac	cca	acc	gaa	att	acc	cgt	432
Leu	Ser	Leu	Glu	Leu	Val	Leu	Thr	Ala	His	Pro	Thr	Glu	Ile	Thr	Arg	
	130					135					140					
cgt	aca	ctg	atc	cac	aaa	atg	gtg	gaa	gtg	aac	gcc	tgt	tta	aaa	cag	480
Arg	Thr	Leu	Ile	His	Lys	Met	Val	Glu	Val	Asn	Ala	Cys	Leu	Lys	Gln	
145					150					155					160	
ctc	gat	aac	aaa	gat	atc	gct	gac	tac	gaa	cac	aac	cag	ctg	atg	cgt	528
Leu	Asp	Asn	Lys	Asp	Ile	Ala	Asp	Tyr	Glu	His	Asn	Gln	Leu	Met	Arg	
				165				170						175		
cgc	ctg	cgc	cag	ttg	atc	gcc	cag	tca	tggt	cat	acc	gat	gaa	atc	cgt	576
Arg	Leu	Arg	Gln	Leu	Ile	Ala	Gln	Ser	Trp	His	Thr	Asp	Glu	Ile	Arg	
			180					185					190			
aag	ctg	cgt	cca	agc	ccg	gta	gat	gaa	gcc	aaa	tggt	ggc	ttt	gcc	gta	624
Lys	Leu	Arg	Pro	Ser	Pro	Val	Asp	Glu	Ala	Lys	Trp	Gly	Phe	Ala	Val	
		195				200						205				
gtg	gaa	aac	agc	ctg	tggt	caa	ggc	gta	cca	aat	tac	ctg	cgc	gaa	ctg	672
Val	Glu	Asn	Ser	Leu	Trp	Gln	Gly	Val	Pro	Asn	Tyr	Leu	Arg	Glu	Leu	
	210					215					220					
aac	gaa	caa	ctg	gaa	gag	aac	ctc	ggc	tac	aaa	ctg	ccc	gtc	gaa	ttt	720
Asn	Glu	Gln	Leu	Glu	Glu	Asn	Leu	Gly	Tyr	Lys	Leu	Pro	Val	Glu	Phe	
225					230					235					240	
gtt	ccg	gtc	cgt	ttt	act	tcg	tggt	atg	ggc	ggc	gac	cgc	gac	ggc	aac	768
Val	Pro	Val	Arg	Phe	Thr	Ser	Trp	Met	Gly	Gly	Asp	Arg	Asp	Gly	Asn	
				245					250					255		
ccg	aac	gtc	act	gcc	gat	atc	acc	cgc	cac	gtc	ctg	cta	ctc	agc	cgc	816
Pro	Asn	Val	Thr	Ala	Asp	Ile	Thr	Arg	His	Val	Leu	Leu	Leu	Ser	Arg	
			260					265						270		
tggt	aaa	gcc	acc	gat	ttg	ttc	ctg	aaa	gat	att	cag	gtg	ctg	gtt	tct	864
Trp	Lys	Ala	Thr	Asp	Leu	Phe	Leu	Lys	Asp	Ile	Gln	Val	Leu	Val	Ser	
		275					280					285				
gaa	ctg	tcg	atg	gtt	gaa	gcg	acc	cct	gaa	ctg	ctg	gcg	ctg	gtt	ggc	912
Glu	Leu	Ser	Met	Val	Glu	Ala	Thr	Pro	Glu	Leu	Leu	Ala	Leu	Val	Gly	
	290					295					300					
gaa	gaa	ggc	gcc	gca	gaa	ccg	tat	cgc	tat	ctg	atg	aaa	aac	ctg	cgt	960
Glu	Glu	Gly	Ala	Ala	Glu	Pro	Tyr	Arg	Tyr	Leu	Met	Lys	Asn	Leu	Arg	

305	310	315	320	
tct cgc ctg atg gcg aca cag gca tgg ctg gaa gcg cgc ctg aaa ggc				1008
Ser Arg Leu Met Ala Thr Gln Ala Trp Leu Glu Ala Arg Leu Lys Gly				
325		330	335	
gaa gaa ctg cca aaa cca gaa ggc ctg ctg aca caa aac gaa gaa ctg				1056
Glu Glu Leu Pro Lys Pro Glu Gly Leu Leu Thr Gln Asn Glu Glu Leu				
340		345	350	
tgg gaa ccg ctc tac gct tgc tac cag tca ctt cag gcg tgt ggc atg				1104
Trp Glu Pro Leu Tyr Ala Cys Tyr Gln Ser Leu Gln Ala Cys Gly Met				
355		360	365	
ggt att atc gcc aac ggc gat ctg ctc gac acc ctg cgc cgc gtg aaa				1152
Gly Ile Ile Ala Asn Gly Asp Leu Leu Asp Thr Leu Arg Arg Val Lys				
370		375	380	
tgt ttc ggc gta ccg ctg gtc cgt att gat atc cgt cag gag agc acg				1200
Cys Phe Gly Val Pro Leu Val Arg Ile Asp Ile Arg Gln Glu Ser Thr				
385		390	395	400
cgt cat acc gaa gcg ctg ggc gag ctg acc cgc tac ctc ggt atc ggc				1248
Arg His Thr Glu Ala Leu Gly Glu Leu Thr Arg Tyr Leu Gly Ile Gly				
405		410	415	
gac tac gaa agc tgg tca gag gcc gac aaa cag gcg ttc ctg atc cgc				1296
Asp Tyr Glu Ser Trp Ser Glu Ala Asp Lys Gln Ala Phe Leu Ile Arg				
420		425	430	
gaa ctg aac tcc aaa cgt ccg ctt ctg ccg cgc aac tgg caa cca agc				1344
Glu Leu Asn Ser Lys Arg Pro Leu Leu Pro Arg Asn Trp Gln Pro Ser				
435		440	445	
gcc gaa acg cgc gaa gtg ctc gat acc tgc cag gtg att gcc gaa gca				1392
Ala Glu Thr Arg Glu Val Leu Asp Thr Cys Gln Val Ile Ala Glu Ala				
450		455	460	
ccg caa ggc tcc att gcc gcc tac gtg atc tgc atg gcg aaa acg ccg				1440
Pro Gln Gly Ser Ile Ala Ala Tyr Val Ile Ser Met Ala Lys Thr Pro				
465		470	475	480
tcc gac gta ctg gct gtc cac ctg ctg ctg aaa gaa gcg ggt atc ggg				1488
Ser Asp Val Leu Ala Val His Leu Leu Leu Lys Glu Ala Gly Ile Gly				
485		490	495	
ttt gcg atg ccg gtt gct ccg ctg ttt gaa acc ctc gat gat ctg aac				1536
Phe Ala Met Pro Val Ala Pro Leu Phe Glu Thr Leu Asp Asp Leu Asn				
500		505	510	
aac gcc aac gat gtc atg acc cag ctg ctc aat att gac tgg tat cgt				1584
Asn Ala Asn Asp Val Met Thr Gln Leu Leu Asn Ile Asp Trp Tyr Arg				
515		520	525	
ggc ctg att cag ggc aaa cag atg gtg atg att ggc tat tcc gac tca				1632
Gly Leu Ile Gln Gly Lys Gln Met Val Met Ile Gly Tyr Ser Asp Ser				
530		535	540	
gca aaa gat gcg gga gtg atg gca gct tcc tgg gcg caa tat cag gca				1680
Ala Lys Asp Ala Gly Val Met Ala Ala Ser Trp Ala Gln Tyr Gln Ala				
545		550	555	560

cag gat gca tta atc aaa acc tgc gaa aaa gcg ggt att gag ctg acg Gln Asp Ala Leu Ile Lys Thr Cys Glu Lys Ala Gly Ile Glu Leu Thr 565 570 575	1728
ttg ttc cac ggt cgc ggc ggt tcc att ggt cgc ggc ggc gca cct gct Leu Phe His Gly Arg Gly Gly Ser Ile Gly Arg Gly Gly Ala Pro Ala 580 585 590	1776
cat gcg gcg ctg ctg tca caa ccg cca gga agc ctg aaa ggc ggc ctg His Ala Ala Leu Leu Ser Gln Pro Pro Gly Ser Leu Lys Gly Gly Leu 595 600 605	1824
cgc gta acc gaa cag ggc gag atg atc cgc ttt aaa tat ggt ctg cca Arg Val Thr Glu Gln Gly Glu Met Ile Arg Phe Lys Tyr Gly Leu Pro 610 615 620	1872
gaa atc acc gtc agc agc ctg tgc ctt tat acc ggg gcg att ctg gaa Glu Ile Thr Val Ser Ser Leu Ser Leu Tyr Thr Gly Ala Ile Leu Glu 625 630 635 640	1920
gcc aac ctg ctg cca ccg ccg gag ccg aaa gag agc tgg cgt cgc att Ala Asn Leu Leu Pro Pro Pro Glu Pro Lys Glu Ser Trp Arg Arg Ile 645 650 655	1968
atg gat gaa ctg tca gtc atc tcc tgc gat gtc tac cgc ggc tac gta Met Asp Glu Leu Ser Val Ile Ser Cys Asp Val Tyr Arg Gly Tyr Val 660 665 670	2016
cgt gaa aac aaa gat ttt gtg cct tac ttc cgc tcc gct acg ccg gaa Arg Glu Asn Lys Asp Phe Val Pro Tyr Phe Arg Ser Ala Thr Pro Glu 675 680 685	2064
caa gaa ctg ggc aaa ctg ccg ttg ggt tca cgt ccg gcg aaa cgt cgc Gln Glu Leu Gly Lys Leu Pro Leu Gly Ser Arg Pro Ala Lys Arg Arg 690 695 700	2112
cca acc ggc ggc gtc gag tca cta cgc gcc att ccg tgg atc ttc gcc Pro Thr Gly Gly Val Glu Ser Leu Arg Ala Ile Pro Trp Ile Phe Ala 705 710 715 720	2160
tgg acg caa aac cgt ctg atg ctc ccc gcc tgg ctg ggt gca ggt acg Trp Thr Gln Asn Arg Leu Met Leu Pro Ala Trp Leu Gly Ala Gly Thr 725 730 735	2208
gcg ctg caa aaa gtg gtc gaa gac ggc aaa cag agc gag ctg gag gct Ala Leu Gln Lys Val Val Glu Asp Gly Lys Gln Ser Glu Leu Glu Ala 740 745 750	2256
atg tgc cgc gat tgg cca ttc ttc tgc acg cgt ctc ggc atg ctg gag Met Cys Arg Asp Trp Pro Phe Phe Ser Thr Arg Leu Gly Met Leu Glu 755 760 765	2304
atg gtc ttc gcc aaa gca gac ctg tgg ctg gcg gaa tac tat gac caa Met Val Phe Ala Lys Ala Asp Leu Trp Leu Ala Glu Tyr Tyr Asp Gln 770 775 780	2352
cgc ctg gta gac aaa gca ctg tgg ccg tta ggt aaa gag tta cgc aac Arg Leu Val Asp Lys Ala Leu Trp Pro Leu Gly Lys Glu Leu Arg Asn 785 790 795 800	2400


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ctg caa gaa gaa gac atc aaa gtg gtg ctg gcg att gcc aac gat tcc 2448
Leu Gln Glu Glu Asp Ile Lys Val Val Leu Ala Ile Ala Asn Asp Ser
      805                      810                      815

cat ctg atg gcc gat ctg ccg tgg att gca gag tct att cag cta cgg 2496
His Leu Met Ala Asp Leu Pro Trp Ile Ala Glu Ser Ile Gln Leu Arg
      820                      825                      830

aat att tac acc gac ccg ctg aac gta ttg cag gcc gag ttg ctg cac 2544
Asn Ile Tyr Thr Asp Pro Leu Asn Val Leu Gln Ala Glu Leu Leu His
      835                      840                      845

cgc tcc cgc cag gca gaa aaa gaa ggc cag gaa ccg gat cct cgc gtc 2592
Arg Ser Arg Gln Ala Glu Lys Glu Gly Gln Glu Pro Asp Pro Arg Val
      850                      855                      860

gaa caa gcg tta atg gtc act att gcc ggg att gcg gca ggt atg cgt 2640
Glu Gln Ala Leu Met Val Thr Ile Ala Gly Ile Ala Ala Gly Met Arg
      865                      870                      875                      880

aat acc ggc taa 2652
Asn Thr Gly *

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 <213> Escherichia coli

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Met Ser Ser Arg Lys Glu Leu Ala Asn Ala Ile Arg Ala Leu Ser Met
  1                      5                      10                      15

gac gca gta cag aaa gcc aaa tcc ggt cac ccg ggt gcc cct atg ggt 96
Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly
      20                      25                      30

atg gct gac att gcc gaa gtc ctg tgg cgt gat ttc ctg aaa cac aac 144
Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
      35                      40                      45

ccg cag aat ccg tcc tgg gct gac cgt gac cgc ttc gtg ctg tcc aac 192
Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
      50                      55                      60

ggc cac ggc tcc atg ctg atc tac agc ctg ctg cac ctc acc ggt tac 240
Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
      65                      70                      75                      80

gat ctg ccg atg gaa gaa ctg aaa aac ttc cgt cag ctg cac tct aaa 288
Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys
      85                      90                      95

act ccg ggt cac ccg gaa gtg ggt tac acc gct ggt gtg gaa acc acc 336
Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr

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100	105	110	
acc ggt ccg ctg ggt cag ggt att gcc aac gca gtc ggt atg gcg att			384
Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile			
115	120	125	
gca gaa aaa acg ctg gcg gcg cag ttt aac cgt ccg ggc cac gac att			432
Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile			
130	135	140	
gtc gac cac tac acc tac gcc ttc atg ggc gac ggc tgc atg atg gaa			480
Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu			
145	150	155	160
ggc atc tcc cac gaa gtt tgc tct ctg gcg ggt acg ctg aag ctg ggt			528
Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly			
165	170	175	
aaa ctg att gca ttc tac gat gac aac ggt att tct atc gat ggt cac			576
Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His			
180	185	190	
gtt gaa ggc tgg ttc acc gac gac acc gca atg cgt ttc gaa gct tac			624
Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr			
195	200	205	
ggc tgg cac gtt att cgc gac atc gac ggt cat gac gcg gca tct atc			672
Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile			
210	215	220	
aaa cgc gca gta gaa gaa gcg cgc gca gtg act gac aaa cct tcc ctg			720
Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu			
225	230	235	240
ctg atg tgc aaa acc atc atc ggt ttc ggt tcc ccg aac aaa gcc ggt			768
Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly			
245	250	255	
acc cac gac tcc cac ggt gcg ccg ctg ggc gac gct gaa att gcc ctg			816
Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu			
260	265	270	
acc cgc gaa caa ctg ggc tgg aaa tat gcg ccg ttc gaa atc ccg tct			864
Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser			
275	280	285	
gaa atc tat gct cag tgg gat gcg aaa gaa gca ggc cag gcg aaa gaa			912
Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu			
290	295	300	
tcc gca tgg aac gag aaa ttc gct gct tac gcg aaa gct tat ccg cag			960
Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln			
305	310	315	320
gaa gcc gct gaa ttt acc cgc cgt atg aaa ggc gaa atg ccg tct gac			1008
Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp			
325	330	335	
ttc gac gct aaa gcg aaa gag ttc atc gct aaa ctg cag gct aat ccg			1056
Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro			
340	345	350	

gcg aaa atc gcc agc cgt aaa gcg tct cag aat gct atc gaa gcg ttc	1104
Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe	
355 360 365	
ggt ccg ctg ttg ccg gaa ttc ctc ggc ggt tct gct gac ctg gcg ccg	1152
Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro	
370 375 380	
tct aac ctg acc ctg tgg tct ggt tct aaa gca atc aac gaa gat gct	1200
Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala	
385 390 395 400	
gcg ggt aac tac atc cac tac ggt gtt cgc gag ttc ggt atg acc gcg	1248
Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala	
405 410 415	
att gct aac ggt atc tcc ctg cac ggt ggc ttc ctg ccg tac acc tcc	1296
Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser	
420 425 430	
acc ttc ctg atg ttc gtg gaa tac gca cgt aac gcc gta cgt atg gct	1344
Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala	
435 440 445	
gcg ctg atg aaa cag cgt cag gtg atg gtt tac acc cac gac tcc atc	1392
Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile	
450 455 460	
ggt ctg ggc gaa gac ggg ccg act cac cag ccg gtt gag cag gtc gct	1440
Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala	
465 470 475 480	
tct ctg cgc gta acc ccg aac atg tct aca tgg cgt ccg tgt gac cag	1488
Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln	
485 490 495	
gtt gaa tcc gcg gtc gcg tgg aaa tac ggt gtt gag cgt cag gac ggc	1536
Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly	
500 505 510	
ccg acc gca ctg atc ctc tcc cgt cag aac ctg gcg cag cag gaa cga	1584
Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Gln Glu Arg	
515 520 525	
act gaa gag caa ctg gca aac atc gcg cgc ggt ggt tat gtg ctg aaa	1632
Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys	
530 535 540	
gac tgc gcc ggt cag ccg gaa ctg att ttc atc gct acc ggt tca gaa	1680
Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu	
545 550 555 560	
gtt gaa ctg gct gtt gct gcc tac gaa aaa ctg act gcc gaa ggc gtg	1728
Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val	
565 570 575	
aaa gcg cgc gtg gtg tcc atg tcy tct acc gac gca ttt gac aag cag	1776
Lys Ala Arg Val Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln	
580 585 590	

gat gct gct tac cgt gaa tcc gta ctg ccg aaa gcg gtt act gca cgc 1824
Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg
595 600 605

gtt gct gta gaa gcg ggt att gct gac tac tgg tac aag tat gtt ggc 1872
Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly
610 615 620

ctg aac ggt gct atc gtc ggt atg acc acc ttc ggt gaa tct gct ccg 1920
Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro
625 630 635 640

gca gag ctg ctg ttt gaa gag ttc ggc ttc act gtt gat aac gtt gtt 1968
Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val
645 650 655

gcg aaa gca aaa gaa ctg ctg taa 1992
Ala Lys Ala Lys Glu Leu Leu *
660

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1 5 10 15

tca gtg cct acc cgt tat cgg gaa cag ctg ctt gag aac gct gcc ggt 96
Ser Val Pro Thr Arg Tyr Arg Glu Gln Leu Leu Glu Asn Ala Ala Gly
20 25 30

caa atg gtt tgc acc att gac att tat cac ccg tgc ctg ctg ctt tac 144
Gln Met Val Cys Thr Ile Asp Ile Tyr His Pro Cys Leu Leu Leu Tyr
35 40 45

ccc ctg cct gaa tgg gaa att atc gag caa aaa tta tcg cgt ctg tcg 192
Pro Leu Pro Glu Trp Glu Ile Ile Glu Gln Lys Leu Ser Arg Leu Ser
50 55 60

agc atg aac ccg gtt gag cgc cgt gtg cag cgc cta ctg tta ggt cat 240
Ser Met Asn Pro Val Glu Arg Arg Val Gln Arg Leu Leu Leu Gly His
65 70 75 80

gcc agc gaa tgt cag atg gat ggc gca ggt cga ttg tta atc gcg cca 288
Ala Ser Glu Cys Gln Met Asp Gly Ala Gly Arg Leu Leu Ile Ala Pro
85 90 95

gta ctg cgg caa cat gcc ggg ctg aca aaa gaa gtg atg ctg gtt gga 336
Val Leu Arg Gln His Ala Gly Leu Thr Lys Glu Val Met Leu Val Gly
100 105 110

cag ttc aac aag ttt gag ctg tgg gat gaa aca acc tgg cat caa cag 384
Gln Phe Asn Lys Phe Glu Leu Trp Asp Glu Thr Thr Trp His Gln Gln

115	120	125	
gtc aag gaa gat atc gac gca gag cag ttg gct acc gga gac tta tcg			432
Val Lys Glu Asp Ile Asp Ala Glu Gln Leu Ala Thr Gly Asp Leu Ser			
130	135	140	
gag cga ctg cag gac ttg tct cta taa			459
Glu Arg Leu Gln Asp Leu Ser Leu *			
145	150		
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Met Met Glu Asn Tyr Lys His Thr Thr Val Leu Leu Asp Glu Ala Val			
1	5	10	15
aat ggc ctc aat atc cgt cct gat ggc atc tac att gat ggg act ttt			96
Asn Gly Leu Asn Ile Arg Pro Asp Gly Ile Tyr Ile Asp Gly Thr Phe			
	20	25	30
ggt cgc ggt ggt cac tca cgt ctg atc ctc tcg cag ctt ggc gaa gag			144
Gly Arg Gly Gly His Ser Arg Leu Ile Leu Ser Gln Leu Gly Glu Glu			
35	40	45	
ggg cgt ttg ctg gcg atc gat cgc gac ccg cag gct atc gcc gtt gcg			192
Gly Arg Leu Leu Ala Ile Asp Arg Asp Pro Gln Ala Ile Ala Val Ala			
50	55	60	
aag act att gat gat ccg cgc ttc tcc atc atc cac gga cct ttc tcc			240
Lys Thr Ile Asp Asp Pro Arg Phe Ser Ile Ile His Gly Pro Phe Ser			
65	70	75	80
gcg ctg ggc gaa tac gtt gcc gag cgc gat ctt atc ggc aag atc gac			288
Ala Leu Gly Glu Tyr Val Ala Glu Arg Asp Leu Ile Gly Lys Ile Asp			
	85	90	95
ggc att ctc ctc gat ctt ggc gtc tct tca ccg caa ctt gat gat gct			336
Gly Ile Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Leu Asp Asp Ala			
100	105	110	
gaa cgt ggc ttt tcc ttt atg cgc gat ggt ccg ctg gac atg cgt atg			384
Glu Arg Gly Phe Ser Phe Met Arg Asp Gly Pro Leu Asp Met Arg Met			
115	120	125	
gac cca acc cgt ggg cag tca gcc gct gaa tgg cta caa acc gca gaa			432
Asp Pro Thr Arg Gly Gln Ser Ala Ala Glu Trp Leu Gln Thr Ala Glu			
130	135	140	
gaa gcc gat atc gcc tgg gta ttg aaa acc tat ggt gaa gag cgt ttt			480
Glu Ala Asp Ile Ala Trp Val Leu Lys Thr Tyr Gly Glu Glu Arg Phe			
145	150	155	160

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gcc aaa cgc att gcc cgc gcc att gtc gag cgt aac cgc gaa cag ccg 528
Ala Lys Arg Ile Ala Arg Ala Ile Val Glu Arg Asn Arg Glu Gln Pro
165 170 175

atg acc cgc acc aaa gaa ctg gcg gaa gtc gtg gct gct gca acg ccg 576
Met Thr Arg Thr Lys Glu Leu Ala Glu Val Val Ala Ala Ala Thr Pro
180 185 190

gtg aaa gat aag ttt aaa cat ccc gcg acc cgt acc ttc cag gcg gtg 624
Val Lys Asp Lys Phe Lys His Pro Ala Thr Arg Thr Phe Gln Ala Val
195 200 205

cgc att tgg gta aac agt gaa ctg gag gag ata gag cag gcg cta aaa 672
Arg Ile Trp Val Asn Ser Glu Leu Glu Glu Ile Glu Gln Ala Leu Lys
210 215 220

agc tcg ctc aac gtg ctg gcc ccg ggt ggg cgg ctt tcg atc atc agc 720
Ser Ser Leu Asn Val Leu Ala Pro Gly Gly Arg Leu Ser Ile Ile Ser
225 230 235

ttc cac tcg ctg gaa gac cgt att gtg aaa cgt ttt atg cgt gaa aac 768
Phe His Ser Leu Glu Asp Arg Ile Val Lys Arg Phe Met Arg Glu Asn
245 250 255

agc cgc ggt ccg caa gtt ccg gca ggg tta ccg atg act gaa gag cag 816
Ser Arg Gly Pro Gln Val Pro Ala Gly Leu Pro Met Thr Glu Glu Gln
260 265 270

ctc aaa aaa ctg ggt ggc cgt cag ctg cga gca cta ggc aag tta atg 864
Leu Lys Lys Leu Gly Gly Arg Gln Leu Arg Ala Leu Gly Lys Leu Met
275 280 285

ccg ggc gaa gaa gag gtg gct gag aac cct cgt gcc cgt agt tca gtt 912
Pro Gly Glu Glu Glu Val Ala Glu Asn Pro Arg Ala Arg Ser Ser Val
290 295 300

ctg cgt att gca gag agg acg aat gca tga 942
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305 310

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<211> 366

<212> DNA

<213> Escherichia coli

<220>

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<222> (1)...(366)

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1 5 10 15

gga agc cac gag cgc cat gca ttg cct ggt gtt atc ggt gac gat ctt 96
Gly Ser His Glu Arg His Ala Leu Pro Gly Val Ile Gly Asp Asp Leu
20 25 30

ttg cga ttt ggg aag ctg cca ctc tgc ctg ttc att tgc att att ttg 144
Leu Arg Phe Gly Lys Leu Pro Leu Cys Leu Phe Ile Cys Ile Ile Leu

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35	40	45	
acg gcg gtg act gtg gta acc acg gcg cac cat acc cgt tta ctg acc			192
Thr Ala Val Thr Val Val Thr Thr Ala His His Thr Arg Leu Leu Thr			
50	55	60	
gct cag cgc gaa caa ctg gtg ctg gag cga gat gct tta gac att gaa			240
Ala Gln Arg Glu Gln Leu Val Leu Glu Arg Asp Ala Leu Asp Ile Glu			
65	70	75	80
tgg cgc aac ctg atc ctt gaa gag aat gcg ctc ggc gac cat agc cgg			288
Trp Arg Asn Leu Ile Leu Glu Glu Asn Ala Leu Gly Asp His Ser Arg			
	85	90	95
gtg gaa agg atc gcc acg gaa aag ctg caa atg cag cat gtt gat ccg			336
Val Glu Arg Ile Ala Thr Glu Lys Leu Gln Met Gln His Val Asp Pro			
	100	105	110
tca caa gaa aat atc gta gtg caa aaa taa			366
Ser Gln Glu Asn Ile Val Val Gln Lys *			
	115	120	
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Met Lys Ala Ala Lys Thr Gln Lys Pro Lys Arg Gln Glu Glu His			
1	5	10	15
gcc aac ttt atc agt tgg cgt ttt gcg ttg tta tgc ggc tgt att ctc			96
Ala Asn Phe Ile Ser Trp Arg Phe Ala Leu Leu Cys Gly Cys Ile Leu			
	20	25	30
ctg gcg ctg gct ttt ctg ctc gga cgc gta gcg tgg tta caa gtt atc			144
Leu Ala Leu Ala Phe Leu Leu Gly Arg Val Ala Trp Leu Gln Val Ile			
	35	40	45
tcc ccg gat atg ctg gtg aaa gag ggc gac atg cgt tct ctt cgc gtt			192
Ser Pro Asp Met Leu Val Lys Glu Gly Asp Met Arg Ser Leu Arg Val			
	50	55	60
cag caa gtt tcc acc tcc cgc ggc atg att act gac cgt tct ggt cgc			240
Gln Gln Val Ser Thr Ser Arg Gly Met Ile Thr Asp Arg Ser Gly Arg			
65	70	75	80
ccg tta gcg gtg agc gtg ccg gta aaa gcg att tgg gct gac ccg aaa			288
Pro Leu Ala Val Ser Val Pro Val Lys Ala Ile Trp Ala Asp Pro Lys			
	85	90	95
gaa gtg cat gac gct ggc ggt atc agc gtc ggt gac cgc tgg aag gcg			336
Glu Val His Asp Ala Gly Gly Ile Ser Val Gly Asp Arg Trp Lys Ala			
	100	105	110

ctg gct aac gcg ctc aat att ccg ctg gat cag ctt tca gcc cgc att	384
Leu Ala Asn Ala Leu Asn Ile Pro Leu Asp Gln Leu Ser Ala Arg Ile	
115 120 125	
aac gcc aac ccg aaa ggg cgc ttt att tat ctg gcg cgt cag gtg aac	432
Asn Ala Asn Pro Lys Gly Arg Phe Ile Tyr Leu Ala Arg Gln Val Asn	
130 135 140	
cct gac atg gcg gac tac atc aaa aaa ctg aaa ctg ccg ggg att cat	480
Pro Asp Met Ala Asp Tyr Ile Lys Lys Leu Lys Leu Pro Gly Ile His	
145 150 155 160	
ctg cgt gaa gag tct cgc cgt tac tat ccg tcc ggc gaa gtg act gct	528
Leu Arg Glu Glu Ser Arg Arg Tyr Tyr Pro Ser Gly Glu Val Thr Ala	
165 170 175	
cac ctc atc ggc ttt act aac gtc gat agt caa ggg att gag ggc gtt	576
His Leu Ile Gly Phe Thr Asn Val Asp Ser Gln Gly Ile Glu Gly Val	
180 185 190	
gag aag agt ttc gat aaa tgg ctt acc ggg cag ccg ggt gag cgc att	624
Glu Lys Ser Phe Asp Lys Trp Leu Thr Gly Gln Pro Gly Glu Arg Ile	
195 200 205	
gtg cgt aaa gac cgc tat ggt cgc gta att gaa gat att tct tct act	672
Val Arg Lys Asp Arg Tyr Gly Arg Val Ile Glu Asp Ile Ser Ser Thr	
210 215 220	
gac agc cag gca gcg cac aac ctg gcg ctg agt att gat gaa cgc ctg	720
Asp Ser Gln Ala Ala His Asn Leu Ala Leu Ser Ile Asp Glu Arg Leu	
225 230 235 240	
cag gcg ctg gtt tat cgc gaa ctg aac aac gcg gtg gcc ttt aac aag	768
Gln Ala Leu Val Tyr Arg Glu Leu Asn Asn Ala Val Ala Phe Asn Lys	
245 250 255	
gct gaa tct ggt agc gcc gtg ctg gtg gat gtc aac acc ggt gaa gtg	816
Ala Glu Ser Gly Ser Ala Val Leu Val Asp Val Asn Thr Gly Glu Val	
260 265 270	
ctg gcg atg gct aac agc ccg tca tac aac cct aac aat ctg agc ggc	864
Leu Ala Met Ala Asn Ser Pro Ser Tyr Asn Pro Asn Asn Leu Ser Gly	
275 280 285	
acg ccg aaa gag gcg atg cgt aac cgt acc atc acc gac gtg ttt gaa	912
Thr Pro Lys Glu Ala Met Arg Asn Arg Thr Ile Thr Asp Val Phe Glu	
290 295 300	
ccg ggc tca acg gtt aaa ccg atg gtg gta atg acc gcg ttg caa cgt	960
Pro Gly Ser Thr Val Lys Pro Met Val Val Met Thr Ala Leu Gln Arg	
305 310 315 320	
ggc gtg gtg cgg gaa aac tcg gta ctc aat acc att cct tat cga att	1008
Gly Val Val Arg Glu Asn Ser Val Leu Asn Thr Ile Pro Tyr Arg Ile	
325 330 335	
aac ggc cac gaa atc aaa gac gtg gca cgc tac agc gaa tta acc ctg	1056
Asn Gly His Glu Ile Lys Asp Val Ala Arg Tyr Ser Glu Leu Thr Leu	
340 345 350	
acc ggg gta tta cag aag tcg agt aac gtc ggt gtt tcc aag ctg gcg	1104

Thr Gly Val Leu Gln Lys Ser Ser Asn Val Gly Val Ser Lys Leu Ala	
355 360 365	
tta gcg atg ccg tcc tca gcg tta gta gat act tac tca cgt ttt gga	1152
Leu Ala Met Pro Ser Ser Ala Leu Val Asp Thr Tyr Ser Arg Phe Gly	
370 375 380	
ctg gga aaa gcg acc aat ttg ggg ttg gtc gga gaa cgc agt ggc tta	1200
Leu Gly Lys Ala Thr Asn Leu Gly Leu Val Gly Glu Arg Ser Gly Leu	
385 390 395 400	
tat cct caa aaa caa cgg tgg tct gac ata gag agg gcc acc ttc tct	1248
Tyr Pro Gln Lys Gln Arg Trp Ser Asp Ile Glu Arg Ala Thr Phe Ser	
405 410 415	
ttc ggc tac ggg cta atg gta aca cca tta cag tta gcg cga gtc tac	1296
Phe Gly Tyr Gly Leu Met Val Thr Pro Leu Gln Leu Ala Arg Val Tyr	
420 425 430	
gca act atc ggc agc tac ggc att tat cgc cca ctg tcg att acc aaa	1344
Ala Thr Ile Gly Ser Tyr Gly Ile Tyr Arg Pro Leu Ser Ile Thr Lys	
435 440 445	
gtt gac ccc ccg gtt ccc ggt gaa cgt gtc ttc ccg gaa tcc att gtc	1392
Val Asp Pro Pro Val Pro Gly Glu Arg Val Phe Pro Glu Ser Ile Val	
450 455 460	
cgc act gtg gtg cat atg atg gaa agc gtg gcg cta cca ggc ggc ggc	1440
Arg Thr Val Val His Met Met Glu Ser Val Ala Leu Pro Gly Gly Gly	
465 470 475 480	
ggc gtg aag gcg gcg att aaa ggc tat cgt atc gcc att aaa acc ggt	1488
Gly Val Lys Ala Ala Ile Lys Gly Tyr Arg Ile Ala Ile Lys Thr Gly	
485 490 495	
acc gcg aaa aag gtc ggg ccg gac ggt cgc tac atc aat aaa tat att	1536
Thr Ala Lys Lys Val Gly Pro Asp Gly Arg Tyr Ile Asn Lys Tyr Ile	
500 505 510	
gct tat acc gca ggc gtt gcg cct gcg agt cag ccg cgc ttc gcg ctg	1584
Ala Tyr Thr Ala Gly Val Ala Pro Ala Ser Gln Pro Arg Phe Ala Leu	
515 520 525	
gtt gtt gtt atc aac gat ccg cag gcg ggt aaa tac tac ggc ggc gcc	1632
Val Val Val Ile Asn Asp Pro Gln Ala Gly Lys Tyr Tyr Gly Gly Ala	
530 535 540	
gtt tcc gcg ccg gtc ttt ggt gcc atc atg ggc ggc gta ttg cgt acc	1680
Val Ser Ala Pro Val Phe Gly Ala Ile Met Gly Gly Val Leu Arg Thr	
545 550 555 560	
atg aac atc gag ccg gat gcg ctg aca acg ggc gat aaa aat gaa ttt	1728
Met Asn Ile Glu Pro Asp Ala Leu Thr Thr Gly Asp Lys Asn Glu Phe	
565 570 575	
gtg att aat caa ggc gag ggg aca ggt ggc aga tcg taa	1767
Val Ile Asn Gln Gly Glu Gly Thr Gly Gly Arg Ser *	
580 585	

<210> 256

<211> 1488

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1488)

<400> 256

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Met Ala Asp Arg Asn Leu Arg Asp Leu Leu Ala Pro Trp Val Pro Asp	
1 5 10 15	
gca cct tcg cga gca ctg cga gag atg aca ctc gac agc cgt gtg gct	96
Ala Pro Ser Arg Ala Leu Arg Glu Met Thr Leu Asp Ser Arg Val Ala	
20 25 30	
gcg gcg ggc gat ctc ttt gta gct gta gta ggt cat cag gcg gac ggg	144
Ala Ala Gly Asp Leu Phe Val Ala Val Val Gly His Gln Ala Asp Gly	
35 40 45	
cgt cga tat atc ccg cag gcg ata gcg caa ggt gtg gct gcc att att	192
Arg Arg Tyr Ile Pro Gln Ala Ile Ala Gln Gly Val Ala Ala Ile Ile	
50 55 60	
gca gag gcg aaa gat gag gcg acc gat ggt gaa atc cgt gaa atg cac	240
Ala Glu Ala Lys Asp Glu Ala Thr Asp Gly Glu Ile Arg Glu Met His	
65 70 75 80	
ggc gta ccg gtc atc tat ctc agc cag ctc aac gag cgt tta tct gca	288
Gly Val Pro Val Ile Tyr Leu Ser Gln Leu Asn Glu Arg Leu Ser Ala	
85 90 95	
ctg gcg ggc cgc ttt tac cat gaa ccc tct gac aat tta cgt ctc gtg	336
Leu Ala Gly Arg Phe Tyr His Glu Pro Ser Asp Asn Leu Arg Leu Val	
100 105 110	
ggc gta acg ggc acc aac ggc aaa acc acg act acc cag ctg ttg gcg	384
Gly Val Thr Gly Thr Asn Gly Lys Thr Thr Thr Gln Leu Leu Ala	
115 120 125	
cag tgg agc caa ctg ctt ggc gaa atc agc gcg gta atg ggc acc gtt	432
Gln Trp Ser Gln Leu Leu Gly Glu Ile Ser Ala Val Met Gly Thr Val	
130 135 140	
ggt aac ggc ctg ctg ggg aaa gtg atc ccg aca gaa aat aca acc ggt	480
Gly Asn Gly Leu Leu Gly Lys Val Ile Pro Thr Glu Asn Thr Thr Gly	
145 150 155 160	
tcg gca gtc gat gtt cag cat gag ctg gcg ggg ctg gtg gat cag ggc	528
Ser Ala Val Asp Val Gln His Glu Leu Ala Gly Leu Val Asp Gln Gly	
165 170 175	
gcg acg ttt tgc gca atg gaa gtt tcc tcc cac ggg ctg gta cag cac	576
Ala Thr Phe Cys Ala Met Glu Val Ser Ser His Gly Leu Val Gln His	
180 185 190	
cgt gtg gcg gca ttg aaa ttt gcg gcg tcg gtc ttt acc aac tta agc	624
Arg Val Ala Ala Leu Lys Phe Ala Ala Ser Val Phe Thr Asn Leu Ser	
195 200 205	

cgc gat cac ctt gat tat cat ggt gat atg gaa cac tac gaa gcc gcg	672
Arg Asp His Leu Asp Tyr His Gly Asp Met Glu His Tyr Glu Ala Ala	
210 215 220	
aaa tgg ctg ctt tat tct gag cat cat tgc ggt cag gcg att att aac	720
Lys Trp Leu Leu Tyr Ser Glu His His Cys Gly Gln Ala Ile Ile Asn	
225 230 235 240	
gcc gac gat gaa gtg ggc cgc cgc tgg ctg gca aaa ctg ccg gac gcg	768
Ala Asp Asp Glu Val Gly Arg Arg Trp Leu Ala Lys Leu Pro Asp Ala	
245 250 255	
gtt gcg gta tca atg gaa gat cat att aat ccg aac tgt cac gga cgc	816
Val Ala Val Ser Met Glu Asp His Ile Asn Pro Asn Cys His Gly Arg	
260 265 270	
tgg ttg aaa gcg acc gaa gtg aac tat cac gac agc ggt gcg acg att	864
Trp Leu Lys Ala Thr Glu Val Asn Tyr His Asp Ser Gly Ala Thr Ile	
275 280 285	
cgc ttt agc tca agt tgg ggc gat ggc gaa att gaa agc cat ctg atg	912
Arg Phe Ser Ser Ser Trp Gly Asp Gly Glu Ile Glu Ser His Leu Met	
290 295 300	
ggc gct ttt aac gtc agc aac ctg ctg ctc gcg ctg gcg aca ctg ttg	960
Gly Ala Phe Asn Val Ser Asn Leu Leu Leu Ala Leu Ala Thr Leu Leu	
305 310 315 320	
gca ctc ggc tat cca ctg gct gat ctg ctg aaa acc gcc gcg cgt ctg	1008
Ala Leu Gly Tyr Pro Leu Ala Asp Leu Leu Lys Thr Ala Ala Arg Leu	
325 330 335	
caa ccg gtt tgc gga cgt atg gaa gtg ttc act gcg cca ggc aaa ccg	1056
Gln Pro Val Cys Gly Arg Met Glu Val Phe Thr Ala Pro Gly Lys Pro	
340 345 350	
acg gtg gtg gtg gat tac gcg cat acg ccg gat gca ctg gaa aaa gcc	1104
Thr Val Val Val Asp Tyr Ala His Thr Pro Asp Ala Leu Glu Lys Ala	
355 360 365	
tta cag gcg gcg cgt ctg cac tgt gcg ggc aag ctg tgg tgt gtc ttt	1152
Leu Gln Ala Ala Arg Leu His Cys Ala Gly Lys Leu Trp Cys Val Phe	
370 375 380	
ggc tgt ggt ggc gat cgc gat aaa ggt aag cgt cca ctg atg ggc gca	1200
Gly Cys Gly Gly Asp Arg Asp Lys Gly Lys Arg Pro Leu Met Gly Ala	
385 390 395 400	
att gcc gaa gag ttt gct gac gtg gcg gtg gtg acg gac gat aac ccg	1248
Ile Ala Glu Glu Phe Ala Asp Val Ala Val Val Thr Asp Asp Asn Pro	
405 410 415	
cgt acc gaa gaa ccg cgt gcc atc atc aac gat att ctg gcg gga atg	1296
Arg Thr Glu Glu Pro Arg Ala Ile Ile Asn Asp Ile Leu Ala Gly Met	
420 425 430	
tta gat gcc gga cat gcc aaa gtg atg gaa ggc cgt gct gaa gcg gtg	1344
Leu Asp Ala Gly His Ala Lys Val Met Glu Gly Arg Ala Glu Ala Val	
435 440 445	
act tgc gcc gtt atg cag gct aaa gag aat gat gtg gta ctg gtc gcg	1392

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Thr Cys Ala Val Met Gln Ala Lys Glu Asn Asp Val Val Leu Val Ala
 450                               455                               460

ggc aaa ggc cat gaa gat tac cag att gtt ggc aat cag cgt ctg gac 1440
Gly Lys Gly His Glu Asp Tyr Gln Ile Val Gly Asn Gln Arg Leu Asp
465                               470                               475                               480

tac tcc gat cgc gtc acg gtg gcg cgt ctg ctg ggg gtg att gca tga 1488
Tyr Ser Asp Arg Val Thr Val Ala Arg Leu Leu Gly Val Ile Ala *
                               485                               490                               495

<210> 257
<211> 1359
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1359)

<400> 257
atg att agc gta acc ctt agc caa ctt acc gac att ctc aac ggt gaa 48
Met Ile Ser Val Thr Leu Ser Gln Leu Thr Asp Ile Leu Asn Gly Glu
 1                               5                               10                               15

ctg caa ggt gca gat atc acc ctt gat gct gta acc act gat acc cga 96
Leu Gln Gly Ala Asp Ile Thr Leu Asp Ala Val Thr Thr Asp Thr Arg
                20                               25                               30

aaa ctg acg ccg ggc tgc ctg ttt gtt gcc ctg aaa ggc gaa cgt ttt 144
Lys Leu Thr Pro Gly Cys Leu Phe Val Ala Leu Lys Gly Glu Arg Phe
                35                               40                               45

gat gcc cac gat ttt gcc gac cag gcg aaa gct ggc ggc gca ggc gca 192
Asp Ala His Asp Phe Ala Asp Gln Ala Lys Ala Gly Gly Ala Gly Ala
                50                               55                               60

cta ctg gtt agc cgt ccg ctg gac atc gac ctg ccg cag tta atc gtc 240
Leu Leu Val Ser Arg Pro Leu Asp Ile Asp Leu Pro Gln Leu Ile Val
 65                               70                               75                               80

aag gat acg cgt ctg gcg ttt ggt gaa ctg gct gca tgg gtt cgc cag 288
Lys Asp Thr Arg Leu Ala Phe Gly Glu Leu Ala Ala Trp Val Arg Gln
                85                               90                               95

caa gtt ccg gcg cgc gtg gtt gct ctg acg ggg tcc tcc ggc aaa acc 336
Gln Val Pro Ala Arg Val Val Ala Leu Thr Gly Ser Ser Gly Lys Thr
                100                               105                               110

tcc gtt aaa gag atg acg gcg gcg att tta agc cag tgc ggc aac acg 384
Ser Val Lys Glu Met Thr Ala Ala Ile Leu Ser Gln Cys Gly Asn Thr
                115                               120                               125

ctt tat acg gca ggc aat ctc aac aac gac atc ggt gta ccg atg acg 432
Leu Tyr Thr Ala Gly Asn Leu Asn Asn Asp Ile Gly Val Pro Met Thr
                130                               135                               140

ctg ttg cgc tta acg ccg gaa tac gat tac gca gtt att gaa ctt ggc 480
Leu Leu Arg Leu Thr Pro Glu Tyr Asp Tyr Ala Val Ile Glu Leu Gly

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145	150	155	160	
gcg aac cat cag ggc gaa ata gcc tgg act gtg agt ctg act cgc ccg				528
Ala Asn His Gln Gly Glu Ile Ala Trp Thr Val Ser Leu Thr Arg Pro				
165		170	175	
gaa gct gcg ctg gtc aac aac ctg gca gcg gcg cat ctg gaa ggt ttt				576
Glu Ala Ala Leu Val Asn Asn Leu Ala Ala Ala His Leu Glu Gly Phe				
180		185	190	
ggc tcg ctt gcg ggt gtc gcg aaa gcg aaa ggt gaa atc ttt agc ggc				624
Gly Ser Leu Ala Gly Val Ala Lys Ala Lys Gly Glu Ile Phe Ser Gly				
195		200	205	
ctg ccg gaa aac ggt atc gcc att atg aac gcc gac aac aac gac tgg				672
Leu Pro Glu Asn Gly Ile Ala Ile Met Asn Ala Asp Asn Asn Asp Trp				
210		215	220	
ctg aac tgg cag agc gta att ggc tca cgc aaa gtg tgg cgt ttc tca				720
Leu Asn Trp Gln Ser Val Ile Gly Ser Arg Lys Val Trp Arg Phe Ser				
225		230	235	240
ccc aat gcc gcc aac agc gat ttc acc gcc acc aat atc cat gtg acc				768
Pro Asn Ala Ala Asn Ser Asp Phe Thr Ala Thr Asn Ile His Val Thr				
245		250	255	
tcg cac ggt acg gaa ttt acc cta caa acc cca acc ggt agc gtc gat				816
Ser His Gly Thr Glu Phe Thr Leu Gln Thr Pro Thr Gly Ser Val Asp				
260		265	270	
gtt ctg ctg ccg ttg ccg ggg cgt cac aat att gcg aat gcg ctg gca				864
Val Leu Leu Pro Leu Pro Gly Arg His Asn Ile Ala Asn Ala Leu Ala				
275		280	285	
gcc gct gcg ctc tcc atg tcc gtg ggc gca acg ctt gat gct atc aaa				912
Ala Ala Ala Leu Ser Met Ser Val Gly Ala Thr Leu Asp Ala Ile Lys				
290		295	300	
gcg ggg ctg gca aat ctg aaa gct gtt cca ggc cgt ctg ttc ccc atc				960
Ala Gly Leu Ala Asn Leu Lys Ala Val Pro Gly Arg Leu Phe Pro Ile				
305		310	315	320
caa ctg gca gaa aac cag ttg ctg ctc gac gac tcc tac aac gcc aat				1008
Gln Leu Ala Glu Asn Gln Leu Leu Leu Asp Asp Ser Tyr Asn Ala Asn				
325		330	335	
gtc ggt tca atg act gca gca gtc cag gta ctg gct gaa atg ccg ggc				1056
Val Gly Ser Met Thr Ala Ala Val Gln Val Leu Ala Glu Met Pro Gly				
340		345	350	
tac cgc gtg ctg gtg gtg ggc gat atg gcg gaa ctg ggc gct gaa agc				1104
Tyr Arg Val Leu Val Val Gly Asp Met Ala Glu Leu Gly Ala Glu Ser				
355		360	365	
gaa gcc tgc cat gta cag gtg ggc gag gcg gca aaa gct gct ggt att				1152
Glu Ala Cys His Val Gln Val Gly Glu Ala Ala Lys Ala Ala Gly Ile				
370		375	380	
gac cgc gtg tta agc gtg ggt aaa caa agc cat gct atc agc acc gcc				1200
Asp Arg Val Leu Ser Val Gly Lys Gln Ser His Ala Ile Ser Thr Ala				
385		390	395	400

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agc ggc gtt ggc gaa cat ttt gct gat aaa act gcg tta att acg cgt 1248
Ser Gly Val Gly Glu His Phe Ala Asp Lys Thr Ala Leu Ile Thr Arg
          405          410          415

ctt aaa tta ctg att gct gag caa cag gta att acg att tta gtt aag 1296
Leu Lys Leu Leu Ile Ala Glu Gln Gln Val Ile Thr Ile Leu Val Lys
          420          425          430

ggt tca cgt agt gcc gcc atg gaa gag gta gta cgc gct tta cag gag 1344
Gly Ser Arg Ser Ala Ala Met Glu Glu Val Val Arg Ala Leu Gln Glu
          435          440          445

aat ggg aca tgt tag 1359
Asn Gly Thr Cys *
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<210> 258
<211> 1083
<212> DNA
<213> Escherichia coli

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<220>
<221> CDS
<222> (1)...(1083)

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<400> 258
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Met Leu Val Trp Leu Ala Glu His Leu Val Lys Tyr Tyr Ser Gly Phe
  1          5          10          15

aac gtc ttt tcc tat ctg acg ttt cgc gcc atc gtc agc ctg ctg acc 96
Asn Val Phe Ser Tyr Leu Thr Phe Arg Ala Ile Val Ser Leu Leu Thr
          20          25          30

gcg ctg ttc atc tca ttg tgg atg ggc ccg cgt atg att gct cat ttg 144
Ala Leu Phe Ile Ser Leu Trp Met Gly Pro Arg Met Ile Ala His Leu
          35          40          45

caa aaa ctt tcc ttt ggt cag gtg gtg cgt aac gac ggt cct gaa tca 192
Gln Lys Leu Ser Phe Gly Gln Val Val Arg Asn Asp Gly Pro Glu Ser
          50          55          60

cac ttc agc aag cgc ggt acg ccg acc atg ggc ggg att atg atc ctg 240
His Phe Ser Lys Arg Gly Thr Pro Thr Met Gly Gly Ile Met Ile Leu
          65          70          75          80

acg gcg att gtg atc tcc gta ctg ctg tgg gct tac ccg tcc aat ccg 288
Thr Ala Ile Val Ile Ser Val Leu Leu Trp Ala Tyr Pro Ser Asn Pro
          85          90          95

tac gtc tgg tgc gtg ttg gtg gtg ctg gta ggt tac ggt gtt att ggc 336
Tyr Val Trp Cys Val Leu Val Val Leu Val Gly Tyr Gly Val Ile Gly
          100          105          110

ttt gtt gat gat tat cgc aaa gtg gtg cgt aaa gac acc aaa ggg ttg 384
Phe Val Asp Asp Tyr Arg Lys Val Val Arg Lys Asp Thr Lys Gly Leu
          115          120          125

atc gct cgt tgg aag tat ttc tgg atg tcg gtc att gcg ctg ggt gtc 432

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Ile	Ala	Arg	Trp	Lys	Tyr	Phe	Trp	Met	Ser	Val	Ile	Ala	Leu	Gly	Val		
130						135					140						
gcc	ttc	gcc	ctg	tac	ctt	gcc	ggc	aaa	gac	acg	ccc	gca	acg	cag	ctg	480	
Ala	Phe	Ala	Leu	Tyr	Leu	Ala	Gly	Lys	Asp	Thr	Pro	Ala	Thr	Gln	Leu		
145					150				155					160			
gtg	gtc	cca	ttc	ttt	aaa	gat	gtg	atg	ccg	cag	ctg	ggg	ctg	ttc	tac	528	
Val	Val	Pro	Phe	Phe	Lys	Asp	Val	Met	Pro	Gln	Leu	Gly	Leu	Phe	Tyr		
				165				170						175			
att	ctg	ctg	gct	tac	ttc	gtc	att	gtg	ggg	act	ggc	aac	gcg	gta	aac	576	
Ile	Leu	Leu	Ala	Tyr	Phe	Val	Ile	Val	Gly	Thr	Gly	Asn	Ala	Val	Asn		
			180					185					190				
ctg	acc	gat	ggg	ctc	gac	ggc	ctg	gca	att	atg	ccg	acc	gta	ttt	gtc	624	
Leu	Thr	Asp	Gly	Leu	Asp	Gly	Leu	Ala	Ile	Met	Pro	Thr	Val	Phe	Val		
		195					200					205					
gcc	ggg	ggg	ttt	gcg	ctg	gtg	ggc	tgg	gcg	acc	ggc	aat	atg	aac	ttt	672	
Ala	Gly	Gly	Phe	Ala	Leu	Val	Ala	Trp	Ala	Thr	Gly	Asn	Met	Asn	Phe		
	210					215					220						
gcc	agc	tac	ttg	cat	ata	ccg	tat	ctg	cga	cac	gcc	ggg	gaa	ctg	gtt	720	
Ala	Ser	Tyr	Leu	His	Ile	Pro	Tyr	Leu	Arg	His	Ala	Gly	Glu	Leu	Val		
225					230				235					240			
att	gtc	tgt	acc	gcg	ata	gtc	ggg	gca	gga	ctg	ggc	ttc	ctg	tgg	ttt	768	
Ile	Val	Cys	Thr	Ala	Ile	Val	Gly	Ala	Gly	Leu	Gly	Phe	Leu	Trp	Phe		
				245				250						255			
aac	acc	tat	ccg	gcg	cag	gtc	ttt	atg	ggc	gat	gta	ggg	tcg	ctg	gcg	816	
Asn	Thr	Tyr	Pro	Ala	Gln	Val	Phe	Met	Gly	Asp	Val	Gly	Ser	Leu	Ala		
			260					265					270				
tta	ggg	ggg	gcg	tta	ggc	att	atc	gcc	gta	ctg	cta	cgt	cag	gaa	ttc	864	
Leu	Gly	Gly	Ala	Leu	Gly	Ile	Ile	Ala	Val	Leu	Leu	Arg	Gln	Glu	Phe		
		275					280					285					
ctg	ctg	gtg	att	atg	ggg	ggc	gtg	ttc	gtg	gta	gaa	acg	ctt	tct	gtc	912	
Leu	Leu	Val	Ile	Met	Gly	Gly	Val	Phe	Val	Val	Glu	Thr	Leu	Ser	Val		
		290					295				300						
atc	ctg	cag	gtc	ggc	tcc	ttt	aaa	ctg	cgc	gga	caa	cgt	att	ttc	cgc	960	
Ile	Leu	Gln	Val	Gly	Ser	Phe	Lys	Leu	Arg	Gly	Gln	Arg	Ile	Phe	Arg		
305					310				315					320			
atg	gca	ccg	att	cat	cac	cac	tat	gaa	ctg	aaa	ggc	tgg	ccg	gaa	ccg	1008	
Met	Ala	Pro	Ile	His	His	His	Tyr	Glu	Leu	Lys	Gly	Trp	Pro	Glu	Pro		
				325				330						335			
cgc	gtc	att	gtg	cgt	ttc	tgg	att	att	tcg	ctg	atg	ctg	gtt	ctg	att	1056	
Arg	Val	Ile	Val	Arg	Phe	Trp	Ile	Ile	Ser	Leu	Met	Leu	Val	Leu	Ile		
			340					345					350				
ggg	ctg	gca	acg	ctg	aag	gta	cgt	taa								1083	
Gly	Leu	Ala	Thr	Leu	Lys	Val	Arg	*									
		355					360										

<210> 259

<211> 1317

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (1317)

<400> 259

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Met Ala Asp Tyr Gln Gly Lys Asn Val Val Ile Ile Gly Leu Gly Leu	
1 5 10 15	
acc ggg ctt tcc tgc gtg gac ttt ttc ctc gct cgc ggt gtg acg ccg	96
Thr Gly Leu Ser Cys Val Asp Phe Phe Leu Ala Arg Gly Val Thr Pro	
20 25 30	
cgc gtt atg gat acg cgt atg aca ccg cct ggc ctg gat aaa tta ccc	144
Arg Val Met Asp Thr Arg Met Thr Pro Pro Gly Leu Asp Lys Leu Pro	
35 40 45	
gaa gcc gta gaa cgc cac acg ggc agt ctg aat gat gaa tgg ctg atg	192
Glu Ala Val Glu Arg His Thr Gly Ser Leu Asn Asp Glu Trp Leu Met	
50 55 60	
gcg gca gat ctg att gtc gcc agt ccc ggt att gca ctg gcg cat cca	240
Ala Ala Asp Leu Ile Val Ala Ser Pro Gly Ile Ala Leu Ala His Pro	
65 70 75 80	
tcc tta agc gct gcc gct gat gcc gga atc gaa atc gtt ggc gat atc	288
Ser Leu Ser Ala Ala Ala Asp Ala Gly Ile Glu Ile Val Gly Asp Ile	
85 90 95	
gag ctg ttc tgt cgc gaa gca caa gca ccg att gtg gcg att acc ggt	336
Glu Leu Phe Cys Arg Glu Ala Gln Ala Pro Ile Val Ala Ile Thr Gly	
100 105 110	
tct aac ggc aaa agc acg gtc acc acg cta gtg ggt gaa atg gcg aaa	384
Ser Asn Gly Lys Ser Thr Val Thr Thr Leu Val Gly Glu Met Ala Lys	
115 120 125	
gcg gcg ggg gtt aac gtt ggt gtg ggt ggc aat att ggc ctg cct gcg	432
Ala Ala Gly Val Asn Val Gly Val Gly Gly Asn Ile Gly Leu Pro Ala	
130 135 140	
ttg atg cta ctg gat gat gag tgt gaa ctg tac gtg ctg gaa ctg tcg	480
Leu Met Leu Leu Asp Asp Glu Cys Glu Leu Tyr Val Leu Glu Leu Ser	
145 150 155 160	
agc ttc cag ctg gaa acc acc tcc agc tta cag gcg gta gca gcg acc	528
Ser Phe Gln Leu Glu Thr Thr Ser Ser Leu Gln Ala Val Ala Ala Thr	
165 170 175	
att ctg aac gtg act gaa gat cat atg gat cgc tat ccg ttt ggt tta	576
Ile Leu Asn Val Thr Glu Asp His Met Asp Arg Tyr Pro Phe Gly Leu	
180 185 190	
caa cag tat cgt gca gca aaa ctg cgc att tac gaa aac gcg aaa gtt	624
Gln Gln Tyr Arg Ala Ala Lys Leu Arg Ile Tyr Glu Asn Ala Lys Val	
195 200 205	

tgc gtg gtt aat gct gat gat gcc tta aca atg ccg att cgc ggt gcg	672
Cys Val Val Asn Ala Asp Asp Ala Leu Thr Met Pro Ile Arg Gly Ala	
210 215 220	
gat gaa cgc tgc gtc agc ttt ggc gtc aac atg ggt gac tat cac ctg	720
Asp Glu Arg Cys Val Ser Phe Gly Val Asn Met Gly Asp Tyr His Leu	
225 230 235 240	
aat cat cag cag ggc gaa acc tgg ctg cgg gtt aaa ggc gag aaa gtg	768
Asn His Gln Gln Gly Glu Thr Trp Leu Arg Val Lys Gly Glu Lys Val	
245 250 255	
ctg aat gtg aaa gag atg aaa ctt tcc ggg cag cat aac tac acc aat	816
Leu Asn Val Lys Glu Met Lys Leu Ser Gly Gln His Asn Tyr Thr Asn	
260 265 270	
gcg ctg gcg gcg ctg gcg ctg gca gat gct gca ggg tta ccg cgt gcc	864
Ala Leu Ala Ala Leu Ala Leu Ala Asp Ala Ala Gly Leu Pro Arg Ala	
275 280 285	
agc agc ctg aaa gcg tta acc aca ttc act ggt ctg ccg cat cgc ttt	912
Ser Ser Leu Lys Ala Leu Thr Thr Phe Thr Gly Leu Pro His Arg Phe	
290 295 300	
gaa gtt gtg ctg gag cat aac ggc gta cgt tgg att aac gat tcg aaa	960
Glu Val Val Leu Glu His Asn Gly Val Arg Trp Ile Asn Asp Ser Lys	
305 310 315 320	
gcg acc aac gtc ggc agt acg gaa gcg gcg ctg aat ggc ctg cac gta	1008
Ala Thr Asn Val Gly Ser Thr Glu Ala Ala Leu Asn Gly Leu His Val	
325 330 335	
gac ggc aca ctg cat ttg ttg ctg ggt ggc gat ggt aaa tcg gcg gac	1056
Asp Gly Thr Leu His Leu Leu Leu Gly Gly Asp Gly Lys Ser Ala Asp	
340 345 350	
ttt agc cca ctg gcg cgt tac ctg aat ggc gat aac gta cgt ctg tat	1104
Phe Ser Pro Leu Ala Arg Tyr Leu Asn Gly Asp Asn Val Arg Leu Tyr	
355 360 365	
tgt ttc ggt cgt gac ggc gcg cag ctg gcg gcg cta cgc ccg gaa gtg	1152
Cys Phe Gly Arg Asp Gly Ala Gln Leu Ala Ala Leu Arg Pro Glu Val	
370 375 380	
gca gaa caa acc gaa act atg gaa cag gcg atg cgc ttg ctg gct ccg	1200
Ala Glu Gln Thr Glu Thr Met Glu Gln Ala Met Arg Leu Leu Ala Pro	
385 390 395 400	
cgt gtt cag ccg ggc gat atg gtt ctg ctc tcc cca gcc tgt gcc agc	1248
Arg Val Gln Pro Gly Asp Met Val Leu Leu Ser Pro Ala Cys Ala Ser	
405 410 415	
ctt gat cag ttc aag aac ttt gaa caa cga ggc aat gag ttt gcc cgt	1296
Leu Asp Gln Phe Lys Asn Phe Glu Gln Arg Gly Asn Glu Phe Ala Arg	
420 425 430	
ctg gcg aag gag tta ggt tga	1317
Leu Ala Lys Glu Leu Gly *	
435	

<210> 260

<211> 1245

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1245)

<400> 260

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1 5 10 15

agt atc ctg gtc tgg atc tcc acg gcg cta aag ggc tgg gtg atg ggc 96
Ser Ile Leu Val Trp Ile Ser Thr Ala Leu Lys Gly Trp Val Met Gly
20 25 30

tcg cgg gaa aaa gat acc gac agc ctg atc atg tac gat cgc acc tta 144
Ser Arg Glu Lys Asp Thr Asp Ser Leu Ile Met Tyr Asp Arg Thr Leu
35 40 45

ctg tgg ctg acc ttc ggc ctc gcg gcg att ggc ttt atc atg gtg acc 192
Leu Trp Leu Thr Phe Gly Leu Ala Ala Ile Gly Phe Ile Met Val Thr
50 55 60

tcg gcg tca atg ccc ata ggg caa cgc tta acc aac gat ccg ttc ttc 240
Ser Ala Ser Met Pro Ile Gly Gln Arg Leu Thr Asn Asp Pro Phe Phe
65 70 75 80

ttc gcg aag cgt gat ggt gtc tat ctg att ttg gcg ttt att ctg gcg 288
Phe Ala Lys Arg Asp Gly Val Tyr Leu Ile Leu Ala Phe Ile Leu Ala
85 90 95

atc att acg ctg cgt ctg ccg atg gag ttc tgg caa cgc tac agt gcc 336
Ile Ile Thr Leu Arg Leu Pro Met Glu Phe Trp Gln Arg Tyr Ser Ala
100 105 110

acg atg ctg ctc gga tct atc atc ctg ctg atg atc gtc ctg gta gtg 384
Thr Met Leu Leu Gly Ser Ile Ile Leu Leu Met Ile Val Leu Val Val
115 120 125

ggt agc tcg gtt aaa ggg gca tcg cgt tgg atc gat ctc ggt ttg ctg 432
Gly Ser Ser Val Lys Gly Ala Ser Arg Trp Ile Asp Leu Gly Leu Leu
130 135 140

cgt atc cag cct gcg gag ctg aca aaa ctg tcg ctg ttt tgc tat atc 480
Arg Ile Gln Pro Ala Glu Leu Thr Lys Leu Ser Leu Phe Cys Tyr Ile
145 150 155 160

gcc aac tat ctg gtg cgt aaa ggc gac gaa gta cgt aat aac ctg cgc 528
Ala Asn Tyr Leu Val Arg Lys Gly Asp Glu Val Arg Asn Asn Leu Arg
165 170 175

ggc ttc ctg aaa ccg atg ggc gtg att ctg gtg ttg gca gtg tta ctg 576
Gly Phe Leu Lys Pro Met Gly Val Ile Leu Val Leu Ala Val Leu Leu
180 185 190

ctg gca cag cca gac ctt ggt acg gtg gtg gtg ttg ttt gtg act acg 624
Leu Ala Gln Pro Asp Leu Gly Thr Val Val Val Leu Phe Val Thr Thr
195 200 205

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ctg gcg atg ttg ttc	ctg gcg gga gcg aaa ttg tgg	cag ttc att gcc	672
Leu Ala Met Leu Phe	Leu Ala Gly Ala Lys Leu Trp	Gln Phe Ile Ala	
210	215	220	
att atc ggt atg ggc	att tca gcg gtt gtg ttg ctg	ata ctc gcc gaa	720
Ile Ile Gly Met Gly	Ile Ser Ala Val Val Leu Leu	Ile Leu Ala Glu	
225	230	235 240	
ccg tac cgt atc cgc	cgt gtt acc gca ttc tgg aac	ccg tgg gaa gat	768
Pro Tyr Arg Ile Arg	Arg Val Thr Ala Phe Trp	Asn Pro Trp Glu Asp	
245	250	255	
ccc ttt ggc agc ggc	tat cag tta acg caa tcg ctg	atg gcg ttt ggt	816
Pro Phe Gly Ser Gly	Tyr Gln Leu Thr Gln Ser Leu	Met Ala Phe Gly	
260	265	270	
cgc ggc gaa ctt tgg	ggg caa ggt tta ggt aac	tcg gta caa aaa ctg	864
Arg Gly Glu Leu Trp	Gly Gln Leu Gly Asn Ser	Val Gln Lys Leu	
275	280	285	
gag tat ctg ccg gaa	gcg cac act gac ttt att	ttc gcc att atc ggc	912
Glu Tyr Leu Pro Glu	Ala His Thr Asp Phe Ile	Phe Ala Ile Ile Gly	
290	295	300	
gaa gaa ctg ggg tat	gtc ggt gtg gtg ctg gca	ctt tta atg gta ttc	960
Glu Glu Leu Gly Tyr	Val Gly Val Val Leu Ala	Leu Leu Met Val Phe	
305	310	315 320	
ttc gtc gct ttt cgc	gcg atg tcg att ggc	cgt aaa gca tta gaa att	1008
Phe Val Ala Phe Arg	Ala Met Ser Ile Gly Arg	Lys Ala Leu Glu Ile	
325	330	335	
gac cac cgt ttt tcc	ggt ttt ctc gcc tgt tct	att ggc atc tgg ttt	1056
Asp His Arg Phe Ser	Gly Phe Leu Ala Cys Ser	Ile Gly Ile Trp Phe	
340	345	350	
agc ttc cag gcg ctg	gtt aac gta ggc gcg gcg	gcg ggg atg tta ccg	1104
Ser Phe Gln Ala Leu	Val Asn Val Gly Ala Ala	Ala Gly Met Leu Pro	
355	360	365	
acc aaa ggt ctg aca	ttg ccg ctg atc agt tac	ggt ggt tcg agc tta	1152
Thr Lys Gly Leu Thr	Leu Pro Leu Ile Ser Tyr	Gly Gly Ser Ser Leu	
370	375	380	
ctg att atg tcg aca	gcc atc atg atg ctg ttg	cgt att gat tat gaa	1200
Leu Ile Met Ser Thr	Ala Ile Met Met Leu Leu	Arg Ile Asp Tyr Glu	
385	390	395 400	
acg cgt ctg gag aaa	gcg cag gcg ttt gta cga	ggt tca cga tga	1245
Thr Arg Leu Glu Lys	Ala Gln Ala Phe Val Arg	Gly Ser Arg *	
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<210> 261

<211> 1068

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (1068)

<400> 261

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gga cat gta ttc ccg gga ctg gcg gtt gcg cac cat cta atg gct cag	96
Gly His Val Phe Pro Gly Leu Ala Val Ala His His Leu Met Ala Gln	
20 25 30	
ggt tgg caa gtt cgc tgg ctg ggg act gcc gac cgt atg gaa gcg gac	144
Gly Trp Gln Val Arg Trp Leu Gly Thr Ala Asp Arg Met Glu Ala Asp	
35 40 45	
tta gtg cca aaa cat ggc atc gaa att gat ttc att cgt atc tct ggt	192
Leu Val Pro Lys His Gly Ile Glu Ile Asp Phe Ile Arg Ile Ser Gly	
50 55 60	
ctg cgt gga aaa ggt ata aaa gca ctg ata gct gcc ccg ctg cgt atc	240
Leu Arg Gly Lys Gly Ile Lys Ala Leu Ile Ala Ala Pro Leu Arg Ile	
65 70 75 80	
ttc aac gcc tgg cgt cag gcg cgg gcg att atg aaa gcg tac aaa cct	288
Phe Asn Ala Trp Arg Gln Ala Arg Ala Ile Met Lys Ala Tyr Lys Pro	
85 90 95	
gac gtg gtg ctc ggt atg gga ggc tac gtg tca ggt cca ggt ggt ctg	336
Asp Val Val Leu Gly Met Gly Gly Tyr Val Ser Gly Pro Gly Gly Leu	
100 105 110	
gcc gcg tgg tcg tta ggc att ccg gtt gta ctt cat gaa caa aac ggt	384
Ala Ala Trp Ser Leu Gly Ile Pro Val Val Leu His Glu Gln Asn Gly	
115 120 125	
att gcg ggc tta acc aat aaa tgg ctg gcg aag att gcc acc aaa gtg	432
Ile Ala Gly Leu Thr Asn Lys Trp Leu Ala Lys Ile Ala Thr Lys Val	
130 135 140	
atg cag gcg ttt cca ggt gct ttc cct aat gcg gaa gta gtg ggt aac	480
Met Gln Ala Phe Pro Gly Ala Phe Pro Asn Ala Glu Val Val Gly Asn	
145 150 155 160	
ccg gtg cgt acc gat gtg ttg gcg ctg ccg ttg ccg cag caa cgt ttg	528
Pro Val Arg Thr Asp Val Leu Ala Leu Pro Leu Pro Gln Gln Arg Leu	
165 170 175	
gct gga cgt gaa ggt ccg gtt cgt gtg ctg gta gtg ggt ggt tct cag	576
Ala Gly Arg Glu Gly Pro Val Arg Val Leu Val Val Gly Gly Ser Gln	
180 185 190	
ggc gca cgc att ctt aac cag aca atg ccg cag gtt gct gcg aaa ctg	624
Gly Ala Arg Ile Leu Asn Gln Thr Met Pro Gln Val Ala Ala Lys Leu	
195 200 205	
ggt gat tca gtc act atc tgg cat cag agc ggc aaa ggt tcg caa caa	672
Gly Asp Ser Val Thr Ile tgg His Gln Ser Gly Lys Gly Ser Gln Gln	
210 215 220	
tcc gtt gaa cag gcg tat gcc gaa gcg ggg caa ccg cag cat aaa gtg	720

Ser Val Glu Gln Ala Tyr Ala Glu Ala Gly Gln Pro Gln His Lys Val
 225 230 235 240
 acg gaa ttt att gat gat atg gcg gcg gcg tat gcg tgg gcg gat gtc 768
 Thr Glu Phe Ile Asp Asp Met Ala Ala Ala Tyr Ala Trp Ala Asp Val
 245 250 255
 gtc gtt tgc cgc tcc ggt gcg tta acg gtg agt gaa atc gcc gcg gca 816
 Val Val Cys Arg Ser Gly Ala Leu Thr Val Ser Glu Ile Ala Ala Ala
 260 265 270
 gga cta ccg gcg ttg ttt gtg ccg ttt caa cat aaa gac cgc cag caa 864
 Gly Leu Pro Ala Leu Phe Val Pro Phe Gln His Lys Asp Arg Gln Gln
 275 280 285
 tac tgg aat gcg cta ccg ctg gaa aaa gcg ggc gca gcc aaa att atc 912
 Tyr Trp Asn Ala Leu Pro Leu Glu Lys Ala Gly Ala Ala Lys Ile Ile
 290 295 300
 gag cag cca cag ctt agc gtg gat gct gtc gcc aac acc ctg gcc ggg 960
 Glu Gln Pro Gln Leu Ser Val Asp Ala Val Ala Asn Thr Leu Ala Gly
 305 310 315 320
 tgg tcg cga gaa acc tta tta acc atg gca gaa cgc gcc cgc gct gca 1008
 Trp Ser Arg Glu Thr Leu Leu Thr Met Ala Glu Arg Ala Arg Ala Ala
 325 330 335
 tcc att ccg gat gcc acc gag cga gtg gca aat gaa gtg agc cgg gtt 1056
 Ser Ile Pro Asp Ala Thr Glu Arg Val Ala Asn Glu Val Ser Arg Val
 340 345 350
 gcc ccg gcg taa 1068
 Ala Arg Ala *
 355
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 <211> 1476
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 <213> Escherichia coli
 <220>
 <221> CDS
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 Met Asn Thr Gln Gln Leu Ala Lys Leu Arg Ser Ile Val Pro Glu Met
 1 5 10 15
 cgt cgc gtt ccg cac ata cat ttt gtc ggc att ggt ggt gcc ggt atg 96
 Arg Arg Val Arg His Ile His Phe Val Gly Ile Gly Gly Ala Gly Met
 20 25 30
 ggc ggt att gcc gaa gtt ctg gcc aat gaa ggt tat cag atc agt ggt 144
 Gly Gly Ile Ala Glu Val Leu Ala Asn Glu Gly Tyr Gln Ile Ser Gly
 35 40 45
 tcc gat tta gcg cca aat ccg gtc acg cag cag tta atg aat ctg ggt 192
 Ser Asp Leu Ala Pro Asn Pro Val Thr Gln Gln Leu Met Asn Leu Gly
 50 55 60

gcg acg att tat ttc aac cat cgc ccg gaa aac gta cgt gat gcc agc	240
Ala Thr Ile Tyr Phe Asn His Arg Pro Glu Asn Val Arg Asp Ala Ser	
65 70 75 80	
gtg gtc gtt gtt tcc agc gcg att tct gcc gat aac ccg gaa att gtc	288
Val Val Val Val Ser Ser Ala Ile Ser Ala Asp Asn Pro Glu Ile Val	
85 90 95	
gcc gct cat gaa gcg cgt att ccg gtg atc cgt cgt gcc gaa atg ctg	336
Ala Ala His Glu Ala Arg Ile Pro Val Ile Arg Arg Ala Glu Met Leu	
100 105 110	
gct gag tta atg cgt ttt cgt cat ggc atc gcc att gcc gga acg cac	384
Ala Glu Leu Met Arg Phe Arg His Gly Ile Ala Ile Ala Gly Thr His	
115 120 125	
ggc aaa acg aca acc acc gcg atg gtt tcc agc atc tac gca gaa gcg	432
Gly Lys Thr Thr Thr Thr Ala Met Val Ser Ser Ile Tyr Ala Glu Ala	
130 135 140	
ggg ctc gac cca acc ttc gtt aac ggc ggg ctg gta aaa gcg gcg ggg	480
Gly Leu Asp Pro Thr Phe Val Asn Gly Gly Leu Val Lys Ala Ala Gly	
145 150 155 160	
gtt cat gcg cgt ttg ggg cat ggt cgg tac ctg att gcc gaa gca gat	528
Val His Ala Arg Leu Gly His Gly Arg Tyr Leu Ile Ala Glu Ala Asp	
165 170 175	
gag agt gat gca tcg ttc ctg cat ctg caa ccg atg gtg gcg att gtc	576
Glu Ser Asp Ala Ser Phe Leu His Leu Gln Pro Met Val Ala Ile Val	
180 185 190	
acc aat atc gaa gcc gac cac atg gat acc tac cag ggc gac ttt gag	624
Thr Asn Ile Glu Ala Asp His Met Asp Thr Tyr Gln Gly Asp Phe Glu	
195 200 205	
aat tta aaa cag act ttt att aat ttt ctg cac aac ctg ccg ttt tac	672
Asn Leu Lys Gln Thr Phe Ile Asn Phe Leu His Asn Leu Pro Phe Tyr	
210 215 220	
ggg cgt gcg gtg atg tgt gtt gat gat ccg gtg atc cgc gaa ttg tta	720
Gly Arg Ala Val Met Cys Val Asp Asp Pro Val Ile Arg Glu Leu Leu	
225 230 235 240	
ccg cga gtg ggg cgt cag acc acg act tac ggc ttc agc gaa gat gcc	768
Pro Arg Val Gly Arg Gln Thr Thr Thr Tyr Gly Phe Ser Glu Asp Ala	
245 250 255	
gac gtg cgt gta gaa gat tat cag cag att ggc ccg cag ggg cac ttt	816
Asp Val Arg Val Glu Asp Tyr Gln Gln Ile Gly Pro Gln Gly His Phe	
260 265 270	
acg ctg ctg cgc cag gac aaa gag ccg atg cgc gtc acc ctg aat gcg	864
Thr Leu Leu Arg Gln Asp Lys Glu Pro Met Arg Val Thr Leu Asn Ala	
275 280 285	
cca ggt cgt cat aac gcg ctg aac gcc gca gct gcg gtt gcg gtt gct	912
Pro Gly Arg His Asn Ala Leu Asn Ala Ala Ala Val Ala Val Ala	
290 295 300	

acg gaa gag ggc att gac gac gag gct att ttg cgg gcg ctt gaa agc 960
 Thr Glu Glu Gly Ile Asp Asp Glu Ala Ile Leu Arg Ala Leu Glu Ser
 305 310 315 320

 ttc cag ggg act ggt cgc cgt ttt gat ttc ctc ggt gaa ttc ccg ctg 1008
 Phe Gln Gly Thr Gly Arg Arg Phe Asp Phe Leu Gly Glu Phe Pro Leu
 325 330 335

 gag cca gtg aat ggt aaa agc ggt acg gca atg ctg gtc gat gac tac 1056
 Glu Pro Val Asn Gly Lys Ser Gly Thr Ala Met Leu Val Asp Asp Tyr
 340 345 350

 ggc cac cac ccg acg gaa gtg gac gcc acc att aaa gcg gcg cgc gca 1104
 Gly His His Pro Thr Glu Val Asp Ala Thr Ile Lys Ala Ala Arg Ala
 355 360 365

 ggc tgg ccg gat aaa aac ctg gta atg ctg ttt cag ccg cac cgt ttt 1152
 Gly Trp Pro Asp Lys Asn Leu Val Met Leu Phe Gln Pro His Arg Phe
 370 375 380

 acc cgt acg cgc gac ctg tat gat gat ttc gcc aat gtg ctg acg cag 1200
 Thr Arg Thr Arg Asp Leu Tyr Asp Asp Phe Ala Asn Val Leu Thr Gln
 385 390 395 400

 gtt gat acc ctg ttg atg ctg gaa gtg tat ccg gct ggc gaa gcg cca 1248
 Val Asp Thr Leu Leu Met Leu Glu Val Tyr Pro Ala Gly Glu Ala Pro
 405 410 415

 att ccg gga gcg gac agc cgt tcg ctg tgt cgc aca att cgt gga cgt 1296
 Ile Pro Gly Ala Asp Ser Arg Ser Leu Cys Arg Thr Ile Arg Gly Arg
 420 425 430

 ggg aaa att gat ccc att ctg gtg ccg gat ccg gcg cgg gta gcc gag 1344
 Gly Lys Ile Asp Pro Ile Leu Val Pro Asp Pro Ala Arg Val Ala Glu
 435 440 445

 atg ctg gca ccg gta tta acc ggt aac gac ctg att ctc gtt cag ggg 1392
 Met Leu Ala Pro Val Leu Thr Gly Asn Asp Leu Ile Leu Val Gln Gly
 450 455 460

 gct ggt aat att gga aaa att gcc cgt tct tta gct gaa atc aaa ctg 1440
 Ala Gly Asn Ile Gly Lys Ile Ala Arg Ser Leu Ala Glu Ile Lys Leu
 465 470 475 480

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<212> DNA

<213> Escherichia coli

<220>

<221> CDS

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<400> 263

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gaa gtt tct ctg aat tct ggc gca gcg gtg tta gcc gga ctg cgt gaa	96			
Glu Val Ser Leu Asn Ser Gly Ala Val Leu Ala Gly Leu Arg Glu				
20	25	30		
ggc ggt att gac gcg tat cct gtc gac ccg aaa gaa gtc gac gtg acg	144			
Gly Gly Ile Asp Ala Tyr Pro Val Asp Pro Lys Glu Val Asp Val Thr				
35	40	45		
caa ctg aag tgc atg ggc ttt cag aaa gtg ttt atc gcg cta cac ggt	192			
Gln Leu Lys Ser Met Gly Phe Gln Lys Val Phe Ile Ala Leu His Gly				
50	55	60		
cgc ggc ggt gaa gat ggt acg ctg cag ggg atg ctc gag ctg atg ggc	240			
Arg Gly Gly Glu Asp Gly Thr Leu Gln Gly Met Leu Glu Leu Met Gly				
65	70	75	80	
ttg cct tat acc gga agc gga gtg atg gca tct gcg ctt tca atg gat	288			
Leu Pro Tyr Thr Gly Ser Gly Val Met Ala Ser Ala Leu Ser Met Asp				
85	90	95		
aaa cta cgc agc aaa ctt cta tgg caa ggt gcc ggt tta ccg gtc gcg	336			
Lys Leu Arg Ser Lys Leu Leu Trp Gln Gly Ala Gly Leu Pro Val Ala				
100	105	110		
ccg tgg gta gcg tta acc cgc gca gag ttt gaa aaa ggc ctg agc gat	384			
Pro Trp Val Ala Leu Thr Arg Ala Glu Phe Glu Lys Gly Leu Ser Asp				
115	120	125		
aag cag tta gca gaa att tct gct ctg ggt ttg ccg gtt atc gtt aag	432			
Lys Gln Leu Ala Glu Ile Ser Ala Leu Gly Leu Pro Val Ile Val Lys				
130	135	140		
ccg agc cgc gaa ggt tcc agt gtg gga atg tca aaa gta gta gca gaa	480			
Pro Ser Arg Glu Gly Ser Ser Val Gly Met Ser Lys Val Val Ala Glu				
145	150	155	160	
aat gct cta caa gat gca tta aga ttg gca ttt cag cac gat gaa gaa	528			
Asn Ala Leu Gln Asp Ala Leu Arg Leu Ala Phe Gln His Asp Glu Glu				
165	170	175		
gta ttg att gaa aaa tgg cta agt ggg ccg gag ttc acg gtt gcg ata	576			
Val Leu Ile Glu Lys Trp Leu Ser Gly Pro Glu Phe Thr Val Ala Ile				
180	185	190		
ctc ggt gaa gaa att tta ccg tca ata cgt att caa ccg tcc gga acc	624			
Leu Gly Glu Glu Ile Leu Pro Ser Ile Arg Ile Gln Pro Ser Gly Thr				
195	200	205		
ttc tat gat tat gag gcg aag tat ctc tct gat gag aca cag tat ttc	672			
Phe Tyr Asp Tyr Glu Ala Lys Tyr Leu Ser Asp Glu Thr Gln Tyr Phe				
210	215	220		
tgc ccc gca ggt ctg gaa gcg tca caa gag gcc aat ttg cag gca tta	720			
Cys Pro Ala Gly Leu Glu Ala Ser Gln Glu Ala Asn Leu Gln Ala Leu				
225	230	235	240	
gtg ctg aaa gca tgg acg acg tta ggt tgc aaa gga tgg gga cgt att	768			
Val Leu Lys Ala Trp Thr Thr Leu Gly Cys Lys Gly Trp Gly Arg Ile				
245	250	255		

gac gtt atg ctg gac agc gat gga cag ttt tat ctg ctg gaa gcc aat 816
 Asp Val Met Leu Asp Ser Asp Gly Gln Phe Tyr Leu Leu Glu Ala Asn
 260 265 270

acc tca ccg ggt atg acc agc cac agc ctg gtg ccg atg gcg gca cgt 864
 Thr Ser Pro Gly Met Thr Ser His Ser Leu Val Pro Met Ala Ala Arg
 275 280 285

cag gca ggt atg agc ttc tcg cag ttg gta gta cga att ctg gaa ctg 912
 Gln Ala Gly Met Ser Phe Ser Gln Leu Val Val Arg Ile Leu Glu Leu
 290 295 300

gcg gac taa 921
 Ala Asp *
 305

<210> 264
 <211> 606
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(606)

<400> 264
 atg gcg ctg cat gac gaa aac gtc gtc tgg cat agc cat ccg gtc act 48
 Met Ala Leu His Asp Glu Asn Val Val Trp His Ser His Pro Val Thr
 1 5 10 15

gtg caa caa cgc gag cta cac cac ggt cat cgt ggt gta gtg ctg tgg 96
 Val Gln Gln Arg Glu Leu His His Gly His Arg Gly Val Val Leu Trp
 20 25 30

ttt acc ggc ctc tcc ggg tcc ggt aaa tca acg gtc gcc ggg gcg ctg 144
 Phe Thr Gly Leu Ser Gly Ser Gly Lys Ser Thr Val Ala Gly Ala Leu
 35 40 45

gag gag gcg tta cat aaa ctc ggc gtc agt acg tat ctg ctg gat ggc 192
 Glu Glu Ala Leu His Lys Leu Gly Val Ser Thr Tyr Leu Leu Asp Gly
 50 55 60

gac aat gtt cgc cac gga tta tgc agc gat ctc ggt ttt agc gat gcc 240
 Asp Asn Val Arg His Gly Leu Cys Ser Asp Leu Gly Phe Ser Asp Ala
 65 70 75 80

gat cgt aaa gag aat atc cgt cgc gtc ggt gaa gtg gcg aat ttg atg 288
 Asp Arg Lys Glu Asn Ile Arg Arg Val Gly Glu Val Ala Asn Leu Met
 85 90 95

gtt gaa gcc gga ctg gtg gtg ctg acc gca ttt atc tcg cca cac cgc 336
 Val Glu Ala Gly Leu Val Val Leu Thr Ala Phe Ile Ser Pro His Arg
 100 105 110

gcc gaa cgc cag atg gtt cgc gaa cgc gta gga gaa ggg cgc ttt atc 384
 Ala Glu Arg Gln Met Val Arg Glu Arg Val Gly Glu Gly Arg Phe Ile
 115 120 125

gaa gtg ttt gtc gat acg ccg ctg gcg att tgc gaa gcc cgc gat ccc 432

Glu Val Phe Val Asp Thr Pro Leu Ala Ile Cys Glu Ala Arg Asp Pro
 130 135 140
 aaa ggc tta tat aag aaa gcg cgt gcc ggt gaa ctg cgc aac ttt acg 480
 Lys Gly Leu Tyr Lys Lys Ala Arg Ala Gly Glu Leu Arg Asn Phe Thr
 145 150 155 160
 gga ata gat tcc gtt tac gaa gcg cct gaa tcg gca gaa att cat ctc 528
 Gly Ile Asp Ser Val Tyr Glu Ala Pro Glu Ser Ala Glu Ile His Leu
 165 170 175
 aat ggt gaa caa tta gta aca aat ttg gta cag caa tta tta gat ctg 576
 Asn Gly Glu Gln Leu Val Thr Asn Leu Val Gln Gln Leu Leu Asp Leu
 180 185 190
 ttg aga cag aac gat att atc aga tcc tga 606
 Leu Arg Gln Asn Asp Ile Ile Arg Ser *
 195 200
 <210> 265
 <211> 1428
 <212> DNA
 <213> Escherichia coli
 <220>
 <221> CDS
 <222> (1)...(1428)
 <400> 265
 atg aac acc gca ctt gca caa caa atc gcc aat gaa ggc ggc gtc gaa 48
 Met Asn Thr Ala Leu Ala Gln Gln Ile Ala Asn Glu Gly Gly Val Glu
 1 5 10 15
 gcc tgg atg att gcg caa caa cat aaa agc ctg ctg cgt ttt ctg acc 96
 Ala Trp Met Ile Ala Gln Gln His Lys Ser Leu Leu Arg Phe Leu Thr
 20 25 30
 tgt ggt agc gtc gat gac ggc aaa agt act ctg att ggt cgt ctg ctg 144
 Cys Gly Ser Val Asp Asp Gly Lys Ser Thr Leu Ile Gly Arg Leu Leu
 35 40 45
 cac gat acc cgc caa atc tac gaa gat cag ctc tca tcg ctg cat aac 192
 His Asp Thr Arg Gln Ile Tyr Glu Asp Gln Leu Ser Ser Leu His Asn
 50 55 60
 gac agt aag cgt cac ggc acc cag ggc gaa aag ctg gat ctg gct ctg 240
 Asp Ser Lys Arg His Gly Thr Gln Gly Glu Lys Leu Asp Leu Ala Leu
 65 70 75 80
 ctg gtg gac ggc ctg caa gct gag cgc gaa cag ggc atc acc att gac 288
 Leu Val Asp Gly Leu Gln Ala Glu Arg Glu Gln Gly Ile Thr Ile Asp
 85 90 95
 gtg gcc tac cgc tat ttc tct acc gag aag cgt aaa ttt att atc gcc 336
 Val Ala Tyr Arg Tyr Phe Ser Thr Glu Lys Arg Lys Phe Ile Ile Ala
 100 105 110
 gac acc cca ggg cac gag cag tac acc cgc aat atg gcg act ggc gca 384
 Asp Thr Pro Gly His Glu Gln Tyr Thr Arg Asn Met Ala Thr Gly Ala
 115 120 125

tcg aca tgt gaa ctg gcg atc tta ctg atc gat gcc cgt aaa ggc gtg Ser Thr Cys Glu Leu Ala Ile Leu Leu Ile Asp Ala Arg Lys Gly Val 130 135 140	432
ctc gat caa acc cgt cgt cac agt ttt atc tcc aca ctg ttg ggg atc Leu Asp Gln Thr Arg Arg His Ser Phe Ile Ser Thr Leu Leu Gly Ile 145 150 155 160	480
aaa cat ctg gtc gtg gcg atc aac aaa atg gat ctg gtg gat tac agt Lys His Leu Val Val Ala Ile Asn Lys Met Asp Leu Val Asp Tyr Ser 165 170 175	528
gaa gag acg ttc acc cgt att cgt gaa gat tat ttg acc ttt gcc ggg Glu Glu Thr Phe Thr Arg Ile Arg Glu Asp Tyr Leu Thr Phe Ala Gly 180 185 190	576
cag ctg ccg ggt aat ctg gat atc cgc ttt gtg ccg ctc tct gca ctg Gln Leu Pro Gly Asn Leu Asp Ile Arg Phe Val Pro Leu Ser Ala Leu 195 200 205	624
gaa ggc gac aac gtg gca tcg caa agt gaa agt atg ccg tgg tac agc Glu Gly Asp Asn Val Ala Ser Gln Ser Glu Ser Met Pro Trp Tyr Ser 210 215 220	672
ggg ccg aca ctg ctc gaa gtg ctg gaa acc gtg gag atc cag cga gtg Gly Pro Thr Leu Leu Glu Val Leu Glu Thr Val Glu Ile Gln Arg Val 225 230 235 240	720
gtg gat gct cag cca atg cgc ttc ccg gtg cag tac gtt aat cgc ccg Val Asp Ala Gln Pro Met Arg Phe Pro Val Gln Tyr Val Asn Arg Pro 245 250 255	768
aat ctc gat ttt cgt ggt tac gcc gga acg ctg gca tcc ggt cgc gtg Asn Leu Asp Phe Arg Gly Tyr Ala Gly Thr Leu Ala Ser Gly Arg Val 260 265 270	816
gaa gtc ggg caa cgt gtc aaa gtg ctg ccc tct ggt gtg gaa tca aac Glu Val Gly Gln Arg Val Lys Val Leu Pro Ser Gly Val Glu Ser Asn 275 280 285	864
gtc gcg cgg atc gtg act ttt gat ggt gat cgc gaa gaa gcc ttt gcc Val Ala Arg Ile Val Thr Phe Asp Gly Asp Arg Glu Glu Ala Phe Ala 290 295 300	912
gga gaa gcg atc acc ctg gtg ctg acg gat gag atc gac atc agc cgt Gly Glu Ala Ile Thr Leu Val Leu Thr Asp Glu Ile Asp Ile Ser Arg 305 310 315 320	960
ggc gat ctg ctg ctg gcg gca gac gaa gcg tta ccg gcg gtg cag agc Gly Asp Leu Leu Ala Ala Asp Glu Ala Leu Pro Ala Val Gln Ser 325 330 335	1008
gcg tcg gtg gat gtg gta tgg atg gcg gaa cag ccg ctt tct cca ggg Ala Ser Val Asp Val Val Trp Met Ala Glu Gln Pro Leu Ser Pro Gly 340 345 350	1056
cag agt tac gac atc aaa att gcc ggt aag aag acg cgc gcg cgt gtt Gln Ser Tyr Asp Ile Lys Ile Ala Gly Lys Lys Thr Arg Ala Arg Val 355 360 365	1104

```

gat ggc att cgc tat cag gtt gat att aat aac ctt acc cag cgt gaa 1152
Asp Gly Ile Arg Tyr Gln Val Asp Ile Asn Asn Leu Thr Gln Arg Glu
370 375 380

gtt gaa aac ctg cca ctg aat ggg atc ggc ctc gtg gat ctc act ttt 1200
Val Glu Asn Leu Pro Leu Asn Gly Ile Gly Leu Val Asp Leu Thr Phe
385 390 395 400

gac gag ccg ctg gtg tta gat cgt tat caa caa aat ccg gtg acg ggt 1248
Asp Glu Pro Leu Val Leu Asp Arg Tyr Gln Gln Asn Pro Val Thr Gly
405 410 415

ggg ctg att ttt atc gat cgc ctg agc aat gtg acc gtg ggt gcc ggt 1296
Gly Leu Ile Phe Ile Asp Arg Leu Ser Asn Val Thr Val Gly Ala Gly
420 425 430

atg gtg cac gag cca gtt agc cag gca act gct gcg cca tct gaa ttc 1344
Met Val His Glu Pro Val Ser Gln Ala Thr Ala Ala Pro Ser Glu Phe
435 440 445

agt gca ttc gaa ctg gaa ttg aat gct ctg gtt cgt cgc cac ttt ccg 1392
Ser Ala Phe Glu Leu Glu Leu Asn Ala Leu Val Arg Arg His Phe Pro
450 455 460

cac tgg ggc gcg cgc gat ttg ctg ggg gat aaa taa 1428
His Trp Gly Ala Arg Asp Leu Leu Gly Asp Lys *
465 470 475

```

<210> 266

<211> 384

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(384)

<400> 266

```

atg cgc cat cgt aag agt ggt cgt caa ctg aac cgc aac agc agc cat 48
Met Arg His Arg Lys Ser Gly Arg Gln Leu Asn Arg Asn Ser Ser His
1 5 10 15

```

```

cgc cag gct atg ttc cgc aat atg gca ggt tca ctg gtt cgt cat gaa 96
Arg Gln Ala Met Phe Arg Asn Met Ala Gly Ser Leu Val Arg His Glu
20 25 30

```

```

atc atc aag acg act ctg cct aaa gcg aaa gag ctg cgc cgc gta gtt 144
Ile Ile Lys Thr Thr Leu Pro Lys Ala Lys Glu Leu Arg Arg Val Val
35 40 45

```

```

gag ccg ctg att act ctt gcc aag act gat agc gtt gct aat cgt cgt 192
Glu Pro Leu Ile Thr Leu Ala Lys Thr Asp Ser Val Ala Asn Arg Arg
50 55 60

```

```

ctg gca ttc gcc cgt act cgt gat aac gag atc gtg gca aaa ctg ttt 240
Leu Ala Phe Ala Arg Thr Arg Asp Asn Glu Ile Val Ala Lys Leu Phe
65 70 75 80

```

```

aac gaa ctg ggc ccg cgt ttc gcg agc cgt gcc ggt ggt tac act cgt 288
Asn Glu Leu Gly Pro Arg Phe Ala Ser Arg Ala Gly Gly Tyr Thr Arg

```

85	90	95	
att ctg aag tgt ggc ttc cgt gca ggc gac aac gcg ccg atg gct tac			336
Ile Leu Lys Cys Gly Phe Arg Ala Gly Asp Asn Ala Pro Met Ala Tyr			
100	105	110	
atc gag ctg gtt gat cgt tca gag aaa gca gaa gct gct gca gag taa			384
Ile Glu Leu Val Asp Arg Ser Glu Lys Ala Glu Ala Ala Glu *			
115	120	125	
<210> 267			
<211> 990			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1) ... (990)			
<400> 267			
atg cag ggt tct gtg aca gag ttt cta aaa ccg cgc ctg gtt gat atc			48
Met Gln Gly Ser Val Thr Glu Phe Leu Lys Pro Arg Leu Val Asp Ile			
1	5	10	15
gag caa gtg agt tcg acg cac gcc aag gtg acc ctt gag cct tta gag			96
Glu Gln Val Ser Ser Thr His Ala Lys Val Thr Leu Glu Pro Leu Glu			
20	25	30	
cg t ggc ttt ggc cat act ctg ggt aac gca ctg cgc cgt att ctg ctc			144
Arg Gly Phe Gly His Thr Leu Gly Asn Ala Leu Arg Arg Ile Leu Leu			
35	40	45	
tca tcg atg ccg ggt tgc gcg gtg acc gag gtt gag att gat ggt gta			192
Ser Ser Met Pro Gly Cys Ala Val Thr Glu Val Glu Ile Asp Gly Val			
50	55	60	
cta cat gag tac agc acc aaa gaa ggc gtt cag gaa gat atc ctg gaa			240
Leu His Glu Tyr Ser Thr Lys Glu Gly Val Gln Glu Asp Ile Leu Glu			
65	70	75	80
atc ctg ctc aac ctg aaa ggg ctg gcg gtg aga gtt cag ggc aaa gat			288
Ile Leu Leu Asn Leu Lys Gly Leu Ala Val Arg Val Gln Gly Lys Asp			
85	90	95	
gaa gtt att ctt acc ttg aat aaa tct ggc att ggc cct gtg act gca			336
Glu Val Ile Leu Thr Leu Asn Lys Ser Gly Ile Gly Pro Val Thr Ala			
100	105	110	
gcc gat atc acc cac gac ggt gat gtc gaa atc gtc aag ccg cag cac			384
Ala Asp Ile Thr His Asp Gly Asp Val Glu Ile Val Lys Pro Gln His			
115	120	125	
gtg atc tgc cac ctg acc gat gag aac gcg tct att agc atg cgt atc			432
Val Ile Cys His Leu Thr Asp Glu Asn Ala Ser Ile Ser Met Arg Ile			
130	135	140	
aaa gtt cag cgc ggt cgt ggt tat gtg ccg gct tct acc cga att cat			480
Lys Val Gln Arg Gly Arg Gly Tyr Val Pro Ala Ser Thr Arg Ile His			
145	150	155	160

```

tcg gaa gaa gat gag cgc cca atc ggc cgt ctg ctg gtc gac gca tgc 528
Ser Glu Glu Asp Glu Arg Pro Ile Gly Arg Leu Leu Val Asp Ala Cys
      165              170              175

tac agc cct gtg gag cgt att gcc tac aat gtt gaa gca gcg cgt gta 576
Tyr Ser Pro Val Glu Arg Ile Ala Tyr Asn Val Glu Ala Ala Arg Val
      180              185              190

gaa cag cgt acc gac ctg gac aag ctg gtc atc gaa atg gaa acc aac 624
Glu Gln Arg Thr Asp Leu Asp Lys Leu Val Ile Glu Met Glu Thr Asn
      195              200              205

ggc aca atc gat cct gaa gag gcg att cgt cgt gcg gca acc att ctg 672
Gly Thr Ile Asp Pro Glu Glu Ala Ile Arg Arg Ala Ala Thr Ile Leu
      210              215              220

gct gaa caa ctg gaa gct ttc gtt gac tta cgt gat gta cgt cag cct 720
Ala Glu Gln Leu Glu Ala Phe Val Asp Leu Arg Asp Val Arg Gln Pro
      225              230              235              240

gaa gtg aaa gaa gag aaa cca gag ttc gat ccg atc ctg ctg cgc cct 768
Glu Val Lys Glu Glu Lys Pro Glu Phe Asp Pro Ile Leu Leu Arg Pro
      245              250              255

gtt gac gat ctg gaa ttg act gtc cgc tct gct aac tgc ctt aaa gca 816
Val Asp Asp Leu Glu Leu Thr Val Arg Ser Ala Asn Cys Leu Lys Ala
      260              265              270

gaa gct atc cac tat atc ggt gat ctg gta cag cgt acc gag gtt gag 864
Glu Ala Ile His Tyr Ile Gly Asp Leu Val Gln Arg Thr Glu Val Glu
      275              280              285

ctc ctt aaa acg cct aac ctt ggt aaa aaa tct ctt act gag att aaa 912
Leu Leu Lys Thr Pro Asn Leu Gly Lys Lys Ser Leu Thr Glu Ile Lys
      290              295              300

gac gtg ctg gct tcc cgt gga ctg tct ctg ggc atg cgc ctg gaa aac 960
Asp Val Leu Ala Ser Arg Gly Leu Ser Leu Gly Met Arg Leu Glu Asn
      305              310              315              320

tgg cca ccg gca agc atc gct gac gag taa 990
Trp Pro Pro Ala Ser Ile Ala Asp Glu *
      325

```

<210> 268

<211> 621

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (621)

<400> 268

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atg gca aga tat ttg ggt cct aag ctc aag ctg agc cgt cgt gag ggc 48
Met Ala Arg Tyr Leu Gly Pro Lys Leu Lys Leu Ser Arg Arg Glu Gly
  1              5              10              15

```

```

acc gac tta ttc ctt aag tct ggc gtt cgc gcg atc gat acc aag tgt 96

```

Thr	Asp	Leu	Phe	Leu	Lys	Ser	Gly	Val	Arg	Ala	Ile	Asp	Thr	Lys	Cys	
		20						25					30			
aaa	att	gaa	caa	gct	cct	ggc	cag	cac	ggg	gcg	cgt	aaa	ccg	cgt	ctg	144
Lys	Ile	Glu	Gln	Ala	Pro	Gly	Gln	His	Gly	Ala	Arg	Lys	Pro	Arg	Leu	
		35					40					45				
tct	gac	tat	ggg	gtg	cag	ttg	cgt	gaa	aag	caa	aaa	gtt	cgc	cgt	atc	192
Ser	Asp	Tyr	Gly	Val	Gln	Leu	Arg	Glu	Lys	Gln	Lys	Val	Arg	Arg	Ile	
	50					55					60					
tat	ggg	gtg	ctg	gag	cgt	cag	ttc	cgt	aac	tac	tac	aaa	gaa	gca	gca	240
Tyr	Gly	Val	Leu	Glu	Arg	Gln	Phe	Arg	Asn	Tyr	Tyr	Lys	Glu	Ala	Ala	
	65				70				75						80	
cgt	ctg	aaa	ggc	aac	acc	ggg	gaa	aac	ctg	ttg	gct	ctg	ctg	gaa	ggg	288
Arg	Leu	Lys	Gly	Asn	Thr	Gly	Glu	Asn	Leu	Leu	Ala	Leu	Leu	Glu	Gly	
			85					90						95		
cgt	ctg	gac	aac	gtt	gta	tac	cgt	atg	ggc	ttc	ggg	gcc	act	cgt	gca	336
Arg	Leu	Asp	Asn	Val	Val	Tyr	Arg	Met	Gly	Phe	Gly	Ala	Thr	Arg	Ala	
			100					105					110			
gaa	gca	cgt	cag	ctg	gtt	agc	cat	aaa	gca	att	atg	gta	aac	ggg	cgt	384
Glu	Ala	Arg	Gln	Leu	Val	Ser	His	Lys	Ala	Ile	Met	Val	Asn	Gly	Arg	
		115					120					125				
gtt	gtt	aac	atc	gct	tct	tat	cag	gtt	agt	ccg	aat	gac	gtt	gta	agc	432
Val	Val	Asn	Ile	Ala	Ser	Tyr	Gln	Val	Ser	Pro	Asn	Asp	Val	Val	Ser	
		130				135					140					
att	cgt	gag	aaa	gcg	aag	aag	cag	tct	cgc	gtg	aaa	gcc	gct	ctg	gag	480
Ile	Arg	Glu	Lys	Ala	Lys	Lys	Gln	Ser	Arg	Val	Lys	Ala	Ala	Leu	Glu	
	145				150					155					160	
ctg	gct	gag	cag	cgt	gaa	aag	cca	acc	tgg	ctg	gaa	gtt	gat	gct	ggc	528
Leu	Ala	Glu	Gln	Arg	Glu	Lys	Pro	Thr	Trp	Leu	Glu	Val	Asp	Ala	Gly	
			165						170					175		
aag	atg	gaa	ggg	acg	ttt	aag	cgt	aag	ccg	gag	cgt	tct	gat	ctg	tct	576
Lys	Met	Glu	Gly	Thr	Phe	Lys	Arg	Lys	Pro	Glu	Arg	Ser	Asp	Leu	Ser	
		180						185					190			
gcg	gac	att	aac	gaa	cac	ctg	atc	gtc	gag	ctt	tac	tcc	aag	taa		621
Ala	Asp	Ile	Asn	Glu	His	Leu	Ile	Val	Glu	Leu	Tyr	Ser	Lys	*		
		195					200					205				

<210> 269

<211> 390

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(390)

<400> 269

atg	gca	aag	gca	cca	att	cgt	gca	cgt	aaa	cgt	gta	aga	aaa	caa	gtc	48
Met	Ala	Lys	Ala	Pro	Ile	Arg	Ala	Arg	Lys	Arg	Val	Arg	Lys	Gln	Val	

1	5	10	15	
tct gac ggc gtg gct cat atc cat gct tct ttc aac aac acc atc gtg	96			
Ser Asp Gly Val Ala His Ile His Ala Ser Phe Asn Asn Thr Ile Val				
20 25 30				
act atc act gat cgt cag ggt aac gcg ttg ggt tgg gca aca gcc ggt	144			
Thr Ile Thr Asp Arg Gln Gly Asn Ala Leu Gly Trp Ala Thr Ala Gly				
35 40 45				
ggg tcc ggt ttc cgt ggt tct cgc aaa tcc act ccg ttt gca gct cag	192			
Gly Ser Gly Phe Arg Gly Ser Arg Lys Ser Thr Pro Phe Ala Ala Gln				
50 55 60				
gtt gca gca gag cgt tgc gct gac gcc gtg aaa gaa tac ggc atc aag	240			
Val Ala Ala Glu Arg Cys Ala Asp Ala Val Lys Glu Tyr Gly Ile Lys				
65 70 75 80				
aat ctg gaa gtt atg gtt aaa ggt ccg ggt cca ggc cgc gaa tct act	288			
Asn Leu Glu Val Met Val Lys Gly Pro Gly Pro Gly Arg Glu Ser Thr				
85 90 95				
att cgt gct ctg aac gcc gca ggt ttc cgc atc act aac att act gat	336			
Ile Arg Ala Leu Asn Ala Ala Gly Phe Arg Ile Thr Asn Ile Thr Asp				
100 105 110				
gtg act ccg atc cct cat aac ggt tgt cgt ccg ccg aaa aaa cgt cgc	384			
Val Thr Pro Ile Pro His Asn Gly Cys Arg Pro Pro Lys Lys Arg Arg				
115 120 125				
gta taa	390			
Val *				

<210> 270

<211> 357

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(357)

<400> 270

gtg gcc cgt ata gca ggc att aac att cct gat cat aag cat gcc gta	48
Met Ala Arg Ile Ala Gly Ile Asn Ile Pro Asp His Lys His Ala Val	
1 5 10 15	
atc gca tta act tcg att tat ggc gtc ggc aag acc cgt tct aaa gcc	96
Ile Ala Leu Thr Ser Ile Tyr Gly Val Gly Lys Thr Arg Ser Lys Ala	
20 25 30	
atc ctg gct gca gcg ggt atc gct gaa gat gtt aag atc agt gag ctg	144
Ile Leu Ala Ala Ala Gly Ile Ala Glu Asp Val Lys Ile Ser Glu Leu	
35 40 45	
tct gaa gga caa atc gac acg ctg cgt gac gaa gtt gcc aaa ttt gtc	192
Ser Glu Gly Gln Ile Asp Thr Leu Arg Asp Glu Val Ala Lys Phe Val	
50 55 60	


```

gtt gaa ggt gat ctg cgc cgt gaa atc agc atg agc atc aag cgc ctg 240
Val Glu Gly Asp Leu Arg Arg Glu Ile Ser Met Ser Ile Lys Arg Leu
65 70 75 80

atg gat ctt ggt tgc tat cgc ggt ttg cgt cat cgt cgt ggt ctc ccg 288
Met Asp Leu Gly Cys Tyr Arg Gly Leu Arg His Arg Arg Gly Leu Pro
85 90 95

gtt cgc ggt cag cgt acc aag acc aac gca cgt acc cgt aag ggt ccg 336
Val Arg Gly Gln Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly Pro
100 105 110

cgc aaa ccg atc aag aaa taa 357
Arg Lys Pro Ile Lys Lys *
115

<210> 271
<211> 1383
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1383)

<400> 271
atg acg caa tta acc atg aaa gac aaa att ggc tac ggg ctg gga gac 48
Met Thr Gln Leu Thr Met Lys Asp Lys Ile Gly Tyr Gly Leu Gly Asp
1 5 10 15

acc gcc tgc ggc ttc gtc tgg cag gcc acg atg ttc ctg ctg gcc tat 96
Thr Ala Cys Gly Phe Val Trp Gln Ala Thr Met Phe Leu Leu Ala Tyr
20 25 30

ttc tac acc gac gtc ttc ggc ctg tgc ggc ggg att atg ggc acg ctg 144
Phe Tyr Thr Asp Val Phe Gly Leu Ser Ala Gly Ile Met Gly Thr Leu
35 40 45

ttt ttg gtc tcc cgc gtg ctc gac gcc gtc acc gac ccg ctg atg ggg 192
Phe Leu Val Ser Arg Val Leu Asp Ala Val Thr Asp Pro Leu Met Gly
50 55 60

ctg ctg gta gac cgc acc cgc acg cgg cac ggc cag ttc cgc ccg ttc 240
Leu Leu Val Asp Arg Thr Arg Thr Arg His Gly Gln Phe Arg Pro Phe
65 70 75 80

ctg ctg tgg ggg gcc atc ccg ttc ggc atc gtc tgc gtg ctg acc ttc 288
Leu Leu Trp Gly Ala Ile Pro Phe Gly Ile Val Cys Val Leu Thr Phe
85 90 95

tac acg ccg gac ttc tcc gca cag ggc aag atc atc tac gcc tgc gtg 336
Tyr Thr Pro Asp Phe Ser Ala Gln Gly Lys Ile Ile Tyr Ala Cys Val
100 105 110

acc tac att ctc ctg acc ctg gtc tac acc ttc gtt aac gtg ccg tac 384
Thr Tyr Ile Leu Leu Thr Leu Val Tyr Thr Phe Val Asn Val Pro Tyr
115 120 125

tgc gcc atg ccg ggc gtc atc acc gcc gac ccg aaa gag cgt cac gcc 432
Cys Ala Met Pro Gly Val Ile Thr Ala Asp Pro Lys Glu Arg His Ala

```

130	135	140	
ctg cag tcc tgg cgc ttc ttc ctg gcg gcg gcg ggc tcg ctc gct atc			480
Leu Gln Ser Trp Arg Phe Phe Leu Ala Ala Gly Ser Leu Ala Ile			
145	150	155	160
agc ggc atc gcg ctg ccg ctg gtg agc atc atc ggc aaa ggg gac gag			528
Ser Gly Ile Ala Leu Pro Leu Val Ser Ile Ile Gly Lys Gly Asp Glu			
	165	170	175
cag gtg ggc tac ttc ggc gcc atg tgc gtg ctg ggg ctg agc ggc gtg			576
Gln Val Gly Tyr Phe Gly Ala Met Cys Val Leu Gly Leu Ser Gly Val			
	180	185	190
gtg ctg ctc tac gtc tgc ttc ttc acg acc aaa gag cgc tac acc ttt			624
Val Leu Leu Tyr Val Cys Phe Phe Thr Thr Lys Glu Arg Tyr Thr Phe			
	195	200	205
gag gtg cag ccg ggc tcg tcg gtg gcg aaa gac ctt aag ctg ctg ctg			672
Glu Val Gln Pro Gly Ser Ser Val Ala Lys Asp Leu Lys Leu Leu Leu			
	210	215	220
ggc aac agc cag tgg cgc atc atg tgc gcg ttc aag atg atg gcg acc			720
Gly Asn Ser Gln Trp Arg Ile Met Cys Ala Phe Lys Met Met Ala Thr			
	225	230	240
tgc tcc aac gtg gtg cgc ggc ggg gcg acg ctc tac ttc gtg aaa tac			768
Cys Ser Asn Val Val Arg Gly Gly Ala Thr Leu Tyr Phe Val Lys Tyr			
	245	250	255
gtg atg gat cac ccg gag ttg gcg acc cag ttt tta ctt tac ggc agc			816
Val Met Asp His Pro Glu Leu Ala Thr Gln Phe Leu Leu Tyr Gly Ser			
	260	265	270
ctc gcc acc atg ttc ggc tcg ctt tgc tcc tca cgc ctg ctg ggc cgc			864
Leu Ala Thr Met Phe Gly Ser Leu Cys Ser Ser Arg Leu Leu Gly Arg			
	275	280	285
ttc gac cgc gtc acc gcc ttc aag tgg atc atc gtc gcc tac tcg ctg			912
Phe Asp Arg Val Thr Ala Phe Lys Trp Ile Ile Val Ala Tyr Ser Leu			
	290	295	300
atc agc ctg ctg att ttc gtc acc ccg gcg gag cac atc gcg ctc att			960
Ile Ser Leu Leu Ile Phe Val Thr Pro Ala Glu His Ile Ala Leu Ile			
	305	310	315
ttt gcc ctc aac atc ctg ttc ctg ttc gtc ttt aat acc acc acg ccg			1008
Phe Ala Leu Asn Ile Leu Phe Leu Phe Val Phe Asn Thr Thr Thr Pro			
	325	330	335
ctg cag tgg ctg atg gct tct gac gtg gtg gac tac gag gag agc cgc			1056
Leu Gln Trp Leu Met Ala Ser Asp Val Val Asp Tyr Glu Glu Ser Arg			
	340	345	350
agc ggt cgc cgc ctc gac ggg ctg gtg ttc tcc acc tac ctg ttc agc			1104
Ser Gly Arg Arg Leu Asp Gly Leu Val Phe Ser Thr Tyr Leu Phe Ser			
	355	360	365
ctg aag att ggc ctg gcg att ggc ggg gcg gtg gtg ggc tgg atc ctg			1152
Leu Lys Ile Gly Leu Ala Ile Gly Gly Ala Val Val Gly Trp Ile Leu			
	370	375	380

gcg tac gtc aac tat tcc gcc agc agc agc gtg cag ccg gtt gag gtg 1200
 Ala Tyr Val Asn Tyr Ser Ala Ser Ser Ser Val Gln Pro Val Glu Val
 385 390 395 400

ctc acc acc atc aaa att ctg ttc tgc gtg gtg ccg gtg gtg ctc tac 1248
 Leu Thr Thr Ile Lys Ile Leu Phe Cys Val Val Pro Val Val Leu Tyr
 405 410 415

gcg ggc atg ttc atc atg ctg tcg ctc tac aag ctc acc gat gcc cgc 1296
 Ala Gly Met Phe Ile Met Leu Ser Leu Tyr Lys Leu Thr Asp Ala Arg
 420 425 430

gtg gag gcc atc agc cgg cag ctg att aag cac cgc gcg gcg cag ggc 1344
 Val Glu Ala Ile Ser Arg Gln Leu Ile Lys His Arg Ala Ala Gln Gly
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gag gcc gtt ccc gac gcc gcg aca gcc gca tcc cat taa 1383
 Glu Ala Val Pro Asp Ala Ala Thr Ala Ala Ser His *
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 Met Glu Ile Thr Asn Pro Ile Leu Thr Gly Phe Asn Pro Asp Pro Ser
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ctg tgc cgc cag ggc gag gac tac tac atc gcc acc tcg acc ttc gag 96
 Leu Cys Arg Gln Gly Glu Asp Tyr Tyr Ile Ala Thr Ser Thr Phe Glu
 20 25 30

tgg ttc ccg ggc gtg cgc atc tac cac tcc cgt gac ctg aaa aac tgg 144
 Trp Phe Pro Gly Val Arg Ile Tyr His Ser Arg Asp Leu Lys Asn Trp
 35 40 45

tcg ctg gtc agc acc ccg ttg gac cgc gtg tcg atg ctg gac atg aag 192
 Ser Leu Val Ser Thr Pro Leu Asp Arg Val Ser Met Leu Asp Met Lys
 50 55 60

ggc aac ccg gac tcc ggc ggc atc tgg gcg ccg tgc ctg agc tac gcc 240
 Gly Asn Pro Asp Ser Gly Gly Ile Trp Ala Pro Cys Leu Ser Tyr Ala
 65 70 75 80

gac ggt aaa ttc tgg ctg ctc tac acc gac gtg aag att gtc gac tcg 288
 Asp Gly Lys Phe Trp Leu Leu Tyr Thr Asp Val Lys Ile Val Asp Ser
 85 90 95

ccg tgg aaa aac ggc cgc aac ttc ctc gtc acc gcg ccc tcc atc gag 336
 Pro Trp Lys Asn Gly Arg Asn Phe Leu Val Thr Ala Pro Ser Ile Glu
 100 105 110

ggg cca tgg agc gag cca atc ccg atg ggc aac ggc ggg ttt gac ccg 384

Gly	Pro	Trp	Ser	Glu	Pro	Ile	Pro	Met	Gly	Asn	Gly	Gly	Phe	Asp	Pro		
	115						120					125					
tcc	ctg	ttc	cac	gac	gac	gat	ggc	cgc	aaa	tac	tat	atc	tac	cgc	ccg	432	
Ser	Leu	Phe	His	Asp	Asp	Asp	Gly	Arg	Lys	Tyr	Tyr	Ile	Tyr	Arg	Pro		
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tgg	ggg	ccg	cgc	cac	cac	agc	aac	ccg	cac	aac	acc	atc	gtg	tta	cag	480	
Trp	Gly	Pro	Arg	His	His	Ser	Asn	Pro	His	Asn	Thr	Ile	Val	Leu	Gln		
	145				150					155				160			
gcg	ttt	gac	ccg	cag	acc	ggc	acg	ctc	tcg	ccc	gag	cgc	aaa	acg	ctg	528	
Ala	Phe	Asp	Pro	Gln	Thr	Gly	Thr	Leu	Ser	Pro	Glu	Arg	Lys	Thr	Leu		
				165				170						175			
ttt	acc	ggc	acg	ccg	ctc	tgc	tac	acc	gaa	ggc	gcg	cac	ctg	tat	cgc	576	
Phe	Thr	Gly	Thr	Pro	Leu	Cys	Tyr	Thr	Glu	Gly	Ala	His	Leu	Tyr	Arg		
			180					185					190				
cac	gcg	gga	tgg	tac	tac	ctg	atg	gcc	gcc	gag	ggc	ggc	acc	agc	tac	624	
His	Ala	Gly	Trp	Tyr	Tyr	Leu	Met	Ala	Ala	Glu	Gly	Gly	Thr	Ser	Tyr		
		195					200					205					
gag	cac	gcc	gtc	gtg	gtg	ctg	cgt	tcc	aaa	aat	atc	gac	ggg	ccg	tac	672	
Glu	His	Ala	Val	Val	Val	Leu	Arg	Ser	Lys	Asn	Ile	Asp	Gly	Pro	Tyr		
	210					215					220						
gag	ctg	cac	ccg	gac	gta	acg	atg	atg	acc	agc	tgg	cac	ctg	ccg	gag	720	
Glu	Leu	His	Pro	Asp	Val	Thr	Met	Met	Thr	Ser	Trp	His	Leu	Pro	Glu		
	225				230					235				240			
aac	ccg	ctg	cag	aag	agc	ggc	cac	ggc	tcg	ctg	ctg	cag	acg	cat	acg	768	
Asn	Pro	Leu	Gln	Lys	Ser	Gly	His	Gly	Ser	Leu	Leu	Gln	Thr	His	Thr		
				245				250						255			
ggt	gaa	tgg	tac	atg	gcc	tac	ctc	acc	agc	cgc	ccg	ctg	cgc	ctg	ccc	816	
Gly	Glu	Trp	Tyr	Met	Ala	Tyr	Leu	Thr	Ser	Arg	Pro	Leu	Arg	Leu	Pro		
			260					265					270				
ggc	gtg	ccg	ctg	ctg	gcc	tcc	ggc	gga	cgc	ggc	tac	tgc	ccg	ctg	ggg	864	
Gly	Val	Pro	Leu	Leu	Ala	Ser	Gly	Gly	Arg	Gly	Tyr	Cys	Pro	Leu	Gly		
	275					280						285					
cgc	gag	acc	ggc	atc	gcc	cgc	att	gaa	tgg	cgc	gac	ggc	tgg	ccg	tac	912	
Arg	Glu	Thr	Gly	Ile	Ala	Arg	Ile	Glu	Trp	Arg	Asp	Gly	Trp	Pro	Tyr		
	290					295					300						
gtg	gaa	ggc	ggc	aag	cac	gcg	cag	ctg	acc	gtg	aaa	ggc	ccg	caa	gta	960	
Val	Glu	Gly	Gly	Lys	His	Ala	Gln	Leu	Thr	Val	Lys	Gly	Pro	Gln	Val		
	305				310					315				320			
gcc	gag	cag	cct	gca	gcc	gtt	ccg	ggc	aac	tgg	cgg	gac	gat	ttc	gac	1008	
Ala	Glu	Gln	Pro	Ala	Ala	Val	Pro	Gly	Asn	Trp	Arg	Asp	Asp	Phe	Asp		
				325				330						335			
gcc	agt	tcg	ctt	gac	ccg	gag	ctg	cag	acc	ctg	cgc	att	ccg	ttc	gac	1056	
Ala	Ser	Ser	Leu	Asp	Pro	Glu	Leu	Gln	Thr	Leu	Arg	Ile	Pro	Phe	Asp		
			340					345					350				
gac	acc	ctc	ggc	tcg	ctc	acc	gcg	cgc	ccg	ggc	ttc	tta	cgg	ctc	tat	1104	
Asp	Thr	Leu	Gly	Ser	Leu	Thr	Ala	Arg	Pro	Gly	Phe	Leu	Arg	Leu	Tyr		

355	360	365	
ggc aac gac tcg ctc aat tcg acc ttc acc caa tcg acc gtg gcg cgc			1152
Gly Asn Asp Ser Leu Asn Ser Thr Phe Thr Gln Ser Thr Val Ala Arg			
370	375	380	
cgc tgg cag cac ttc gcc ttc cgg gca gaa acg cgg atg gag ttc tcg			1200
Arg Trp Gln His Phe Ala Phe Arg Ala Glu Thr Arg Met Glu Phe Ser			
385	390	395	400
ccg gtg cac ttc cag cag agc gcg ggg ctg acc tgc tac tac aac agc			1248
Pro Val His Phe Gln Gln Ser Ala Gly Leu Thr Cys Tyr Tyr Asn Ser			
	405	410	415
aaa aac tgg agc tac tgc ttt gtg gac tac gag gag gga cag ggt aga			1296
Lys Asn Trp Ser Tyr Cys Phe Val Asp Tyr Glu Glu Gly Gln Gly Arg			
	420	425	430
acc atc aaa gtt atc cag ctc gac cac aac gtg ccg tcg tgg ccg ctg			1344
Thr Ile Lys Val Ile Gln Leu Asp His Asn Val Pro Ser Trp Pro Leu			
	435	440	445
cac gag cag ccc att ccg gtg ccg gaa cat gcg gag agc gtc tgg ctg			1392
His Glu Gln Pro Ile Pro Val Pro Glu His Ala Glu Ser Val Trp Leu			
	450	455	460
ccg gtg gac gtg gat acg ctg gtc tac cgc tac agc tac tcg ttt gat			1440
Arg Val Asp Val Asp Thr Leu Val Tyr Arg Tyr Ser Tyr Ser Phe Asp			
	465	470	475
ggc gag acg tgg cac acc gtg ccg gtg acg tat gag gcg tgg aag ctg			1488
Gly Glu Thr Trp His Thr Val Pro Val Thr Tyr Glu Ala Trp Lys Leu			
	485	490	495
tcg gac gac tac atc ggc ggg cgc ggc ttc ttc acc ggc gcg ttt gtg			1536
Ser Asp Asp Tyr Ile Gly Gly Arg Gly Phe Phe Thr Gly Ala Phe Val			
	500	505	510
ggc ctg cac tgc gag gac atc agc ggc gac ggc tgc tac gcg gac ttc			1584
Gly Leu His Cys Glu Asp Ile Ser Gly Asp Gly Cys Tyr Ala Asp Phe			
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gac tac ttc acc tac gag ccg gtc taa			1611
Asp Tyr Phe Thr Tyr Glu Pro Val *			
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Met His Met Lys Lys Ile Ile Phe Ala Phe Ile Ile Leu Phe Val Phe			
1	5	10	15

tta ctc cct atg att att ttt tac caa ccc tgg gtc aat gca tta ccg	96
Leu Leu Pro Met Ile Ile Phe Tyr Gln Pro Trp Val Asn Ala Leu Pro	
20 25 30	
tca acg ccc cga cac gca agt cct gag caa tta gaa aaa aca gtt cgt	144
Ser Thr Pro Arg His Ala Ser Pro Glu Gln Leu Glu Lys Thr Val Arg	
35 40 45	
tat ctt aca caa act gtg cat cca cgt agt gcc gac aat att gat aat	192
Tyr Leu Thr Gln Thr Val His Pro Arg Ser Ala Asp Asn Ile Asp Asn	
50 55 60	
ctg aat agy tcc gca gaa tat ata aaa gag gtc ttt gtc agt agc ggt	240
Leu Asn Arg Ser Ala Glu Tyr Ile Lys Glu Val Phe Val Ser Ser Gly	
65 70 75 80	
gcc aga gtt acc tcg cag gac gtc ccc att acg ggt ggc ccc tac aaa	288
Ala Arg Val Thr Ser Gln Asp Val Pro Ile Thr Gly Gly Pro Tyr Lys	
85 90 95	
aac att gtt gct gat tat ggt cct gcc gat gga ccg ctg att att att	336
Asn Ile Val Ala Asp Tyr Gly Pro Ala Asp Gly Pro Leu Ile Ile Ile	
100 105 110	
ggg gcg cat tat gac tct gcc agc agt tat gaa aac gat caa ttg acc	384
Gly Ala His Tyr Asp Ser Ala Ser Ser Tyr Glu Asn Asp Gln Leu Thr	
115 120 125	
tat acg ccg ggc gcg gat gat aac gcc agc ggt gtg gca gga tta ctc	432
Tyr Thr Pro Gly Ala Asp Asp Asn Ala Ser Gly Val Ala Gly Leu Leu	
130 135 140	
gaa ctg gca cgt ttg tta cat cag caa gta ccg aaa aca ggc gtg cag	480
Glu Leu Ala Arg Leu His Gln Gln Val Pro Lys Thr Gly Val Gln	
145 150 155 160	
ctg gtc gcc tat gcg tcg gaa gaa ccg ccc ttc ttt cgt agc gat gaa	528
Leu Val Ala Tyr Ala Ser Glu Glu Pro Pro Phe Phe Arg Ser Asp Glu	
165 170 175	
atg ggg agc gcg gtg cat gca gct tcg ctt gag cgt cca gtg aaa tta	576
Met Gly Ser Ala Val His Ala Ala Ser Leu Glu Arg Pro Val Lys Leu	
180 185 190	
atg ata gca ctg gag atg att ggc tat tac gac tct gcg cct gga agc	624
Met Ile Ala Leu Glu Met Ile Gly Tyr Tyr Asp Ser Ala Pro Gly Ser	
195 200 205	
cag aat tac cct tac ccg gca atg tcc tgg ctt tat ccc gat cgg gga	672
Gln Asn Tyr Pro Tyr Pro Ala Met Ser Trp Leu Tyr Pro Asp Arg Gly	
210 215 220	
gac ttt att gcc gtg gtc ggc aga ata cag gat atc aac gcc gtt cgt	720
Asp Phe Ile Ala Val Val Gly Arg Ile Gln Asp Ile Asn Ala Val Arg	
225 230 235 240	
cag gta aaa gcg gca ttg ttg tca tct cag gat tta tct gtt tat tct	768
Gln Val Lys Ala Ala Leu Leu Ser Ser Gln Asp Leu Ser Val Tyr Ser	
245 250 255	
atg aat acc cca ggg ttt att ccc ggt att gat ttc tct gac cac ctg	816

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Met Asn Thr Pro Gly Phe Ile Pro Gly Ile Asp Phe Ser Asp His Leu
      260                      265                      270

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Asn Tyr Trp Gln His Asp Ile Pro Ala Ile Met Ile Thr Asp Thr Ala
      275                      280                      285

ttt tat cgt aat aaa caa tac cac ttg ccc ggt gat acc gca gac aga 912
Phe Tyr Arg Asn Lys Gln Tyr His Leu Pro Gly Asp Thr Ala Asp Arg
      290                      295                      300

ttg aat tat cag aaa atg gct cag gta gtg gat ggt gtt ata act ttg 960
Leu Asn Tyr Gln Lys Met Ala Gln Val Val Asp Gly Val Ile Thr Leu
      305                      310                      315                      320

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<213> Escherichia coli

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      1                      5                      10                      15

gcc gct gcc gtg gcg ctg gcg cta ccg gca aaa gcc aac acc tgg ccg 96
Ala Ala Ala Val Ala Leu Ala Leu Pro Ala Lys Ala Asn Thr Trp Pro
      20                      25                      30

ctg ccg cca gcg ggc agt cgt ctg gtt ggc gaa aac aaa ttt cat gtg 144
Leu Pro Pro Ala Gly Ser Arg Leu Val Gly Glu Asn Lys Phe His Val
      35                      40                      45

gtg gaa aat gac ggt ggt tct ctg gaa gcc atc gcc aaa aaa tac aac 192
Val Glu Asn Asp Gly Gly Ser Leu Glu Ala Ile Ala Lys Lys Tyr Asn
      50                      55                      60

gtc ggc ttt ctc gct ctg tta cag gct aac ccc ggc gtt gat cct tac 240
Val Gly Phe Leu Ala Leu Leu Gln Ala Asn Pro Gly Val Asp Pro Tyr
      65                      70                      75                      80

gta ccg cgc gcg ggc agc gtg tta acg atc ccg ttg caa acc cta ctt 288
Val Pro Arg Ala Gly Ser Val Leu Thr Ile Pro Leu Gln Thr Leu Leu
      85                      90                      95

cca gat gcg ccg cgc gaa ggc att gtg atc aac att gcg gag ctg cgt 336
Pro Asp Ala Pro Arg Glu Gly Ile Val Ile Asn Ile Ala Glu Leu Arg
      100                      105                      110

ctc tat tac tac ccg ccg ggt aaa aat tcg gta acc gtg tat cca ata 384
Leu Tyr Tyr Tyr Pro Pro Gly Lys Asn Ser Val Thr Val Tyr Pro Ile
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ggt att ggt cag tta ggt ggt gac acg ctg aca ccg aca atg gtg acc 432
Gly Ile Gly Gln Leu Gly Gly Asp Thr Leu Thr Pro Thr Met Val Thr
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Thr Val Ser Asp Lys Arg Ala Asn Pro Thr Trp Thr Pro Thr Ala Asn
145 150 155 160

atc cgc gcc cgt tat aaa gca cag gga att gag ttg cct gcg gta gtg 528
Ile Arg Ala Arg Tyr Lys Ala Gln Gly Ile Glu Leu Pro Ala Val Val
165 170 175

ccg gct gga ctg gat aac cca atg ggc cat cat gcg att cgt ctg gcg 576
Pro Ala Gly Leu Asp Asn Pro Met Gly His His Ala Ile Arg Leu Ala
180 185 190

gcc tat ggc ggc gtt tat ttg ctt cat ggt acg aac gcc gat ttc ggc 624
Ala Tyr Gly Gly Val Tyr Leu Leu His Gly Thr Asn Ala Asp Phe Gly
195 200 205

att ggc atg cgg gta agt tct ggc tgt att cgt ctg cgg gat gac gat 672
Ile Gly Met Arg Val Ser Ser Gly Cys Ile Arg Leu Arg Asp Asp Asp
210 215 220

atc aaa aca ctc ttt agc cag gtc acc cca ggc acc aaa gtg aat atc 720
Ile Lys Thr Leu Phe Ser Gln Val Thr Pro Gly Thr Lys Val Asn Ile
225 230 235 240

atc aac act ccg ata aaa gtc tct gcc gaa cca aac ggt gcg cgt ctg 768
Ile Asn Thr Pro Ile Lys Val Ser Ala Glu Pro Asn Gly Ala Arg Leu
245 250 255

gtt gaa gta cat cag ccg ctg tca gag aag att gat gac gat ccg cag 816
Val Glu Val His Gln Pro Leu Ser Glu Lys Ile Asp Asp Asp Pro Gln
260 265 270

ctg ctg cca att acg ctg aat agc gca atg caa tca ttt aaa gat gca 864
Leu Leu Pro Ile Thr Leu Asn Ser Ala Met Gln Ser Phe Lys Asp Ala
275 280 285

gca caa act gac gct gaa gtg atg caa cat gtg atg gat gtc cgt tcc 912
Ala Gln Thr Asp Ala Glu Val Met Gln His Val Met Asp Val Arg Ser
290 295 300

ggg atg ccg gtg gat gtc cgc cgt cat caa gtg agc cca caa acg ctg 960
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Thr Val Asn Ile Ser Ala Arg Ile Ile Pro Leu Leu Ile Ile His Gln	
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aga tat aaa att cct atg cca aaa gtt cag gcc gac ggc ctg cca ttg	144
Arg Tyr Lys Ile Pro Met Pro Lys Val Gln Ala Asp Gly Leu Pro Leu	
35 40 45	
ccc cag cga tac ggt gcg ata tta acc att gtg att ggt att tcg atg	192
Pro Gln Arg Tyr Gly Ala Ile Leu Thr Ile Val Ile Gly Ile Ser Met	
50 55 60	
gcc gtc ctt gac ggc gca atc gcc aac gtc gcc ctg cca aca atc gcc	240
Ala Val Leu Asp Gly Ala Ile Ala Asn Val Ala Leu Pro Thr Ile Ala	
65 70 75 80	
acg gac ctt cat gcc acg cca gcc agt tcc atc tgg gta gtg aac gcc	288
Thr Asp Leu His Ala Thr Pro Ala Ser Ser Ile Trp Val Val Asn Ala	
85 90 95	
tat caa atc gcc att gtc atc tcc ctg ctc tcg ttt tcg ttt ctg gcc	336
Tyr Gln Ile Ala Ile Val Ile Ser Leu Leu Ser Phe Ser Phe Leu Gly	
100 105 110	
gat atg ttt ggc tat cga cgt att tat aaa tgc ggt ctg gtc gtt ttt	384
Asp Met Phe Gly Tyr Arg Arg Ile Tyr Lys Cys Gly Leu Val Val Phe	
115 120 125	
ctg ttg tct tca ctg ttc tgc gcc ctt tct gat tcg ctg caa atg ctc	432
Leu Leu Ser Ser Leu Phe Cys Ala Leu Ser Asp Ser Leu Gln Met Leu	
130 135 140	
acc ctt gcg cgt gtc ata caa ggt ttc ggc ggt gca gcg ttg atg agc	480
Thr Leu Ala Arg Val Ile Gln Gly Phe Gly Gly Ala Ala Leu Met Ser	
145 150 155 160	
gtt aat acc gca ctt atc cgc ctg atc tat cca caa cgt ttt ctg ggt	528
Val Asn Thr Ala Leu Ile Arg Leu Ile Tyr Pro Gln Arg Phe Leu Gly	
165 170 175	
aga ggg atg ggc ata aac tcg ttt att gtt gcc gtc tct tct gct gcc	576
Arg Gly Met Gly Ile Asn Ser Phe Ile Val Ala Val Ser Ser Ala Ala	
180 185 190	
ggg ccg aca att gct gca gca atc ctc tcc atc gca tcc tgg aaa tgg	624
Gly Pro Thr Ile Ala Ala Ala Ile Leu Ser Ile Ala Ser Trp Lys Trp	
195 200 205	
tta ttt tta atc aac gta ccg tta ggt att atc gcc ctg ctt ctg gcg	672
Leu Phe Leu Ile Asn Val Pro Leu Gly Ile Ile Ala Leu Leu Leu Ala	
210 215 220	
atg cgt ttt ctg cca ccc aat ggt tct cgc gcc agt aaa ccc cgt ttc	720
Met Arg Phe Leu Pro Pro Asn Gly Ser Arg Ala Ser Lys Pro Arg Phe	

225	230	235	240	
gac ctg ccc agc gcc gtg atg aac gcg tta acc ttc ggc ctg ctt atc				768
Asp Leu Pro Ser Ala Val Met Asn Ala Leu Thr Phe Gly Leu Leu Ile	245	250	255	
act gcg ttg agt ggt ttc gct cag ggg caa tcg ctg acg tta att gct				816
Thr Ala Leu Ser Gly Phe Ala Gln Gly Gln Ser Leu Thr Leu Ile Ala	260	265	270	
gcg gaa ctg gtg gta atg gtt gtt gtt ggt att ttc ttt att cgc cgc				864
Ala Glu Leu Val Val Met Val Val Gly Ile Phe Phe Ile Arg Arg	275	280	285	
cag ctt tct ctt ccc gta ccg ctg cta ccg gtg gat tta ctg cgt atc				912
Gln Leu Ser Leu Pro Val Pro Leu Leu Pro Val Asp Leu Leu Arg Ile	290	295	300	
ccg ctg ttt tca ctt tct att tgc aca tct gtt tgc tct ttc tgc gca				960
Pro Leu Phe Ser Leu Ser Ile Cys Thr Ser Val Cys Ser Phe Cys Ala	310	315	320	
caa atg ctg gca atg gtt tcc ctg ccc ttt tac ctg caa acc gtg ctc				1008
Gln Met Leu Ala Met Val Ser Leu Pro Phe Tyr Leu Gln Thr Val Leu	325	330	335	
ggg cgt agt gaa gtc gaa aca ggt tta ctt ctg aca ccg tgg ccg tta				1056
Gly Arg Ser Glu Val Glu Thr Gly Leu Leu Leu Thr Pro Trp Pro Leu	340	345	350	
gca acg atg gtg atg gct ccg ctg gca ggc tat ttg att gaa cgc gta				1104
Ala Thr Met Val Met Ala Pro Leu Ala Gly Tyr Leu Ile Glu Arg Val	355	360	365	
cat gca gga ttg ctg ggg gct tta ggg ttg ttc atc atg gct gcg ggg				1152
His Ala Gly Leu Leu Gly Ala Leu Gly Leu Phe Ile Met Ala Ala Gly	370	375	380	
ctt ttt tcc ctg gtt ctg ctg ccc gcg tca cct gcg gat atc aat att				1200
Leu Phe Ser Leu Val Leu Leu Pro Ala Ser Pro Ala Asp Ile Asn Ile	385	390	395	400
atc tgg ccg atg atc tta tgt ggt gct gga ttt ggc tta ttc cag tca				1248
Ile Trp Pro Met Ile Leu Cys Gly Ala Gly Phe Gly Leu Phe Gln Ser	405	410	415	
ccc aat aac cac acc att att acc tcc gcg cct cgc gaa cgt agc ggt				1296
Pro Asn Asn His Thr Ile Ile Thr Ser Ala Pro Arg Glu Arg Ser Gly	420	425	430	
gga gcc agt ggc atg tta gga acg gct cgt cta ctg ggt cag agt agc				1344
Gly Ala Ser Gly Met Leu Gly Thr Ala Arg Leu Leu Gly Gln Ser Ser	435	440	445	
ggc gcg gcg ctg gtg gcg ctg atg cta aat cag ttt gga gat aat ggt				1392
Gly Ala Ala Leu Val Ala Leu Met Leu Asn Gln Phe Gly Asp Asn Gly	450	455	460	
aca cac gtc tcg ctg atg gct gcg gct att ctg gca gtg att gct gcc				1440
Thr His Val Ser Leu Met Ala Ala Ala Ile Leu Ala Val Ile Ala Ala	465	470	475	480

tgt gtc agt ggt tta cgt atc act cag cca cga tcc agg gca taa 1485
 Cys Val Ser Gly Leu Arg Ile Thr Gln Pro Arg Ser Arg Ala *
 485 490

<210> 276

<211> 1434

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1434)

<400> 276

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 Met Lys Val Thr Leu Pro Glu Phe Glu Arg Ala Gly Val Met Val Val
 1 5 10 15

ggt gat gtg atg ctg gat cgt tac tgg tac ggc ccc acc agt cgt atc 96
 Gly Asp Val Met Leu Asp Arg Tyr Trp Tyr Gly Pro Thr Ser Arg Ile
 20 25 30

tcg ccg gaa gcg ccg gtg ccc gtg gtt aaa gtg aat acc atc gaa gaa 144
 Ser Pro Glu Ala Pro Val Pro Val Lys Val Asn Thr Ile Glu Glu
 35 40 45

cgt ccg ggc ggc gcg gct aac gtg gcg atg aat atc gct tct ctc ggt 192
 Arg Pro Gly Gly Ala Ala Asn Val Ala Met Asn Ile Ala Ser Leu Gly
 50 55 60

gct aat gca cgc ctg gtc ggg ttg acg ggc att gac gat gca gcg cgc 240
 Ala Asn Ala Arg Leu Val Gly Leu Thr Gly Ile Asp Asp Ala Ala Arg
 65 70 75 80

gcg ctg agt aaa tct ctg gcc gac gtc aac gtc aaa tgc gac ttc gtt 288
 Ala Leu Ser Lys Ser Leu Ala Asp Val Asn Val Lys Cys Asp Phe Val
 85 90 95

tct gta ccg acg cat ccg acc att acc aaa tta cgg gta ctt tcc cgc 336
 Ser Val Pro Thr His Pro Thr Ile Thr Lys Leu Arg Val Leu Ser Arg
 100 105 110

aac caa cag ctg atc cgt ctg gat ttt gaa gaa ggt ttc gaa ggt gtt 384
 Asn Gln Gln Leu Ile Arg Leu Asp Phe Glu Glu Gly Phe Glu Gly Val
 115 120 125

gat ccg cag ccg ctg cac gag cgg att aat cag gcg ctg agt tcg att 432
 Asp Pro Gln Pro Leu His Glu Arg Ile Asn Gln Ala Leu Ser Ser Ile
 130 135 140

ggc gcg ctg gtg ctt tct gac tac gcc aaa ggt gcg ctg gca agc gta 480
 Gly Ala Leu Val Leu Ser Asp Tyr Ala Lys Gly Ala Leu Ala Ser Val
 145 150 155 160

cag cag atg atc caa ctg gcg cgt aaa gcg ggt gtt ccg gtg ctg att 528
 Gln Gln Met Ile Gln Leu Ala Arg Lys Ala Gly Val Pro Val Leu Ile
 165 170 175

gat cca aaa ggt acc gat ttt gag cgc tac cgc ggc gct acg ctg tta	576
Asp Pro Lys Gly Thr Asp Phe Glu Arg Tyr Arg Gly Ala Thr Leu Leu	
180 185 190	
acg ccg aat ctc tcg gaa ttt gaa gct gtt gtc ggt aaa tgt aag acc	624
Thr Pro Asn Leu Ser Glu Phe Glu Ala Val Val Gly Lys Cys Lys Thr	
195 200 205	
gaa gaa gag att gtt gag cgc ggc atg aaa ctg att gcc gat tac gaa	672
Glu Glu Glu Ile Val Glu Arg Gly Met Lys Leu Ile Ala Asp Tyr Glu	
210 215 220	
ctc tcg gct ctg tta gtg acc cgt tcc gaa cag ggt atg tcg ctg ctg	720
Leu Ser Ala Leu Leu Val Thr Arg Ser Glu Gln Gly Met Ser Leu Leu	
225 230 235 240	
caa ccg ggt aaa gcg ccg ctg cat atg cca acc caa gcg cag gaa gtg	768
Gln Pro Gly Lys Ala Pro Leu His Met Pro Thr Gln Ala Gln Glu Val	
245 250 255	
tat gac gtt acc ggt gcg ggc gac acg gtg att ggc gtc ctg gcg gca	816
Tyr Asp Val Thr Gly Ala Gly Asp Thr Val Ile Gly Val Leu Ala Ala	
260 265 270	
acg ctg gca gcg ggt aat tcg ctg gaa gaa gcc tgc ttc ttt gcc aat	864
Thr Leu Ala Ala Gly Asn Ser Leu Glu Glu Ala Cys Phe Phe Ala Asn	
275 280 285	
gcg gcg gct ggc gtg gtg gtc ggc aaa ctg gga acc tcc acg gtt tcg	912
Ala Ala Ala Gly Val Val Val Gly Lys Leu Gly Thr Ser Thr Val Ser	
290 295 300	
ccg atc gag ctg gaa aat gct gta cgt gga cgt gca gat aca ggc ttt	960
Pro Ile Glu Leu Glu Asn Ala Val Arg Gly Arg Ala Asp Thr Gly Phe	
305 310 315 320	
ggc gtg atg acc gaa gag gaa ctg aag ctg gcc gta gcg gca gcg cgt	1008
Gly Val Met Thr Glu Glu Glu Leu Lys Leu Ala Val Ala Ala Ala Arg	
325 330 335	
aaa cgt ggt gaa aaa gtg gtg atg acc aac ggt gtc ttt gac atc ctg	1056
Lys Arg Gly Glu Lys Val Val Met Thr Asn Gly Val Phe Asp Ile Leu	
340 345 350	
cac gcc ggg cac gtc tct tat ctg gca aat gcc cgc aag ctg ggt gac	1104
His Ala Gly His Val Ser Tyr Leu Ala Asn Ala Arg Lys Leu Gly Asp	
355 360 365	
cgc ttg att gtt gcc gtc aac agc gat gcc tcc acc aaa cgg ctg aaa	1152
Arg Leu Ile Val Ala Val Asn Ser Asp Ala Ser Thr Lys Arg Leu Lys	
370 375 380	
ggg gat tcc cgc ccg gta aac cca ctc gaa cag cgt atg att gtg ctg	1200
Gly Asp Ser Arg Pro Val Asn Pro Leu Glu Gln Arg Met Ile Val Leu	
385 390 395 400	
ggc gca ctg gaa gcg gtc gac tgg gta gtg tcg ttt gaa gag gac acg	1248
Gly Ala Leu Glu Ala Val Asp Trp Val Val Ser Phe Glu Glu Asp Thr	
405 410 415	
ccg cag cgc ttg atc gcc ggg atc ttg cca gat ctg ctg gtg aaa ggc	1296

Pro Gln Arg Leu Ile Ala Gly Ile Leu Pro Asp Leu Leu Val Lys Gly
 420 425 430

ggc gac tat aaa cca gaa gag att gcc ggg agt aaa gaa gtc tgg gcc 1344
 Gly Asp Tyr Lys Pro Glu Glu Ile Ala Gly Ser Lys Glu Val Trp Ala
 435 440 445

aac ggt ggc gaa gtg ttg gtg ctc aac ttt gaa gac ggt tgc tcg acg 1392
 Asn Gly Gly Glu Val Leu Val Leu Asn Phe Glu Asp Gly Cys Ser Thr
 450 455 460

acc aac atc atc aag aag atc caa cag gat aaa aaa ggc taa 1434
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 465 470 475

<210> 277

<211> 2841

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(2841)

<400> 277

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gag cgg ctg cca gag cct tta gcc gag gaa tca ctt agc gca cag gcg 96
 Glu Arg Leu Pro Glu Pro Leu Ala Glu Glu Ser Leu Ser Ala Gln Ala
 20 25 30

aag tca gta ctt act ttt agt gat ttt gtg cag gac agc gtg att gcg 144
 Lys Ser Val Leu Thr Phe Ser Asp Phe Val Gln Asp Ser Val Ile Ala
 35 40 45

cat cca gag tgg ctg acg gaa ctg gaa agc caa ccg ccg cag gcc gac 192
 His Pro Glu Trp Leu Thr Glu Leu Glu Ser Gln Pro Pro Gln Ala Asp
 50 55 60

gaa tgg cag cat tac gcg gca tgg ttg cag gag gcg ctc tgt aat gtg 240
 Glu Trp Gln His Tyr Ala Ala Trp Leu Gln Glu Ala Leu Cys Asn Val
 65 70 75 80

agt gac gaa gcc ggg tta atg cgc gag ctg cgg cta ttc cgg cgg cgc 288
 Ser Asp Glu Ala Gly Leu Met Arg Glu Leu Arg Leu Phe Arg Arg Arg
 85 90 95

att atg gtg cgc atc gcc tgg gcg caa acg ctg gca ctg gtt act gaa 336
 Ile Met Val Arg Ile Ala Trp Ala Gln Thr Leu Ala Leu Val Thr Glu
 100 105 110

gag agc ata ttg cag cag ctc agc tat ctg gcg gag acg ctg att gtt 384
 Glu Ser Ile Leu Gln Gln Leu Ser Tyr Leu Ala Glu Thr Leu Ile Val
 115 120 125

gcg gcg cgt gac tgg ctg tat gac gcc tgc tgc cgc gag tgg gga acg 432
 Ala Ala Arg Asp Trp Leu Tyr Asp Ala Cys Cys Arg Glu Trp Gly Thr

130	135	140	
ccg tgc aat gcg cag ggc gaa gcg caa ccg ctg ctg att tta ggc atg			480
Pro Cys Asn Ala Gln Gly Glu Ala Gln Pro Leu Leu Ile Leu Gly Met			
145	150	155	160
ggt aag ctg ggc ggt ggg gag ctg aat ttc tcc tct gat atc gat ctg			528
Gly Lys Leu Gly Gly Gly Glu Leu Asn Phe Ser Ser Asp Ile Asp Leu			
	165	170	175
att ttt gcc tgg ccg gaa cat ggt tgt acg cag ggt gga cgc cgg gaa			576
Ile Phe Ala Trp Pro Glu His Gly Cys Thr Gln Gly Gly Arg Arg Glu			
	180	185	190
ctg gat aac gcg cag ttt ttt acc cgc atg ggg cag cgg ctg att aaa			624
Leu Asp Asn Ala Gln Phe Phe Thr Arg Met Gly Gln Arg Leu Ile Lys			
	195	200	205
gtg ctg gat caa cca acg cag gat ggc ttc gtc tat cgc gtg gat atg			672
Val Leu Asp Gln Pro Thr Gln Asp Gly Phe Val Tyr Arg Val Asp Met			
	210	215	220
cgg ctg cgt ccg ttt ggc gaa agt ggc ccg ctg gtg ctg agc ttt gcc			720
Arg Leu Arg Pro Phe Gly Glu Ser Gly Pro Leu Val Leu Ser Phe Ala			
	225	230	240
gcg ttg gaa gat tat tac cag gag cag ggg cgc gac tgg gag cgt tac			768
Ala Leu Glu Asp Tyr Tyr Gln Glu Gln Gly Arg Asp Trp Glu Arg Tyr			
	245	250	255
gcg atg gtc aag gcg ccg att atg ggc gat agc gaa ggc gtc tat gct			816
Ala Met Val Lys Ala Arg Ile Met Gly Asp Ser Glu Gly Val Tyr Ala			
	260	265	270
aac gag ttg cgt gcg atg ctg cgc ccg ttt gtt ttc cgt cgt tac atc			864
Asn Glu Leu Arg Ala Met Leu Arg Pro Phe Val Phe Arg Arg Tyr Ile			
	275	280	285
gat ttc agc gtg att cag tcg ctg cgc aac atg aaa ggg atg att gcc			912
Asp Phe Ser Val Ile Gln Ser Leu Arg Asn Met Lys Gly Met Ile Ala			
	290	295	300
cgt gaa gtg cgt cga cgt ggt ttg acc gac aat atc aaa ctc ggc gca			960
Arg Glu Val Arg Arg Arg Gly Leu Thr Asp Asn Ile Lys Leu Gly Ala			
	305	310	315
ggc ggc att cgc gaa att gaa ttt atc gtt cag gtg ttc cag ctc att			1008
Gly Gly Ile Arg Glu Ile Glu Phe Ile Val Gln Val Phe Gln Leu Ile			
	325	330	335
cgc ggc gga cgc gaa ccg tcg ctg caa tcg cgc tct tta ctg cca acg			1056
Arg Gly Gly Arg Glu Pro Ser Leu Gln Ser Arg Ser Leu Leu Pro Thr			
	340	345	350
ctc agc gcc att gcc gag ctg cat ctg ctt tct gaa aac gat gct gaa			1104
Leu Ser Ala Ile Ala Glu Leu His Leu Leu Ser Glu Asn Asp Ala Glu			
	355	360	365
caa ttg cga gtg gcg tat ctg ttc ctg cgg cgt ctg gaa aac ctg ctg			1152
Gln Leu Arg Val Ala Tyr Leu Phe Leu Arg Arg Leu Glu Asn Leu Leu			
	370	375	380

caa agc att aac gac gaa caa acc cag acg ctt cct tct gat gag ctt	1200
Gln Ser Ile Asn Asp Glu Gln Thr Gln Thr Leu Pro Ser Asp Glu Leu	
385 390 395 400	
aat cgt gcg cgg ctg gcg tgg gcg atg gac ttt gct gac tgg ccg caa	1248
Asn Arg Ala Arg Leu Ala Trp Ala Met Asp Phe Ala Asp Trp Pro Gln	
405 410 415	
ctg acc ggg gcg ctg acc gca cat atg acc aat gtg cgc cgg gtg ttt	1296
Leu Thr Gly Ala Leu Thr Ala His Met Thr Asn Val Arg Arg Val Phe	
420 425 430	
aat gaa ttg att ggc gac gat gaa agt gaa act cag gaa gag tcg ctg	1344
Asn Glu Leu Ile Gly Asp Asp Glu Ser Glu Thr Gln Glu Glu Ser Leu	
435 440 445	
tcg gaa cag tgg cgt gag ctg tgg cag gat gcg ttg cag gaa gat gac	1392
Ser Glu Gln Trp Arg Glu Leu Trp Gln Asp Ala Leu Gln Glu Asp Asp	
450 455 460	
act acg cca gtg ctg gcg cat ctt agc gag gat gat cgc aaa cag gtg	1440
Thr Thr Pro Val Leu Ala His Leu Ser Glu Asp Asp Arg Lys Gln Val	
465 470 475 480	
cta acg ctg att gcc gat ttc cgc aaa gag ctg gat aag cgc acc atc	1488
Leu Thr Leu Ile Ala Asp Phe Arg Lys Glu Leu Asp Lys Arg Thr Ile	
485 490 495	
ggg ccg cga gga cgt cag gtg ctc gac cat ctg atg ccg cat ctg cta	1536
Gly Pro Arg Gly Arg Gln Val Leu Asp His Leu Met Pro His Leu Leu	
500 505 510	
agt gat gtc tgt gcg cgt gaa gac gct gcc gtt acg ctg tcg cgc att	1584
Ser Asp Val Cys Ala Arg Glu Asp Ala Ala Val Thr Leu Ser Arg Ile	
515 520 525	
acc gcc ttg ctg gtg ggg att gtt acc cgc acc acc tat tta gaa ttg	1632
Thr Ala Leu Leu Val Gly Ile Val Thr Arg Thr Thr Tyr Leu Glu Leu	
530 535 540	
ctc agt gaa ttc ccc gcg gcg ctt aaa cat ttg att tct ctg tgt gcc	1680
Leu Ser Glu Phe Pro Ala Ala Leu Lys His Leu Ile Ser Leu Cys Ala	
545 550 555 560	
gcg tcg ccg atg att gcc agc cag ctg gcg cgt tat cca tta ttg ctg	1728
Ala Ser Pro Met Ile Ala Ser Gln Leu Ala Arg Tyr Pro Leu Leu Leu	
565 570 575	
gat gaa ttg ctc gat cca aac acc ctt tac cag ccg acg gcg acc gat	1776
Asp Glu Leu Leu Asp Pro Asn Thr Leu Tyr Gln Pro Thr Ala Thr Asp	
580 585 590	
gcc tac cgc gat gag ttg cgc cag tat ttg ctg cgc gtg ccg gaa gat	1824
Ala Tyr Arg Asp Glu Leu Arg Gln Tyr Leu Leu Arg Val Pro Glu Asp	
595 600 605	
gac gaa gag caa cag ctt gag gcg ctg cgt cag ttc aaa cag gcg cag	1872
Asp Glu Glu Gln Gln Leu Glu Ala Leu Arg Gln Phe Lys Gln Ala Gln	
610 615 620	

ctg tta cgc atc gcc gca gcg gat atc gcc ggt acg cta ccg gtg atg	1920
Leu Leu Arg Ile Ala Ala Ala Asp Ile Ala Gly Thr Leu Pro Val Met	
625 630 635 640	
aaa gtg agc gat cac tta acc tgg ctg gcg gaa gcc atg ata gat gcc	1968
Lys Val Ser Asp His Leu Thr Trp Leu Ala Glu Ala Met Ile Asp Ala	
645 650 655	
gtc gtt cag cag gcg tgg gtt caa atg gtt gcc cgc tac ggt aag ccg	2016
Val Val Gln Gln Ala Trp Val Gln Met Val Ala Arg Tyr Gly Lys Pro	
660 665 670	
aat cac ctg aac gaa cgc gaa ggg cgt ggt ttt gcg gtg gtc ggc tac	2064
Asn His Leu Asn Glu Arg Glu Gly Arg Gly Phe Ala Val Val Gly Tyr	
675 680 685	
ggc aag ctg ggc ggc tgg gag tta ggc tac agt tcc gat ctt gac ctt	2112
Gly Lys Leu Gly Gly Trp Glu Leu Gly Tyr Ser Ser Asp Leu Asp Leu	
690 695 700	
atc ttc ctc cat gat tgc cca atg gat gcg atg act gac ggt gag ccg	2160
Ile Phe Leu His Asp Cys Pro Met Asp Ala Met Thr Asp Gly Glu Arg	
705 710 715 720	
gaa atc gac ggg ccg cag ttt tat ctg cgt ctg gcg caa cgc att atg	2208
Glu Ile Asp Gly Arg Gln Phe Tyr Leu Arg Leu Ala Gln Arg Ile Met	
725 730 735	
cat ctg ttc agt acg cgt acc tct tcc ggc att ttg tat gaa gtg gat	2256
His Leu Phe Ser Thr Arg Thr Ser Ser Gly Ile Leu Tyr Glu Val Asp	
740 745 750	
gct cga ctg cgt ccg tcc ggg gcg gcg gga atg ctg gtg aca tcc gca	2304
Ala Arg Leu Arg Pro Ser Gly Ala Ala Gly Met Leu Val Thr Ser Ala	
755 760 765	
gaa gca ttt gcc gat tat cag aaa aac gag gcc tgg acg tgg gaa cat	2352
Glu Ala Phe Ala Asp Tyr Gln Lys Asn Glu Ala Trp Thr Trp Glu His	
770 775 780	
cag gcg ctg gtg cgt gcg cgt gta gtg tac ggc gat ccg cag ctc acc	2400
Gln Ala Leu Val Arg Ala Arg Val Val Tyr Gly Asp Pro Gln Leu Thr	
785 790 795 800	
gcg cac ttt gac gca gtg cgt cgc gag att atg acg ctg ccg cgt gaa	2448
Ala His Phe Asp Ala Val Arg Arg Glu Ile Met Thr Leu Pro Arg Glu	
805 810 815	
ggt aaa act ctg caa acg gaa gtg cgg gaa atg cgc gag aaa atg cgc	2496
Gly Lys Thr Leu Gln Thr Glu Val Arg Glu Met Arg Glu Lys Met Arg	
820 825 830	
gct cat ctc ggc aat aaa cat cgc gat cgc ttt gat atc aaa gct gat	2544
Ala His Leu Gly Asn Lys His Arg Asp Arg Phe Asp Ile Lys Ala Asp	
835 840 845	
gaa ggg gga att acc gat atc gaa ttt att acc caa tat ctg gtg ttg	2592
Glu Gly Gly Ile Thr Asp Ile Glu Phe Ile Thr Gln Tyr Leu Val Leu	
850 855 860	
cgc tac gct cat gaa aaa ccg aag tta acg cgc tgg tca gac aac gtg	2640

Arg	Tyr	Ala	His	Glu	Lys	Pro	Lys	Leu	Thr	Arg	Trp	Ser	Asp	Asn	Val	
865					870					875					880	
cgt	att	ctg	gaa	cta	ctg	gcg	caa	aac	gac	att	atg	gaa	gag	cag	gaa	2688
Arg	Ile	Leu	Glu	Leu	Leu	Ala	Gln	Asn	Asp	Ile	Met	Glu	Glu	Gln	Glu	
			885						890					895		
gcg	atg	gcg	ctg	acc	cgt	gct	tac	act	acg	ctt	cgc	gat	gaa	ctt	cat	2736
Ala	Met	Ala	Leu	Thr	Arg	Ala	Tyr	Thr	Thr	Leu	Arg	Asp	Glu	Leu	His	
			900					905					910			
cat	ctg	gca	tta	cag	gaa	ttg	ccg	ggc	cat	gtg	tcg	gag	gat	tgc	ttc	2784
His	Leu	Ala	Leu	Gln	Glu	Leu	Pro	Gly	His	Val	Ser	Glu	Asp	Cys	Phe	
		915					920					925				
acc	gca	gag	cgt	gaa	ctg	gtg	ccg	gca	agc	tgg	cag	aag	tgg	ctg	gtg	2832
Thr	Ala	Glu	Arg	Glu	Leu	Val	Arg	Ala	Ser	Trp	Gln	Lys	Trp	Leu	Val	
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gaa	gaa	tga														2841
Glu	Glu	*														
945																
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Met	Ala	Gln	Glu	Ile	Glu	Leu	Lys	Phe	Ile	Val	Asn	His	Ser	Ala	Val	
1				5					10					15		
gag	gcg	ttg	cgt	gac	cat	ctc	aat	acg	ctg	ggc	ggc	gag	cac	cat	gac	96
Glu	Ala	Leu	Arg	Asp	His	Leu	Asn	Thr	Leu	Gly	Gly	Glu	His	His	Asp	
			20					25					30			
ccc	gtg	cag	ttg	ctg	aat	att	tac	tac	gaa	acg	ccg	gat	aac	tgg	ctg	144
Pro	Val	Gln	Leu	Leu	Asn	Ile	Tyr	Tyr	Glu	Thr	Pro	Asp	Asn	Trp	Leu	
		35				40						45				
cgt	ggg	cac	gat	atg	ggc	tta	cgt	att	cgt	ggc	gaa	aac	ggg	cgc	tat	192
Arg	Gly	His	Asp	Met	Gly	Leu	Arg	Ile	Arg	Gly	Glu	Asn	Gly	Arg	Tyr	
	50					55					60					
gag	atg	acc	atg	aaa	gtt	gca	gga	aga	gtg	aca	ggc	ggc	tta	cat	cag	240
Glu	Met	Thr	Met	Lys	Val	Ala	Gly	Arg	Val	Thr	Gly	Gly	Leu	His	Gln	
	65				70				75					80		
cgc	ccg	gaa	tat	aac	gtg	gcg	ttg	agc	gaa	ccg	acg	ctc	gac	ctg	gcg	288
Arg	Pro	Glu	Tyr	Asn	Val	Ala	Leu	Ser	Glu	Pro	Thr	Leu	Asp	Leu	Ala	
				85					90					95		
cag	tta	ccg	acg	gaa	gtc	tgg	ccg	aac	ggc	gaa	ttg	ccc	gcc	gat	ctc	336
Gln	Leu	Pro	Thr	Glu	Val	Trp	Pro	Asn	Gly	Glu	Leu	Pro	Ala	Asp	Leu	
		100					105						110			

gcc tcc cgc gtg cag ccg ctg ttc agc acc gat ttt tat cgc gaa aaa	384
Ala Ser Arg Val Gln Pro Leu Phe Ser Thr Asp Phe Tyr Arg Glu Lys	
115 120 125	
tgg ctg gtg gcg gtc gat ggt agc caa att gaa atc gcc ctc gac cag	432
Trp Leu Val Ala Val Asp Gly Ser Gln Ile Glu Ile Ala Leu Asp Gln	
130 135 140	
ggg gaa gtg aaa gcg ggt gaa ttt gct gaa cct atc tgt gag ctg gaa	480
Gly Glu Val Lys Ala Gly Glu Phe Ala Glu Pro Ile Cys Glu Leu Glu	
145 150 155 160	
ctg gaa ctg ctt agc gcc gac acg cgc gcg gtg ctg aaa ctg gcg aac	528
Leu Glu Leu Leu Ser Gly Asp Thr Arg Ala Val Leu Lys Leu Ala Asn	
165 170 175	
caa ctg gta tcg caa acc gga tta cgc cag gcc agc ctg agc aaa gcg	576
Gln Leu Val Ser Gln Thr Gly Leu Arg Gln Gly Ser Leu Ser Lys Ala	
180 185 190	
gcg cgt gcc tat cat ctg gcg cag gcc aat ccg gcg cgt gaa atc aaa	624
Ala Arg Gly Tyr His Leu Ala Gln Gly Asn Pro Ala Arg Glu Ile Lys	
195 200 205	
ccg acc acc att ttg cat gtt gcg gca aaa gcc gat gtg gaa cag ggg	672
Pro Thr Thr Ile Leu His Val Ala Ala Lys Ala Asp Val Glu Gln Gly	
210 215 220	
ctg gaa gcg gcg ctc gag ctg gcg tta gcg caa tgg cag tat cat gaa	720
Leu Glu Ala Ala Leu Glu Leu Ala Leu Ala Gln Trp Gln Tyr His Glu	
225 230 235 240	
gaa ctg tgg gta cgc gcc aac gat gcg gcg aaa gaa cag gtg ctg gca	768
Glu Leu Trp Val Arg Gly Asn Asp Ala Ala Lys Glu Gln Val Leu Ala	
245 250 255	
gcc att agc ctg gtc cgt cat acg ctg atg ctg ttc ggt ggt att gtg	816
Ala Ile Ser Leu Val Arg His Thr Leu Met Leu Phe Gly Gly Ile Val	
260 265 270	
ccg cgt aaa gcg agc act cac tta cgt gat ctg ctg act caa tgc gag	864
Pro Arg Lys Ala Ser Thr His Leu Arg Asp Leu Leu Thr Gln Cys Glu	
275 280 285	
gcg acc att gct tct gcg gtg tct gcc gtg acg gcg gtc tac tct acc	912
Ala Thr Ile Ala Ser Ala Val Ser Ala Val Thr Ala Val Tyr Ser Thr	
290 295 300	
gaa acg gca atg gcg aag ctg gcg ttg acc gaa tgg ttg gta agc aaa	960
Glu Thr Ala Met Ala Lys Leu Ala Leu Thr Glu Trp Leu Val Ser Lys	
305 310 315 320	
gca tgg cag cca ttt tta gat gcc aaa gcg cag gcc aaa atc agc gac	1008
Ala Trp Gln Pro Phe Leu Asp Ala Lys Ala Gln Gly Lys Ile Ser Asp	
325 330 335	
tcc ttc aaa cgc ttt gcc gat atc cat ctt tcc cgc cat gcc gct gaa	1056
Ser Phe Lys Arg Phe Ala Asp Ile His Leu Ser Arg His Ala Ala Glu	
340 345 350	

ctg aaa agc gtt ttc tgc cag ccg tta ggc gat cgc tac cgt gac cag 1104
 Leu Lys Ser Val Phe Cys Gln Pro Leu Gly Asp Arg Tyr Arg Asp Gln
 355 360 365

ttg cca cgc ctg acg cgt gat att gac tca ata ctg ttg ctg gcg ggt 1152
 Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Leu Ala Gly
 370 375 380

tac tat gat cct gtc gtc gcg caa gcc tgg ctg gag aac tgg cag ggg 1200
 Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly
 385 390 395 400

ctg cat cac gct att gcg acc ggg caa cgc atc gaa att gaa cat ttc 1248
 Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe
 405 410 415

cgt aat gag gca aac aat cag gaa ccg ttc tgg ttg cac agc gga aaa 1296
 Arg Asn Glu Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys
 420 425 430

cgt taa 1302
 Arg *

<210> 279
 <211> 624
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(624)

<400> 279
 gtg ctc aac aaa ctc tcc tta ctg ctg aaa gac gca ggt att tcg ctt 48
 Met Leu Asn Lys Leu Ser Leu Leu Leu Lys Asp Ala Gly Ile Ser Leu
 1 5 10 15

acc gat cac cag aaa aac cag ctt att gcc tac gtg aat atg ctg cat 96
 Thr Asp His Gln Lys Asn Gln Leu Ile Ala Tyr Val Asn Met Leu His
 20 25 30

aaa tgg aac aaa gcg tac aac ctg act tcg gtc cgc gat cct aat gag 144
 Lys Trp Asn Lys Ala Tyr Asn Leu Thr Ser Val Arg Asp Pro Asn Glu
 35 40 45

atg ctg gta cgc cat att ctc gat agc att gtg gtg gca ccg tat ctg 192
 Met Leu Val Arg His Ile Leu Asp Ser Ile Val Val Ala Pro Tyr Leu
 50 55 60

caa ggt gaa cgg ttt atc gat gtc ggc acc gga cca gga ctg cca ggc 240
 Gln Gly Glu Arg Phe Ile Asp Val Gly Thr Gly Pro Gly Leu Pro Gly
 65 70 75 80

att cca ctc tct atc gtg cgt cct gaa gcc cat ttc act ctg ttg gat 288
 Ile Pro Leu Ser Ile Val Arg Pro Glu Ala His Phe Thr Leu Leu Asp
 85 90 95

agc ctt ggt aaa cgc gtg cgt ttc ctt cgt cag gtg caa cat gag ctt 336
 Ser Leu Gly Lys Arg Val Arg Phe Leu Arg Gln Val Gln His Glu Leu

100	105	110	
aaa ctg gag aat att gaa cca gta cag agc agg gta gaa gag ttt cct			384
Lys Leu Glu Asn Ile Glu Pro Val Gln Ser Arg Val Glu Glu Phe Pro			
115	120	125	
tca gag ccg cca ttt gat ggc gta att agc cgc gct ttt gcc tct ctg			432
Ser Glu Pro Pro Phe Asp Gly Val Ile Ser Arg Ala Phe Ala Ser Leu			
130	135	140	
aac gat atg gtg agc tgg tgc cac cat ctt cct ggt gag caa ggc cgt			480
Asn Asp Met Val Ser Trp Cys His His Leu Pro Gly Glu Gln Gly Arg			
145	150	155	160
ttc tac gcg ctg aaa ggg caa atg ccg gaa gat gaa atc gct ttg ttg			528
Phe Tyr Ala Leu Lys Gly Gln Met Pro Glu Asp Glu Ile Ala Leu Leu			
165	170	175	
ccc gaa gaa tat cag gtc gaa tca gtg gtt aaa ctt cag gtt cca gcc			576
Pro Glu Glu Tyr Gln Val Glu Ser Val Val Lys Leu Gln Val Pro Ala			
180	185	190	
ctg gat ggc gaa cgt cat ctg gtg gtg att aaa gca aat aaa att taa			624
Leu Asp Gly Glu Arg His Leu Val Val Ile Lys Ala Asn Lys Ile *			
195	200	205	

<210> 280

<211> 1890

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1890)

<400> 280

atg ttt tat ccg gat cct ttt gac gtc atc atc att ggc ggg ggt cat	48
Met Phe Tyr Pro Asp Pro Phe Asp Val Ile Ile Ile Gly Gly Gly His	
1 5 10 15	
gca ggc acc gag gcc gcg atg gcc gcg gcg cgt atg ggt caa cag act	96
Ala Gly Thr Glu Ala Ala Met Ala Ala Ala Arg Met Gly Gln Gln Thr	
20 25 30	
ctg ctt ttg aca cac aat atc gac act ctg ggg cag atg agc tgc aac	144
Leu Leu Leu Thr His Asn Ile Asp Thr Leu Gly Gln Met Ser Cys Asn	
35 40 45	
ccg gcg atc ggc ggt att ggg aag gga cat ctg gta aaa gaa gtg gat	192
Pro Ala Ile Gly Gly Ile Gly Lys Gly His Leu Val Lys Glu Val Asp	
50 55 60	
gca ctc ggc ggt ctg atg gcg aaa gcg atc gat cag gcg ggt atc cag	240
Ala Leu Gly Gly Leu Met Ala Lys Ala Ile Asp Gln Ala Gly Ile Gln	
65 70 75 80	
ttt agg ata cta aac gca agc aaa gga ccg gcg gtt cgc gct acc cga	288
Phe Arg Ile Leu Asn Ala Ser Lys Gly Pro Ala Val Arg Ala Thr Arg	
85 90 95	

gct cag gcg gat cgt gtg ctc tac cgt cag gcg gta cgt acg gcg ctg	336
Ala Gln Ala Asp Arg Val Leu Tyr Arg Gln Ala Val Arg Thr Ala Leu	
100 105 110	
gag aac caa ccg aac ctg atg atc ttc cag cag gcg gtt gaa gat ctt	384
Glu Asn Gln Pro Asn Leu Met Ile Phe Gln Gln Ala Val Glu Asp Leu	
115 120 125	
att gtc gaa aac gat cgc gtg gtc ggt gct gtt acc caa atg gga ctg	432
Ile Val Glu Asn Asp Arg Val Val Gly Ala Val Thr Gln Met Gly Leu	
130 135 140	
aag ttc cgt gcc aaa gcc gtc gtg ctc acc gtt ggg acg ttc ctc gac	480
Lys Phe Arg Ala Lys Ala Val Val Leu Thr Val Gly Thr Phe Leu Asp	
145 150 155 160	
ggt aaa att cat atc ggt ctg gat aat tac agc ggt ggc cgt gct ggt	528
Gly Lys Ile His Ile Gly Leu Asp Asn Tyr Ser Gly Gly Arg Ala Gly	
165 170 175	
gat ccg ccg tcc att ccg ctt tct cgc cgt ttg cgt gaa ctg ccg ctg	576
Asp Pro Pro Ser Ile Pro Leu Ser Arg Arg Leu Arg Glu Leu Pro Leu	
180 185 190	
cgc gtt ggt cgt ctg aaa acc ggg aca cca ccg cgt att gat gct cga	624
Arg Val Gly Arg Leu Lys Thr Gly Thr Pro Pro Arg Ile Asp Ala Arg	
195 200 205	
acc atc gac ttt agc gta ctg gcg caa cag cat ggc gat aac cca atg	672
Thr Ile Asp Phe Ser Val Leu Ala Gln Gln His Gly Asp Asn Pro Met	
210 215 220	
ccg gta ttc tcg ttt atg ggc aat gcg tcc cag cat ccc cag cag gtg	720
Pro Val Phe Ser Phe Met Gly Asn Ala Ser Gln His Pro Gln Gln Val	
225 230 235 240	
ccg tgt tat atc act cat acc aac gag aaa acc cat gat gtg atc cgc	768
Pro Cys Tyr Ile Thr His Thr Asn Glu Lys Thr His Asp Val Ile Arg	
245 250 255	
agt aac ctc gat cgt agc cca atg tac gca ggg gtg atc gaa ggt gtc	816
Ser Asn Leu Asp Arg Ser Pro Met Tyr Ala Gly Val Ile Glu Gly Val	
260 265 270	
ggc cca cgc tac tgc ccg tcg atc gaa gac aaa gtc atg cgc ttc gcc	864
Gly Pro Arg Tyr Cys Pro Ser Ile Glu Asp Lys Val Met Arg Phe Ala	
275 280 285	
gac aga aat cag cat cag atc ttc ctt gaa ccg gaa gga ctg acc tct	912
Asp Arg Asn Gln His Gln Ile Phe Leu Glu Pro Glu Gly Leu Thr Ser	
290 295 300	
aat gaa att tat ccg aac ggt atc tcc acc agc ctg ccg ttc gat gtg	960
Asn Glu Ile Tyr Pro Asn Gly Ile Ser Thr Ser Leu Pro Phe Asp Val	
305 310 315 320	
cag atg caa atc gtc cgc tct atg cag ggg atg gaa aac gcg aag atc	1008
Gln Met Gln Ile Val Arg Ser Met Gln Gly Met Glu Asn Ala Lys Ile	
325 330 335	

gtg cgt ccg ggt tat gcc att gag tat gac ttc ttc gat cct cgc gac	1056
Val Arg Pro Gly Tyr Ala Ile Glu Tyr Asp Phe Phe Asp Pro Arg Asp	
340 345 350	
ctg aaa ccg acg ctg gag agc aag ttt atc cag ggg ctg ttc ttt gct	1104
Leu Lys Pro Thr Leu Glu Ser Lys Phe Ile Gln Gly Leu Phe Phe Ala	
355 360 365	
ggg cag att aac ggc act acc ggt tac gaa gaa gcc gct gcg caa ggt	1152
Gly Gln Ile Asn Gly Thr Thr Gly Tyr Glu Glu Ala Ala Ala Gln Gly	
370 375 380	
ttg ctg gcc ggt ctt aac gct gcc cgt ctg tct gct gac aaa gaa ggt	1200
Leu Leu Ala Gly Leu Asn Ala Ala Arg Leu Ser Ala Asp Lys Glu Gly	
385 390 395 400	
tgg gct ccg gca cgt tct cag gcg tat ctc ggc gta cta gtt gat gac	1248
Trp Ala Pro Ala Arg Ser Gln Ala Tyr Leu Gly Val Leu Val Asp Asp	
405 410 415	
ctg tgc act tta gga acc aaa gaa ccg tat cgt atg ttt act tcg cgc	1296
Leu Cys Thr Leu Gly Thr Lys Glu Pro Tyr Arg Met Phe Thr Ser Arg	
420 425 430	
gca gaa tat cgt ctg atg cta cgc gaa gat aat gcg gat ctg cgt ttg	1344
Ala Glu Tyr Arg Leu Met Leu Arg Glu Asp Asn Ala Asp Leu Arg Leu	
435 440 445	
act gaa atc ggt cgt gaa ctg ggc ctg gtg gat gac gaa cgt tgg gcg	1392
Thr Glu Ile Gly Arg Glu Leu Gly Leu Val Asp Asp Glu Arg Trp Ala	
450 455 460	
cgc ttt aac gag aaa ctt gag aat atc gag cgt gag cgt cag cgt ctg	1440
Arg Phe Asn Glu Lys Leu Glu Asn Ile Glu Arg Glu Arg Gln Arg Leu	
465 470 475 480	
aaa tcg acc tgg gta acc ccg tcg gcg gaa gct gca gcc gaa gtg aat	1488
Lys Ser Thr Trp Val Thr Pro Ser Ala Glu Ala Ala Ala Glu Val Asn	
485 490 495	
gct cac ctg act gcg ccg ctt tcc cgt gaa gcc agt ggt gaa gat ctg	1536
Ala His Leu Thr Ala Pro Leu Ser Arg Glu Ala Ser Gly Glu Asp Leu	
500 505 510	
ctg cgt cgt ccg gaa atg act tat gaa aaa tta acc acg ctg acg ccg	1584
Leu Arg Arg Pro Glu Met Thr Tyr Glu Lys Leu Thr Thr Leu Thr Pro	
515 520 525	
ttt gcc cct gcg ttg aca gac gaa cag gcg gcg gaa cag gtt gag att	1632
Phe Ala Pro Ala Leu Thr Asp Glu Gln Ala Ala Glu Gln Val Glu Ile	
530 535 540	
cag gtt aaa tac gaa ggt tat atc gcg cgc cag caa gat gag atc gaa	1680
Gln Val Lys Tyr Glu Gly Tyr Ile Ala Arg Gln Gln Asp Glu Ile Glu	
545 550 555 560	
aag cag ctg cgt aac gag aac acc ctg cta ccc gcg aca ctg gat tac	1728
Lys Gln Leu Arg Asn Glu Asn Thr Leu Leu Pro Ala Thr Leu Asp Tyr	
565 570 575	
cgc cag gta tcc ggt ctt tct aac gaa gtg atc gcc aaa ctt aac gat	1776

Arg	Gln	Val	Ser	Gly	Leu	Ser	Asn	Glu	Val	Ile	Ala	Lys	Leu	Asn	Asp	
			580					585					590			
cac	aaa	cca	gcc	tct	atc	ggc	caa	gct	tcg	cgt	att	tct	ggc	gtc	acg	1824
His	Lys	Pro	Ala	Ser	Ile	Gly	Gln	Ala	Ser	Arg	Ile	Ser	Gly	Val	Thr	
		595					600					605				
cct	gcg	gcc	atc	tcc	att	ctg	ctg	gtg	tgg	ctg	aaa	aaa	cag	ggt	atg	1872
Pro	Ala	Ala	Ile	Ser	Ile	Leu	Leu	Val	Trp	Leu	Lys	Lys	Gln	Gly	Met	
	610					615				620						
ctg	cgt	cgt	agc	gca	taa											1890
Leu	Arg	Arg	Ser	Ala	*											
625																
<210> 281																
<211> 444																
<212> DNA																
<213> Escherichia coli																
<220>																
<221> CDS																
<222> (1)...(444)																
<400> 281																
atg	gca	gat	atc	act	ctt	atc	agc	ggc	agc	acc	ctc	ggc	ggt	gcc	gaa	48
Met	Ala	Asp	Ile	Thr	Leu	Ile	Ser	Gly	Ser	Thr	Leu	Gly	Gly	Ala	Glu	
1				5					10					15		
tat	gta	gca	gaa	cac	ctg	gct	gaa	aag	ctg	gaa	gag	gcg	ggt	ttt	acc	96
Tyr	Val	Ala	Glu	His	Leu	Ala	Glu	Lys	Leu	Glu	Glu	Ala	Gly	Phe	Thr	
			20					25					30			
acc	gaa	acg	ctg	cac	ggt	ccg	ctg	tta	gaa	gat	tta	cct	gcc	tca	ggg	144
Thr	Glu	Thr	Leu	His	Gly	Pro	Leu	Leu	Glu	Asp	Leu	Pro	Ala	Ser	Gly	
			35				40					45				
atc	tgg	ctg	gtt	atc	agc	tcc	acc	cac	ggt	gcc	gga	gat	att	ccg	gac	192
Ile	Trp	Leu	Val	Ile	Ser	Ser	Thr	His	Gly	Ala	Gly	Asp	Ile	Pro	Asp	
	50					55					60					
aac	ctt	tct	cct	ttc	tat	gaa	gca	ttg	cag	gaa	cag	aag	ccc	gat	ctt	240
Asn	Leu	Ser	Pro	Phe	Tyr	Glu	Ala	Leu	Gln	Glu	Gln	Lys	Pro	Asp	Leu	
65					70				75					80		
tct	gca	gtc	cgc	ttt	ggc	gca	atc	ggt	att	ggc	agt	cgt	gaa	tat	gac	288
Ser	Ala	Val	Arg	Phe	Gly	Ala	Ile	Gly	Ile	Gly	Ser	Arg	Glu	Tyr	Asp	
				85				90						95		
acc	ttt	tgt	ggg	gct	atc	gat	aaa	ctc	gag	gca	gaa	ctc	aaa	aat	tcc	336
Thr	Phe	Cys	Gly	Ala	Ile	Asp	Lys	Leu	Glu	Ala	Glu	Leu	Lys	Asn	Ser	
			100					105					110			
ggt	gca	aaa	cag	aca	ggc	gaa	aca	ctg	aag	atc	aac	att	ctt	gat	cac	384
Gly	Ala	Lys	Gln	Thr	Gly	Glu	Thr	Leu	Lys	Ile	Asn	Ile	Leu	Asp	His	
		115					120					125				
gac	att	ccg	gaa	gat	ccg	gca	gaa	gaa	tgg	ctg	gga	tcg	tgg	gtt	aat	432
Asp	Ile	Pro	Glu	Asp	Pro	Ala	Glu	Glu	Trp	Leu	Gly	Ser	Trp	Val	Asn	
	130					135					140					

tta ctc aaa taa
 Leu Leu Lys *
 145

444

<210> 282
 <211> 456
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(456)

<400> 282
 gtg ggt cag cga aac gtt tcg ctg atg gag aaa aaa atg aaa aaa ggc 48
 Met Gly Gln Arg Asn Val Ser Leu Met Glu Lys Lys Met Lys Lys Gly
 1 5 10 15
 acc gtt ctt aat tct gat att tca tcg gtg atc tcc cgt ctg gga cat 96
 Thr Val Leu Asn Ser Asp Ile Ser Ser Val Ile Ser Arg Leu Gly His
 20 25 30
 acc gat acg ctg gtg gtg tgt gat gct ggt tta ccc atc ccc aaa agt 144
 Thr Asp Thr Leu Val Val Cys Asp Ala Gly Leu Pro Ile Pro Lys Ser
 35 40 45
 aca acg cgt atc gat atg gca tta acc cag ggt gta cct tct ttt atg 192
 Thr Thr Arg Ile Asp Met Ala Leu Thr Gln Gly Val Pro Ser Phe Met
 50 55 60
 cag gtg ctg ggc gtc gtc aca aat gaa atg cag gtc gag gcg gcc att 240
 Gln Val Leu Gly Val Val Thr Asn Glu Met Gln Val Glu Ala Ala Ile
 65 70 75 80
 atc gcg gaa gag atc aaa cac cat aat ccg caa ctc cac gaa acg ttg 288
 Ile Ala Glu Glu Ile Lys His His Asn Pro Gln Leu His Glu Thr Leu
 85 90 95
 ctc act cac ctt gag cag ctg caa aaa cac cag gga aat acc att gaa 336
 Leu Thr His Leu Glu Gln Leu Gln Lys His Gln Gly Asn Thr Ile Glu
 100 105 110
 att cgt tac acc acg cat gaa caa ttc aaa caa caa acc gca gaa agt 384
 Ile Arg Tyr Thr Thr His Glu Gln Phe Lys Gln Gln Thr Ala Glu Ser
 115 120 125
 cag gcg gta att cgc agc gga gaa tgt tct ccg tat gcg aat atc att 432
 Gln Ala Val Ile Arg Ser Gly Glu Cys Ser Pro Tyr Ala Asn Ile Ile
 130 135 140
 ctc tgt gct ggc gtg acg ttc tga 456
 Leu Cys Ala Gly Val Thr Phe *
 145 150

<210> 283
 <211> 1506
 <212> DNA
 <213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (1506)

<400> 283

atg gaa gca tta ctt cag ctt aaa ggc atc gat aaa gcc ttc ccg ggc	48
Met Glu Ala Leu Leu Gln Leu Lys Gly Ile Asp Lys Ala Phe Pro Gly	
1 5 10 15	
gta aaa gcc ctc tcg ggc gca gcg tta aat gtc tat ccg ggc cgc gtg	96
Val Lys Ala Leu Ser Gly Ala Ala Leu Asn Val Tyr Pro Gly Arg Val	
20 25 30	
atg gcg ctg gtg ggc gaa aac ggc gcg ggt aaa tcc acc atg atg aaa	144
Met Ala Leu Val Gly Glu Asn Gly Ala Gly Lys Ser Thr Met Met Lys	
35 40 45	
gtg ctt act ggc atc tat act cgc gat gcc ggt acg ctt tta tgg ctg	192
Val Leu Thr Gly Ile Tyr Thr Arg Asp Ala Gly Thr Leu Leu Trp Leu	
50 55 60	
ggg aaa gaa acg aca ttt acc ggg cca aaa tct tcc cag gaa gcc ggg	240
Gly Lys Glu Thr Thr Phe Thr Gly Pro Lys Ser Ser Gln Glu Ala Gly	
65 70 75 80	
att ggg att atc cat cag gaa ctg aac ctg atc ccg cag ttg acc att	288
Ile Gly Ile Ile His Gln Glu Leu Asn Leu Ile Pro Gln Leu Thr Ile	
85 90 95	
gcc gaa aac att ttc ctc ggt cgt gag ttt gtt aat cgc ttt ggc aaa	336
Ala Glu Asn Ile Phe Leu Gly Arg Glu Phe Val Asn Arg Phe Gly Lys	
100 105 110	
att gac tgg aaa acc atg tat gcc gaa gcg gat aaa ttg ctg gct aaa	384
Ile Asp Trp Lys Thr Met Tyr Ala Glu Ala Asp Lys Leu Leu Ala Lys	
115 120 125	
ctt aac ctg cgc ttt aaa agc gac aag ctg gtg ggc gat ctt tcc atc	432
Leu Asn Leu Arg Phe Lys Ser Asp Lys Leu Val Gly Asp Leu Ser Ile	
130 135 140	
ggg gac cag caa atg gtt gaa atc gcc aaa gtg ctg agc ttt gag tcg	480
Gly Asp Gln Gln Met Val Glu Ile Ala Lys Val Leu Ser Phe Glu Ser	
145 150 155 160	
aaa gtc atc att atg gat gaa ccg acc gat gcg ctg acc gat acc gaa	528
Lys Val Ile Ile Met Asp Glu Pro Thr Asp Ala Leu Thr Asp Thr Glu	
165 170 175	
acc gaa tcc ctg ttc cgc gtc atc cgc gag ctg aaa tcg caa ggc cgc	576
Thr Glu Ser Leu Phe Arg Val Ile Arg Glu Leu Lys Ser Gln Gly Arg	
180 185 190	
ggg att gtc tat atc tcc cac cgc atg aaa gaa atc ttc gag att tgc	624
Gly Ile Val Tyr Ile Ser His Arg Met Lys Glu Ile Phe Glu Ile Cys	
195 200 205	
gat gac gtt acc gtt ttt cgt gat ggg caa ttt att gct gag cgc gaa	672
Asp Asp Val Thr Val Phe Arg Asp Gly Gln Phe Ile Ala Glu Arg Glu	
210 215 220	

gtg gca tca ctg acc gaa gat tcg ctg att gag atg atg gtg ggt cgc	720
Val Ala Ser Leu Thr Glu Asp Ser Leu Ile Glu Met Met Val Gly Arg	
225 230 235 240	
aag ctg gaa gat caa tat ccg cac ctg gac aaa gcg ccg gga gat atc	768
Lys Leu Glu Asp Gln Tyr Pro His Leu Asp Lys Ala Pro Gly Asp Ile	
245 250 255	
cgc ctg aaa gtc gat aat ctc tgc gga cct ggc gtt aac gat gtc tct	816
Arg Leu Lys Val Asp Asn Leu Cys Gly Pro Gly Val Asn Asp Val Ser	
260 265 270	
ttt act tta cgc aaa ggc gaa att ctt ggc gtc tct ggt ttg atg ggc	864
Phe Thr Leu Arg Lys Gly Glu Ile Leu Gly Val Ser Gly Leu Met Gly	
275 280 285	
gca ggt cgt acc gaa ctg atg aaa gtg ctc tac ggc gca cta ccg cgc	912
Ala Gly Arg Thr Glu Leu Met Lys Val Leu Tyr Gly Ala Leu Pro Arg	
290 295 300	
acc agc ggt tac gtc acc ctg gat ggg cat gaa gtc gtt acc cgt tca	960
Thr Ser Gly Tyr Val Thr Leu Asp Gly His Glu Val Val Thr Arg Ser	
305 310 315 320	
ccg cag gat ggc ctg gca aac ggc att gtg tat atc tcc gaa gac cgt	1008
Pro Gln Asp Gly Leu Ala Asn Gly Ile Val Tyr Ile Ser Glu Asp Arg	
325 330 335	
aaa cgt gac ggt tta gtg ttg ggc atg tca gta aaa gag aac atg tcg	1056
Lys Arg Asp Gly Leu Val Leu Gly Met Ser Val Lys Glu Asn Met Ser	
340 345 350	
ctg aca gcg ctg cgc tac ttc agc cgc gct ggc ggc agt ttg aag cat	1104
Leu Thr Ala Leu Arg Tyr Phe Ser Arg Ala Gly Gly Ser Leu Lys His	
355 360 365	
gcc gat gaa cag cag gct gtg agt gat ttc att cgt ctg ttt aat gtg	1152
Ala Asp Glu Gln Gln Ala Val Ser Asp Phe Ile Arg Leu Phe Asn Val	
370 375 380	
aaa act ccg tcg atg gaa cag gca att ggt ctg ctt tcc ggt ggc aat	1200
Lys Thr Pro Ser Met Glu Gln Ala Ile Gly Leu Leu Ser Gly Gly Asn	
385 390 395 400	
cag caa aaa gtg gcg att gcc cgc ggt ctg atg aca cgc ccc aaa gtg	1248
Gln Gln Lys Val Ala Ile Ala Arg Gly Leu Met Thr Arg Pro Lys Val	
405 410 415	
ttg atc ctt gat gaa cct acc cgt ggc gta gat gtc ggc gcg aaa aaa	1296
Leu Ile Leu Asp Glu Pro Thr Arg Gly Val Asp Val Gly Ala Lys Lys	
420 425 430	
gag atc tat caa ctg att aac cag ttc aaa gcc gat ggc ttg agc atc	1344
Glu Ile Tyr Gln Leu Ile Asn Gln Phe Lys Ala Asp Gly Leu Ser Ile	
435 440 445	
att ctg gtg tca tcg gag atg cca gaa gta tta ggc atg agc gat cgc	1392
Ile Leu Val Ser Ser Glu Met Pro Glu Val Leu Gly Met Ser Asp Arg	
450 455 460	

atc atc gtc atg cat gaa ggg cat ctc agc ggg gaa ttt act cgt gag 1440
 Ile Ile Val Met His Glu Gly His Leu Ser Gly Glu Phe Thr Arg Glu
 465 470 475 480

cag gcc acc cag gaa gtg tta atg gct gcc gct gtg ggc aag ctt aat 1488
 Gln Ala Thr Gln Glu Val Leu Met Ala Ala Val Gly Lys Leu Asn
 485 490 495

cgc gtg aat cag gag taa 1506
 Arg Val Asn Gln Glu *
 500

<210> 284

<211> 966

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(966)

<400> 284

atg aca acc cag act gtc tct ggt cgc cgt tat ttc acg aaa gcg tgg 48
 Met Thr Thr Gln Thr Val Ser Gly Arg Tyr Phe Thr Lys Ala Trp
 1 5 10 15

ctg atg gag cag aaa tcg ctt atc gct ctg ctg gtg ctg atc gcg att 96
 Leu Met Glu Gln Lys Ser Leu Ile Ala Leu Leu Val Leu Ile Ala Ile
 20 25 30

gtc tcg acg tta agc ccg aac ttt ttc acc atc aat aac tta ttc aat 144
 Val Ser Thr Leu Ser Pro Asn Phe Phe Thr Ile Asn Asn Leu Phe Asn
 35 40 45

att ctc cag caa acc tca gtg aac gcc att atg gcg gtc ggg atg acg 192
 Ile Leu Gln Gln Thr Ser Val Asn Ala Ile Met Ala Val Gly Met Thr
 50 55 60

ctg gtg atc ctg acg tcg ggc atc gac tta tcg gta ggt tct ctg ttg 240
 Leu Val Ile Leu Thr Ser Gly Ile Asp Leu Ser Val Gly Ser Leu Leu
 65 70 75 80

gcg ctg acc ggc gca gtt gct gca tct atc gtc ggc att gaa gtc aat 288
 Ala Leu Thr Gly Ala Val Ala Ala Ser Ile Val Gly Ile Glu Val Asn
 85 90 95

gcg ctg gtg gct gtc gct gct gct ctc gcg tta ggt gcc gca att ggt 336
 Ala Leu Val Ala Val Ala Ala Leu Ala Leu Gly Ala Ala Ile Gly
 100 105 110

gcg gta acc ggg gtg att gta gcg aaa ggt cgc gtc cag gcg ttt atc 384
 Ala Val Thr Gly Val Ile Val Ala Lys Gly Arg Val Gln Ala Phe Ile
 115 120 125

gct acg ctg gtt atg atg ctt tta ctg cgc ggc gtg acc atg gtt tat 432
 Ala Thr Leu Val Met Met Leu Leu Arg Gly Val Thr Met Val Tyr
 130 135 140

acc aac ggt agc cca gtg aat acc ggc ttt act gag aac gcc gat ctg 480
 Thr Asn Gly Ser Pro Val Asn Thr Gly Phe Thr Glu Asn Ala Asp Leu

145	150	155	160	
ttt ggc tgg ttt ggt att ggt cgt ccg ctg ggc gta ccg acg cca gtc	528			
Phe Gly Trp Phe Gly Ile Gly Arg Pro Leu Gly Val Pro Thr Pro Val				
165	170	175		
tgg atc atg ggg att gtc ttc ctc gcg gcc tgg tac atg ctg cat cac	576			
Trp Ile Met Gly Ile Val Phe Leu Ala Ala Trp Tyr Met Leu His His				
180	185	190		
acg cgt ctg ggg cgt tac atc tac gcg ctg ggc ggc aac gaa gcg gca	624			
Thr Arg Leu Gly Arg Tyr Ile Tyr Ala Leu Gly Gly Asn Glu Ala Ala				
195	200	205		
acg cgt ctt tct ggt atc aac gtc aat aaa atc aaa atc atc gtc tat	672			
Thr Arg Leu Ser Gly Ile Asn Val Asn Lys Ile Lys Ile Ile Val Tyr				
210	215	220		
tct ctt tgt ggt ctg ctg gca tct ctg gcc ggg atc att gaa gtg gcg	720			
Ser Leu Cys Gly Leu Leu Ala Ser Leu Ala Gly Ile Ile Glu Val Ala				
225	230	235	240	
cgt ctc tcc tcc gca caa ccc acg gcg ggg act ggc tat gag ctg gat	768			
Arg Leu Ser Ser Ala Gln Pro Thr Ala Gly Thr Gly Tyr Glu Leu Asp				
245	250	255		
gct att gct gcg gtg gtt ctg ggc ggt acg agt ctg gcg ggc gga aaa	816			
Ala Ile Ala Ala Val Val Leu Gly Gly Thr Ser Leu Ala Gly Gly Lys				
260	265	270		
ggc cgc att gtt ggg acg ttg atc ggc gca tta att ctt ggc ttc ctt	864			
Gly Arg Ile Val Gly Thr Leu Ile Gly Ala Leu Ile Leu Gly Phe Leu				
275	280	285		
aat aat gga ttg aat ttg tta ggt gtt tcc tcc tat tac cag atg atc	912			
Asn Asn Gly Leu Asn Leu Leu Gly Val Ser Ser Tyr Tyr Gln Met Ile				
290	295	300		
gtc aaa gcg gtg gtg att ttg ctg gcg gtg ctg gta gac aac aaa aag	960			
Val Lys Ala Val Val Ile Leu Leu Ala Val Leu Val Asp Asn Lys Lys				
305	310	315	320	
cag taa				966
Gln *				

<210> 285

<211> 891

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (891)

<400> 285

atg aac atg aaa aaa ctg gct acc ctg gtt tcc gct gtt gcg cta agc	48
Met Asn Met Lys Lys Leu Ala Thr Leu Val Ser Ala Val Ala Leu Ser	
1	5
	10
	15

gcc acc gtc agt gcg aat gcg atg gca aaa gac acc atc gcg ctg gtg	96
Ala Thr Val Ser Ala Asn Ala Met Ala Lys Asp Thr Ile Ala Leu Val	
20 25 30	
gtc tcc acg ctt aac aac ccg ttc ttt gta tcg ctg aaa gat ggc gcg	144
Val Ser Thr Leu Asn Asn Pro Phe Phe Val Ser Leu Lys Asp Gly Ala	
35 40 45	
cag aaa gag gcg gat aaa ctt ggc tat aac ctg gtg gtg ctg gac tcc	192
Gln Lys Glu Ala Asp Lys Leu Gly Tyr Asn Leu Val Val Leu Asp Ser	
50 55 60	
cag aac aac ccg gcg aaa gag ctg gcg aac gtg cag gac tta acc gtt	240
Gln Asn Asn Pro Ala Lys Glu Leu Ala Asn Val Gln Asp Leu Thr Val	
65 70 75 80	
cgc ggc aca aaa att ctg ctg att aac ccg acc gac tcc gac gca gtg	288
Arg Gly Thr Lys Ile Leu Leu Ile Asn Pro Thr Asp Ser Asp Ala Val	
85 90 95	
ggc aat gct gtg aag atg gct aac cag gcg aac atc ccg gtt atc act	336
Gly Asn Ala Val Lys Met Ala Asn Gln Ala Asn Ile Pro Val Ile Thr	
100 105 110	
ctt gac cgc cag gca acg aaa ggt gaa gtg gtg agc cac att gct tct	384
Leu Asp Arg Gln Ala Thr Lys Gly Glu Val Val Ser His Ile Ala Ser	
115 120 125	
gat aac gta ctg ggc ggc aaa atc gct ggt gat tac atc gcg aag aaa	432
Asp Asn Val Leu Gly Gly Lys Ile Ala Gly Asp Tyr Ile Ala Lys Lys	
130 135 140	
gcg ggt gaa ggt gcc aaa gtt atc gag ctg caa ggc att gct ggt aca	480
Ala Gly Glu Gly Ala Lys Val Ile Glu Leu Gln Gly Ile Ala Gly Thr	
145 150 155 160	
tcc gca gcc cgt gaa cgt ggc gaa ggc ttc cag cag gcc gtt gct gct	528
Ser Ala Ala Arg Glu Arg Gly Glu Gly Phe Gln Gln Ala Val Ala Ala	
165 170 175	
cac aag ttt aat gtt ctt gcc agc cag cca gca gat ttt gat cgc att	576
His Lys Phe Asn Val Leu Ala Ser Gln Pro Ala Asp Phe Asp Arg Ile	
180 185 190	
aaa ggt ttg aac gta atg cag aac ctg ttg acc gct cat ccg gat gtt	624
Lys Gly Leu Asn Val Met Gln Asn Leu Leu Thr Ala His Pro Asp Val	
195 200 205	
cag gct gta ttc gcg cag aat gat gaa atg gcg ctg ggc gcg ctg cgc	672
Gln Ala Val Phe Ala Gln Asn Asp Glu Met Ala Leu Gly Ala Leu Arg	
210 215 220	
gca ctg caa act gcc ggt aaa tcg gat gtg atg gtc gtc gga ttt gac	720
Ala Leu Gln Thr Ala Gly Lys Ser Asp Val Met Val Val Gly Phe Asp	
225 230 235 240	
ggc aca ccg gat ggc gaa aaa gcg gtg aat gat ggc aaa cta gca gcg	768
Gly Thr Pro Asp Gly Glu Lys Ala Val Asn Asp Gly Lys Leu Ala Ala	
245 250 255	
act atc gct cag cta ccc gat cag att ggc gcg aaa ggc gtc gaa acc	816

```

Thr Ile Ala Gln Leu Pro Asp Gln Ile Gly Ala Lys Gly Val Glu Thr
      260                      265                      270

gca gat aaa gtg ctg aaa ggc gag aaa gtt cag gct aag tat ccg gtt 864
Ala Asp Lys Val Leu Lys Gly Glu Lys Val Gln Ala Lys Tyr Pro Val
      275                      280                      285

gat ctg aaa ctg gtt gtt aag cag tag 891
Asp Leu Lys Leu Val Val Lys Gln *
      290                      295

<210> 286
<211> 930
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(930)

<400> 286
atg caa aac gca ggc agc ctc gtt gtt ctt ggc agc att aat gct gac 48
Met Gln Asn Ala Gly Ser Leu Val Val Leu Gly Ser Ile Asn Ala Asp
  1                      5                      10                      15

cac att ctt aat ctt caa tct ttt cct act cca ggc gaa acc gta acc 96
His Ile Leu Asn Leu Gln Ser Phe Pro Thr Pro Gly Glu Thr Val Thr
      20                      25                      30

ggt aac cac tat cag gtt gca ttt ggc ggc aaa ggc gcg aat cag gct 144
Gly Asn His Tyr Gln Val Ala Phe Gly Gly Lys Gly Ala Asn Gln Ala
      35                      40                      45

gtg gct gct ggg cgt agc ggt gcg aat atc gcg ttt att gcc tgt acg 192
Val Ala Ala Gly Arg Ser Gly Ala Asn Ile Ala Phe Ile Ala Cys Thr
      50                      55                      60

ggt gat gac agc att ggt gag agc gtt cgc cag cag ctc gcc act gat 240
Gly Asp Asp Ser Ile Gly Glu Ser Val Arg Gln Gln Leu Ala Thr Asp
      65                      70                      75                      80

aac att gat att act ccg gtc agc gtg atc aaa ggc gaa tca aca ggt 288
Asn Ile Asp Ile Thr Pro Val Ser Val Ile Lys Gly Glu Ser Thr Gly
      85                      90                      95

gtg gcg ctg att ttt gtt aat ggc gaa ggt gag aat gtc atc ggt att 336
Val Ala Leu Ile Phe Val Asn Gly Glu Gly Glu Asn Val Ile Gly Ile
      100                      105                      110

cat gcc ggc gct aat gct gcc ctt tcc ccg gcg ctg gtg gaa gcg caa 384
His Ala Gly Ala Asn Ala Ala Leu Ser Pro Ala Leu Val Glu Ala Gln
      115                      120                      125

cgt gag cgt att gcc aac gcg tca gca tta tta atg cag ctg gaa tca 432
Arg Glu Arg Ile Ala Asn Ala Ser Ala Leu Leu Met Gln Leu Glu Ser
      130                      135                      140

cca ctc gaa agt gtg atg gca gcg gcg aaa atc gcc cat caa aat aag 480
Pro Leu Glu Ser Val Met Ala Ala Ala Lys Ile Ala His Gln Asn Lys
      145                      150                      155                      160

```

act atc gtt gcg ctt aac ccg gct ccg gct cgc gaa ctt cct gac gaa 528
 Thr Ile Val Ala Leu Asn Pro Ala Pro Ala Arg Glu Leu Pro Asp Glu
 165 170 175

ctg ctg gcg ctg gtg gac att att acg cca aac gaa acg gaa gca gaa 576
 Leu Leu Ala Leu Val Asp Ile Ile Thr Pro Asn Glu Thr Glu Ala Glu
 180 185 190

aag ctc acc ggt att cgt gtt gaa aat gat gaa gat gca gcg aag gcg 624
 Lys Leu Thr Thr Gly Ile Arg Val Glu Asn Asp Glu Asp Ala Ala Lys Ala
 195 200 205

gcg cag gta ctg cat gaa aaa ggt atc cgt act gta ctg att act tta 672
 Ala Gln Val Leu His Glu Lys Gly Ile Arg Thr Val Leu Ile Thr Leu
 210 215 220

gga agt cgt ggt gta tgg gct agc gtg aat ggt gaa ggt cag cgc gtt 720
 Gly Ser Arg Gly Val Trp Ala Ser Val Asn Gly Glu Gly Gln Arg Val
 225 230 235 240

cct gga ttc cgg gtg cag gct gtc gat acc att gct gcc gga gat acc 768
 Pro Gly Phe Arg Val Gln Ala Val Asp Thr Ile Ala Ala Gly Asp Thr
 245 250 255

ttt aac ggt gcg tta atc acg gca ttg ctg gaa gaa aaa cca ttg cca 816
 Phe Asn Gly Ala Leu Ile Thr Ala Leu Leu Glu Glu Lys Pro Leu Pro
 260 265 270

gag gcg att cgt ttt gcc cat gct gcc gct gcg att gcc gta aca cgt 864
 Glu Ala Ile Arg Phe Ala His Ala Ala Ala Ala Ile Ala Val Thr Arg
 275 280 285

aaa ggc gca caa cct tcc gta ccg tgg cgt gaa gag atc gac gca ttt 912
 Lys Gly Ala Gln Pro Ser Val Pro Trp Arg Glu Glu Ile Asp Ala Phe
 290 295 300

tta gac agg cag agg tga 930
 Leu Asp Arg Gln Arg *
 305

<210> 287

<211> 38

<212> PRT

<213> Escherichia coli

<400> 287

Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
 1 5 10 15
 Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
 20 25 30
 His Lys Gln Arg Gln Gly
 35

<210> 288

<211> 443

<212> PRT

<213> Escherichia coli

<400> 288

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Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
 1      5      10      15
Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
 20      25      30
Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
 35      40      45
Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe
 50      55      60
Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu
 65      70      75      80
Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Ile Gln Leu Leu Thr
 85      90      95
Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly
100      105      110
Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala
115      120      125
Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly
130      135      140
Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala
145      150      155      160
Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu
165      170      175
Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Ile Phe
180      185      190
Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu
195      200      205
Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Leu Val Ala
210      215      220
Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly
225      230      235      240
Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg
245      250      255
Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala
260      265      270
Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala
275      280      285
Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr
290      295      300
Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu
305      310      315      320
Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val
325      330      335
Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe
340      345      350
Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys
355      360      365
Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile
370      375      380
Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr
385      390      395      400
Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe
405      410      415
Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala
420      425      430
Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg
435      440

```

<210> 289

<211> 144

<212> PRT

<213> Escherichia coli

<400> 289

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Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly
 1           5           10           15
Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly
           20           25           30
Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Gly Val Arg Arg
           35           40           45
Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe
           50           55           60
Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser
65           70           75           80
Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys
           85           90           95
Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu
           100          105          110
Ala Gly Glu Val Thr Thr Pro Val Thr Val Arg Gly Leu Arg Val Thr
           115          120          125
Lys Gly Ala Arg Ala Ala Ile Glu Ala Ala Gly Gly Lys Ile Glu Glu
           130          135          140

```

<210> 290

<211> 59

<212> PRT

<213> Escherichia coli

<400> 290

```

Met Ala Lys Thr Ile Lys Ile Thr Gln Thr Arg Ser Ala Ile Gly Arg
 1           5           10           15
Leu Pro Lys His Lys Ala Thr Leu Leu Gly Leu Gly Leu Arg Arg Ile
           20           25           30
Gly His Thr Val Glu Arg Glu Asp Thr Pro Ala Ile Arg Gly Met Ile
           35           40           45
Asn Ala Val Ser Phe Met Val Lys Val Glu Glu
           50           55

```

<210> 291

<211> 167

<212> PRT

<213> Escherichia coli

<400> 291

```

Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile
 1           5           10           15
Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser
           20           25           30
Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe
           35           40           45
Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met
           50           55           60
Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr
65           70           75           80
Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met
           85           90           95
Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg
           100          105          110
Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr

```

```

      115      120      125
Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
  130      135      140
Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser
  145      150      155      160
Val Glu Glu Ile Leu Gly Lys
      165

```

<210> 292

<211> 117

<212> PRT

<213> Escherichia coli

<400> 292

```

Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
  1      5      10      15
Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
      20      25      30
Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu
      35      40      45
Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr
      50      55      60
Thr Gly Asn Lys Asp Ala Ala Ala Ala Val Gly Lys Ala Val Ala Glu
  65      70      75      80
Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly
      85      90      95
Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu
      100      105      110
Ala Gly Leu Gln Phe
      115

```

<210> 293

<211> 177

<212> PRT

<213> Escherichia coli

<400> 293

```

Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
  1      5      10      15
Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu
      20      25      30
Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
      35      40      45
Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
      50      55      60
Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
  65      70      75      80
Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
      85      90      95
Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
      100      105      110
Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
      115      120      125
Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val
      130      135      140
Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys
  145      150      155      160
Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys
      165      170      175

```

Lys

<210> 294
 <211> 130
 <212> PRT
 <213> Escherichia coli

<400> 294
 Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn
 1 5 10 15
 Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu
 20 25 30
 Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp
 35 40 45
 Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys
 50 55 60
 Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg
 65 70 75 80
 Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met
 85 90 95
 Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr
 100 105 110
 Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr
 115 120 125
 Val Ala
 130

<210> 295
 <211> 101
 <212> PRT
 <213> Escherichia coli

<400> 295
 Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu
 1 5 10 15
 Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser
 20 25 30
 Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu
 35 40 45
 Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys
 50 55 60
 Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser
 65 70 75 80
 Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu
 85 90 95
 Lys Lys Ala Ser Trp
 100

<210> 296
 <211> 179
 <212> PRT
 <213> Escherichia coli

<400> 296
 Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu
 1 5 10 15
 Met Thr Glu Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu

20 25 30
 Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys
 35 40 45
 Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys
 50 55 60
 Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg
 65 70 75 80
 Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met
 85 90 95
 Trp Glu Phe Phe Glu Arg Leu Ile Thr Ile Ala Val Pro Arg Ile Arg
 100 105 110
 Asp Phe Arg Gly Leu Ser Ala Lys Ser Phe Asp Gly Arg Gly Asn Tyr
 115 120 125
 Ser Met Gly Val Arg Glu Gln Ile Ile Phe Pro Glu Ile Asp Tyr Asp
 130 135 140
 Lys Val Asp Arg Val Arg Gly Leu Asp Ile Thr Ile Thr Thr Thr Ala
 145 150 155 160
 Lys Ser Asp Glu Glu Gly Arg Ala Leu Leu Ala Ala Phe Asp Phe Pro
 165 170 175
 Phe Arg Lys

<210> 297

<211> 104

<212> PRT

<213> Escherichia coli

<400> 297

Met Ala Ala Lys Ile Arg Arg Asp Asp Glu Val Ile Val Leu Thr Gly
 1 5 10 15
 Lys Asp Lys Gly Lys Arg Gly Lys Val Lys Asn Val Leu Ser Ser Gly
 20 25 30
 Lys Val Ile Val Glu Gly Ile Asn Leu Val Lys Lys His Gln Lys Pro
 35 40 45
 Val Pro Ala Leu Asn Gln Pro Gly Gly Ile Val Glu Lys Glu Ala Ala
 50 55 60
 Ile Gln Val Ser Asn Val Ala Ile Phe Asn Ala Ala Thr Gly Lys Ala
 65 70 75 80
 Asp Arg Val Gly Phe Arg Phe Glu Asp Gly Lys Lys Val Arg Phe Phe
 85 90 95
 Lys Ser Asn Ser Glu Thr Ile Lys
 100

<210> 298

<211> 123

<212> PRT

<213> Escherichia coli

<400> 298

Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala
 1 5 10 15
 Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr
 20 25 30
 Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro
 35 40 45
 Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg
 50 55 60
 Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp
 65 70 75 80

Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly
 85 90 95
 Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe
 100 105 110
 Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu
 115 120

<210> 299

<211> 485

<212> PRT

<213> Escherichia coli

<400> 299

Met Gly Ile Tyr Phe Thr Asn Ser Asp Asp Gln Ile Tyr Phe Lys Arg
 1 5 10 15
 Ser Glu Gly Met Ser Asp Ile Asn His Ala Gly Ser Asp Leu Ile Phe
 20 25 30
 Glu Leu Glu Asp Arg Pro Pro Phe His Gln Ala Leu Val Gly Ala Ile
 35 40 45
 Thr His Leu Leu Ala Ile Phe Val Pro Met Val Thr Pro Ala Leu Ile
 50 55 60
 Val Gly Ala Ala Leu Gln Leu Ser Ala Glu Thr Thr Ala Tyr Leu Val
 65 70 75 80
 Ser Met Ala Met Ile Ala Ser Gly Ile Gly Thr Trp Leu Gln Val Asn
 85 90 95
 Arg Tyr Gly Ile Val Gly Ser Gly Leu Leu Ser Ile Gln Ser Val Asn
 100 105 110
 Phe Ser Phe Val Thr Val Met Ile Ala Leu Gly Ser Ser Met Lys Ser
 115 120 125
 Asp Gly Phe His Glu Glu Leu Ile Met Ser Ser Leu Leu Gly Val Ser
 130 135 140
 Phe Val Gly Ala Phe Leu Val Val Gly Ser Ser Phe Ile Leu Pro Tyr
 145 150 155 160
 Leu Arg Arg Val Ile Thr Pro Thr Val Ser Gly Ile Val Val Leu Met
 165 170 175
 Ile Gly Leu Ser Leu Ile Lys Val Gly Ile Ile Asp Phe Gly Gly Gly
 180 185 190
 Phe Ala Ala Lys Ser Ser Gly Thr Phe Gly Asn Tyr Glu His Leu Gly
 195 200 205
 Val Gly Leu Leu Val Leu Ile Val Val Ile Gly Phe Asn Cys Cys Arg
 210 215 220
 Ser Pro Leu Leu Arg Met Gly Gly Ile Ala Ile Gly Leu Cys Val Gly
 225 230 235 240
 Tyr Ile Ala Ser Leu Cys Leu Gly Met Val Asp Phe Ser Ser Met Arg
 245 250 255
 Asn Leu Pro Leu Ile Thr Ile Pro His Pro Phe Lys Tyr Gly Phe Ser
 260 265 270
 Phe Ser Phe His Gln Phe Leu Val Val Gly Thr Ile Tyr Leu Leu Ser
 275 280 285
 Val Leu Glu Ala Val Gly Asp Ile Thr Ala Thr Ala Met Val Ser Arg
 290 295 300
 Arg Pro Ile Gln Gly Glu Glu Tyr Gln Ser Arg Leu Lys Gly Gly Val
 305 310 315 320
 Leu Ala Asp Gly Leu Val Ser Val Ile Ala Ser Ala Val Gly Ser Leu
 325 330 335
 Pro Leu Thr Thr Phe Ala Gln Asn Asn Gly Val Ile Gln Met Thr Gly
 340 345 350
 Val Ala Ser Arg Tyr Val Gly Arg Thr Ile Ala Val Met Leu Val Ile
 355 360 365
 Leu Gly Leu Phe Pro Met Ile Gly Gly Phe Phe Thr Thr Ile Pro Ser

370	375	380
Ala Val Leu Gly Gly	Ala Met Thr Leu Met Phe Ser Met Ile Ala Ile	
385	390	395
Ala Gly Ile Arg Ile	Ile Thr Asn Gly Leu Lys Arg Arg Glu Thr	400
	405	410
Leu Ile Val Ala Thr	Ser Leu Gly Leu Gly Leu Gly Val Ser Tyr Asp	415
	420	425
Pro Glu Ile Phe Lys Ile	Leu Pro Ala Ser Ile Tyr Val Leu Val Glu	430
	435	440
Asn Pro Ile Cys Ala Gly	Gly Leu Thr Ala Ile Leu Leu Asn Ile Ile	445
	450	455
Leu Pro Gly Gly Tyr Arg	Gln Glu Asn Val Leu Pro Gly Ile Thr Ser	460
465	470	475
Ala Glu Glu Met Asp		480
	485	

<210> 300

<211> 439

<212> PRT

<213> Escherichia coli

<400> 300

Met Met Ser Gly Glu His Thr Leu Lys Ala Val Arg Gly Ser Phe Ile	
1 5 10 15	
Asp Val Thr Arg Thr Ile Asp Asn Pro Glu Glu Ile Ala Ser Ala Leu	
20 25 30	
Arg Phe Ile Glu Asp Gly Leu Leu Leu Ile Lys Gln Gly Lys Val Glu	
35 40 45	
Trp Phe Gly Glu Trp Glu Asn Gly Lys His Gln Ile Pro Asp Thr Ile	
50 55 60	
Arg Val Arg Asp Tyr Arg Gly Lys Leu Ile Val Pro Gly Phe Val Asp	
65 70 75 80	
Thr His Ile His Tyr Pro Gln Ser Glu Met Val Gly Ala Tyr Gly Glu	
85 90 95	
Gln Leu Leu Glu Trp Leu Asn Lys His Thr Phe Pro Thr Glu Arg Arg	
100 105 110	
Tyr Glu Asp Leu Glu Tyr Ala Arg Glu Met Ser Ala Phe Phe Ile Lys	
115 120 125	
Gln Leu Leu Arg Asn Gly Thr Thr Thr Ala Leu Val Phe Gly Thr Val	
130 135 140	
His Pro Gln Ser Val Asp Ala Leu Phe Glu Ala Ala Ser His Ile Asn	
145 150 155 160	
Met Arg Met Ile Ala Gly Lys Val Met Met Asp Arg Asn Ala Pro Asp	
165 170 175	
Tyr Leu Leu Asp Thr Ala Glu Ser Ser Tyr His Gln Ser Lys Glu Leu	
180 185 190	
Ile Glu Arg Trp His Lys Asn Gly Arg Leu Leu Tyr Ala Ile Thr Pro	
195 200 205	
Arg Phe Ala Pro Thr Ser Ser Pro Glu Gln Met Ala Met Ala Gln Arg	
210 215 220	
Leu Lys Glu Glu Tyr Pro Asp Thr Trp Val His Thr His Leu Cys Glu	
225 230 235 240	
Asn Lys Asp Glu Ile Ala Trp Val Lys Ser Leu Tyr Pro Asp His Asp	
245 250 255	
Gly Tyr Leu Asp Val Tyr His Gln Tyr Gly Leu Thr Gly Lys Asn Cys	
260 265 270	
Val Phe Ala His Cys Val His Leu Glu Glu Lys Glu Trp Asp Arg Leu	
275 280 285	
Ser Glu Thr Lys Ser Ser Ile Ala Phe Cys Pro Thr Ser Asn Leu Tyr	
290 295 300	

Leu Gly Ser Gly Leu Phe Asn Leu Lys Lys Ala Trp Gln Lys Lys Val
 305 310 315 320
 Lys Val Gly Met Gly Thr Asp Ile Gly Ala Gly Thr Thr Phe Asn Met
 325 330 335
 Leu Gln Thr Leu Asn Glu Ala Tyr Lys Val Leu Gln Leu Gln Gly Tyr
 340 345 350
 Arg Leu Ser Ala Tyr Glu Ala Phe Tyr Leu Ala Thr Leu Gly Gly Ala
 355 360 365
 Lys Ser Leu Gly Leu Asp Asp Leu Ile Gly Asn Phe Leu Pro Gly Lys
 370 375 380
 Glu Ala Asp Phe Val Val Met Glu Pro Thr Ala Thr Pro Leu Gln Gln
 385 390 395 400
 Leu Arg Tyr Asp Asn Ser Val Ser Leu Val Asp Lys Leu Phe Val Met
 405 410 415
 Met Thr Leu Gly Asp Asp Arg Ser Ile Tyr Arg Thr Tyr Val Asp Gly
 420 425 430
 Arg Leu Val Tyr Glu Arg Asn
 435

<210> 301
 <211> 189
 <212> PRT
 <213> Escherichia coli

<400> 301
 Met Ser Gly Asp Ile Leu Gln Thr Pro Asp Ala Pro Lys Pro Gln Gly
 1 5 10 15
 Ala Leu Asp Asn Tyr Phe Lys Ile Thr Ala Arg Gly Ser Thr Val Arg
 20 25 30
 Gln Glu Val Leu Ala Gly Leu Thr Thr Phe Leu Ala Met Val Tyr Ser
 35 40 45
 Val Ile Val Val Pro Gly Met Leu Gly Lys Ala Gly Phe Pro Pro Ala
 50 55 60
 Ala Val Phe Val Ala Thr Cys Leu Val Ala Gly Phe Gly Ser Leu Leu
 65 70 75 80
 Met Gly Leu Trp Ala Asn Leu Pro Met Ala Ile Gly Cys Ala Ile Ser
 85 90 95
 Leu Thr Ala Phe Thr Ala Phe Ser Leu Val Leu Gly Gln Gln Ile Ser
 100 105 110
 Val Pro Val Ala Leu Gly Ala Val Phe Leu Met Gly Val Ile Phe Thr
 115 120 125
 Ala Ile Ser Val Thr Gly Val Arg Thr Trp Ile Leu Arg Asn Leu Pro
 130 135 140
 Met Gly Ile Ala His Gly Thr Gly Ile Gly Ile Gly Leu Phe Leu Leu
 145 150 155 160
 Leu Ile Ala Ala Asn Gly Val Gly Met Val Ile Lys Asn Pro Ile Glu
 165 170 175
 Gly Leu Gln Trp Arg Ser Val Arg Leu Pro Pro Ser Arg
 180 185

<210> 302
 <211> 276
 <212> PRT
 <213> Escherichia coli

<400> 302
 Met Ala Leu Gly Ala Phe Thr Ser Phe Pro Val Met Met Ser Leu Leu
 1 5 10 15
 Gly Leu Ala Val Ile Phe Gly Leu Glu Lys Cys Arg Val Pro Gly Gly

```

      20      25      30
Ile Leu Leu Val Ile Ile Ala Ile Ser Ile Ile Gly Leu Ile Phe Asp
      35      40      45
Pro Ala Val Lys Tyr His Gly Leu Val Ala Met Pro Ser Leu Thr Gly
      50      55      60
Glu Asp Gly Lys Ser Leu Ile Phe Ser Leu Asp Ile Met Gly Ala Leu
      65      70      75      80
Gln Pro Thr Val Leu Pro Ser Val Leu Ala Leu Val Met Thr Ala Val
      85      90      95
Phe Asp Ala Thr Gly Thr Ile Arg Ala Val Ala Gly Gln Ala Asn Leu
      100      105      110
Leu Asp Lys Asp Asn Gln Ile Ile Asn Gly Gly Lys Ala Leu Thr Ser
      115      120      125
Asp Ser Val Ser Ser Ile Phe Ser Gly Leu Val Gly Ala Ala Pro Ala
      130      135      140
Ala Val Tyr Ile Glu Ser Ala Ala Gly Thr Ala Ala Gly Gly Lys Thr
      145      150      155      160
Gly Leu Thr Ala Thr Val Val Gly Ala Leu Phe Leu Leu Ile Leu Phe
      165      170      175
Leu Ser Pro Leu Ser Phe Leu Ile Pro Gly Tyr Ala Thr Ala Pro Ala
      180      185      190
Leu Met Tyr Val Gly Leu Leu Met Leu Ser Asn Val Ser Lys Leu Asp
      195      200      205
Phe Asn Asp Phe Ile Asp Ala Met Ala Gly Leu Val Cys Ala Val Phe
      210      215      220
Ile Val Leu Thr Cys Asn Ile Val Thr Gly Ile Met Leu Gly Phe Val
      225      230      235      240
Thr Leu Val Val Gly Arg Val Phe Ala Arg Glu Trp Gln Lys Leu Asn
      245      250      255
Ile Gly Thr Val Ile Ile Thr Ala Ala Leu Val Ala Phe Tyr Ala Gly
      260      265      270
Gly Trp Ala Ile
      275

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<210> 303

<211> 466

<212> PRT

<213> Escherichia coli

<400> 303

```

Met Asn Ser Glu Gly Gly Lys Pro Gly Asn Val Leu Thr Val Asn Gly
1      5      10      15
Asn Tyr Thr Gly Asn Asn Gly Leu Met Thr Phe Asn Ala Thr Leu Gly
      20      25      30
Gly Asp Asn Ser Pro Thr Asp Lys Met Asn Val Lys Gly Asp Thr Gln
      35      40      45
Gly Asn Thr Arg Val Arg Val Asp Asn Ile Gly Gly Val Gly Ala Gln
      50      55      60
Thr Val Asn Gly Ile Glu Leu Ile Glu Val Gly Gly Asn Ser Ala Gly
      65      70      75      80
Asn Phe Ala Leu Thr Thr Gly Thr Val Glu Ala Gly Ala Tyr Val Tyr
      85      90      95
Thr Leu Ala Lys Gly Lys Gly Asn Asp Glu Lys Asn Trp Tyr Leu Thr
      100      105      110
Ser Lys Trp Asp Gly Val Thr Pro Ala Asp Thr Pro Asp Pro Ile Asn
      115      120      125
Asn Pro Pro Val Val Asp Pro Glu Gly Pro Ser Val Tyr Arg Pro Glu
      130      135      140
Ala Gly Ser Tyr Ile Ser Asn Ile Ala Ala Ala Asn Ser Leu Phe Ser
      145      150      155      160

```


His Arg Leu His Asp Arg Leu Gly Glu Pro Gln Tyr Thr Asp Ser Leu
 165 170
 His Ser Gln Gly Ser Ala Ser Ser Met Trp Met Arg His Val Gly Gly
 180 185 190
 His Glu Arg Ser Arg Ala Gly Asp Gly Gln Leu Asn Thr Gln Ala Asn
 195 200 205
 Arg Tyr Val Leu Gln Leu Gly Gly Asp Leu Ala Gln Trp Ser Ser Asn
 210 215 220
 Ala Gln Asp Arg Trp His Leu Gly Val Met Ala Gly Tyr Ala Asn Gln
 225 230 235 240
 His Ser Asn Thr Gln Ser Asn Arg Val Gly Tyr Lys Ser Asp Gly Arg
 245 250 255
 Ile Ser Gly Tyr Ser Ala Gly Leu Tyr Ala Thr Trp Tyr Gln Asn Asp
 260 265 270
 Ala Asn Lys Thr Gly Ala Tyr Val Asp Ser Trp Ala Leu Tyr Asn Trp
 275 280 285
 Phe Asp Asn Ser Val Ser Ser Asp Asn Arg Ser Ala Asp Asp Tyr Asp
 290 295 300
 Ser Arg Gly Val Thr Ala Ser Val Glu Gly Gly Tyr Thr Phe Glu Ala
 305 310 315 320
 Gly Thr Phe Ser Gly Ser Glu Gly Thr Leu Asn Thr Trp Tyr Val Gln
 325 330 335
 Pro Gln Ala Gln Ile Thr Trp Met Gly Val Lys Asp Ser Asp His Thr
 340 345 350
 Arg Lys Asp Gly Thr Arg Ile Glu Thr Glu Gly Asp Gly Asn Val Gln
 355 360 365
 Thr Arg Leu Gly Val Lys Thr Tyr Leu Asn Ser His His Gln Arg Asp
 370 375 380
 Asp Gly Lys Gln Arg Glu Phe Gln Pro Tyr Ile Glu Ala Asn Trp Ile
 385 390 395 400
 Asn Asn Ser Lys Val Tyr Ala Val Lys Met Asn Gly Gln Thr Val Gly
 405 410 415
 Arg Glu Gly Ala Arg Asn Leu Gly Glu Val Arg Thr Gly Val Glu Ala
 420 425 430
 Lys Val Asn Asn Asn Leu Ser Leu Trp Gly Asn Val Gly Val Gln Leu
 435 440 445
 Gly Asp Lys Gly Tyr Ser Asp Thr Gln Gly Met Leu Gly Val Lys Tyr
 450 455 460
 Ser Trp
 465

<210> 304

<211> 1325

<212> PRT

<213> Escherichia coli

<400> 304

Met Asn Arg Ile Tyr Arg Val Ile Trp Asn Cys Thr Leu Gln Val Phe
 1 5 10 15
 Gln Ala Cys Ser Glu Leu Thr Arg Arg Ala Gly Lys Thr Ser Thr Val
 20 25 30
 Asn Leu Arg Lys Ser Ser Gly Leu Thr Thr Lys Phe Ser Arg Leu Thr
 35 40 45
 Leu Gly Val Leu Leu Ala Leu Ser Gly Ser Ala Ser Gly Ala Ser Leu
 50 55 60
 Glu Val Asp Asn Asp Gln Ile Thr Asn Ile Asp Thr Asp Val Ala Tyr
 65 70 75 80
 Asp Ala Tyr Leu Val Gly Trp Tyr Gly Thr Gly Val Leu Asn Ile Leu
 85 90 95
 Ala Gly Gly Asn Ala Ser Leu Thr Thr Ile Thr Thr Ser Val Ile Gly

[illegible]

Val Asp Gly Gln Asn Ser Leu Leu Glu Thr Phe Asn Met Tyr Val Gly
 595 600 605
 Thr Ser Gly Thr Gly Thr Leu Thr Leu Thr Asn Asn Gly Thr Leu Asn
 610 615 620
 Val Glu Gly Gly Glu Val Tyr Leu Gly Val Phe Glu Pro Ala Val Gly
 625 630 635 640
 Thr Leu Asn Ile Gly Ala Ala His Gly Glu Ala Ala Ala Asp Ala Gly
 645 650 655
 Phe Ile Thr Asn Ala Thr Lys Val Glu Phe Gly Leu Gly Glu Gly Val
 660 665 670
 Phe Val Phe Asn His Thr Asn Asn Ser Asp Ala Gly Tyr Gln Val Asp
 675 680 685
 Met Leu Ile Thr Gly Asp Asp Lys Asp Gly Lys Val Ile His Asp Ala
 690 695 700
 Gly His Thr Val Phe Asn Ala Gly Asn Thr Tyr Ser Gly Lys Thr Leu
 705 710 715 720
 Val Asn Asp Gly Leu Leu Thr Ile Ala Ser His Thr Ala Asp Gly Val
 725 730 735
 Thr Gly Met Gly Ser Ser Glu Val Thr Ile Ala Asn Pro Gly Thr Leu
 740 745 750
 Asp Ile Leu Ala Ser Thr Asn Ser Ala Gly Asp Tyr Thr Leu Thr Asn
 755 760 765
 Ala Leu Lys Gly Asp Gly Leu Met Arg Val Gln Leu Ser Ser Ser Asp
 770 775 780
 Lys Met Phe Gly Phe Thr His Ala Thr Gly Thr Glu Phe Ala Gly Val
 785 790 795 800
 Ala Gln Leu Lys Asp Ser Thr Phe Thr Leu Glu Arg Asp Asn Thr Ala
 805 810 815
 Ala Leu Thr His Ala Met Leu Gln Ser Asp Ser Glu Asn Thr Thr Ser
 820 825 830
 Val Lys Val Gly Glu Gln Ser Ile Gly Gly Leu Ala Met Asn Gly Gly
 835 840 845
 Thr Ile Ile Phe Asp Thr Asp Ile Pro Ala Ala Thr Leu Ala Glu Gly
 850 855 860
 Tyr Ile Ser Val Asp Thr Leu Val Val Gly Ala Gly Asp Tyr Thr Trp
 865 870 875 880
 Lys Gly Arg Asn Tyr Gln Val Asn Gly Thr Gly Asp Val Leu Ile Asp
 885 890 895
 Val Pro Lys Pro Trp Asn Asp Pro Met Ala Asn Asn Pro Leu Thr Thr
 900 905 910
 Leu Asn Leu Leu Glu His Asp Asp Ser His Val Gly Val Gln Leu Val
 915 920 925
 Lys Ala Gln Thr Val Ile Gly Ser Gly Gly Ser Leu Thr Leu Arg Asp
 930 935 940
 Leu Gln Gly Asp Glu Val Glu Ala Asp Lys Thr Leu His Ile Ala Gln
 945 950 955 960
 Asn Gly Thr Val Val Ala Glu Gly Asp Tyr Gly Phe Arg Leu Thr Thr
 965 970 975
 Ala Pro Gly Asn Gly Leu Tyr Val Asn Tyr Gly Leu Lys Ala Leu Asn
 980 985 990
 Ile His Gly Gly Gln Lys Leu Thr Leu Ala Glu His Gly Gly Ala Tyr
 995 1000 1005
 Gly Ala Thr Ala Asp Met Ser Ala Lys Ile Gly Gly Glu Gly Asp Leu
 1010 1015 1020
 Ala Ile Asn Thr Val Arg Gln Val Ser Leu Ser Asn Gly Gln Asn Asp
 1025 1030 1035 1040
 Tyr Gln Gly Ala Thr Tyr Val Gln Met Gly Thr Leu Arg Thr Asp Ala
 1045 1050 1055
 Asp Gly Ala Leu Gly Asn Thr Arg Glu Leu Asn Ile Ser Asn Ala Ala
 1060 1065 1070
 Ile Val Asp Leu Asn Gly Ser Thr Gln Thr Val Glu Thr Phe Thr Gly

1075	1080	1085
Gln Met Gly Ser Thr Val Leu Phe Lys Glu Gly Ala Leu Thr Val Asn		
1090	1095	1100
Lys Gly Gly Ile Ser Gln Gly Glu Leu Thr Gly Gly Asn Leu Asn		
1105	1110	1115
Val Thr Gly Gly Thr Leu Ala Ile Glu Gly Leu Asn Ala Arg Tyr Asn		1120
	1125	1130
Ala Leu Thr Ser Ile Ser Pro Asn Ala Glu Val Ser Leu Asp Asn Thr		1135
	1140	1145
Gln Gly Leu Gly Arg Gly Asn Ile Ala Asn Asp Gly Leu Leu Thr Leu		1150
	1155	1160
Lys Asn Val Thr Gly Glu Leu Arg Asn Ser Ile Ser Gly Lys Gly Ile		1165
	1170	1175
Val Ser Ala Thr Ala Arg Thr Asp Val Glu Leu Asp Gly Asp Asn Ser		1180
1185	1190	1195
Arg Phe Val Gly Gln Phe Asn Ile Asp Thr Gly Ser Ala Leu Ser Val		1200
	1205	1210
Asn Glu Gln Lys Asn Leu Gly Asp Ala Ser Val Ile Asn Asn Gly Leu		1215
	1220	1225
Leu Thr Ile Ser Thr Glu Arg Ser Trp Ala Met Thr His Ser Ile Ser		1230
	1235	1240
Gly Ser Gly Asp Val Thr Lys Leu Gly Thr Gly Ile Leu Thr Leu Asn		1245
	1250	1255
Asn Asp Ser Ala Ala Tyr Gln Gly Thr Thr Asp Ile Val Gly Gly Glu		1260
1265	1270	1275
Ile Ala Phe Gly Ser Asp Ser Ala Ile Asn Met Ala Ser Gln His Ile		1280
	1285	1290
Asn Ile His Asn Ser Gly Val Met Ser Gly Asn Val Thr Thr Ala Gly		1295
	1300	1305
Asp Met Asn Val Met Pro Gly Gly Gly Thr Ala Cys Arg		1310
	1315	1320
		1325

<210> 305

<211> 251

<212> PRT

<213> Escherichia coli

<400> 305

Met Thr Glu Ala Gln Arg His Gln Ile Leu Leu Glu Met Leu Ala Gln		
1	5	10
Leu Gly Phe Val Thr Val Glu Lys Val Val Glu Arg Leu Gly Ile Ser		15
	20	25
Pro Ala Thr Ala Arg Arg Asp Ile Asn Lys Leu Asp Glu Ser Gly Lys		30
	35	40
Leu Lys Lys Val Arg Asn Gly Ala Glu Ala Ile Thr Gln Gln Arg Pro		45
	50	55
Arg Trp Thr Pro Met Asn Leu His Gln Ala Gln Asn His Asp Glu Lys		60
65	70	75
Val Arg Ile Ala Lys Ala Ala Ser Gln Leu Val Asn Pro Gly Glu Ser		80
	85	90
Val Val Ile Asn Cys Gly Ser Thr Ala Phe Leu Leu Gly Arg Glu Met		95
	100	105
Cys Gly Lys Pro Val Gln Ile Ile Thr Asn Tyr Leu Pro Leu Ala Asn		110
	115	120
Tyr Leu Ile Asp Gln Glu His Asp Ser Val Ile Ile Met Gly Gly Gln		125
	130	135
Tyr Asn Lys Ser Gln Ser Ile Thr Leu Ser Pro Gln Gly Ser Glu Asn		140
145	150	155
Ser Leu Tyr Ala Gly His Trp Met Phe Thr Ser Gly Lys Gly Leu Thr		160
	165	170
		175

Ala Glu Gly Leu Tyr Lys Thr Asp Met Leu Thr Ala Met Ala Glu Gln
 180 185 190
 Lys Met Leu Ser Val Val Gly Lys Leu Val Val Leu Val Asp Ser Ser
 195 200 205
 Lys Ile Gly Glu Arg Ala Gly Met Leu Phe Ser Arg Ala Asp Gln Ile
 210 215 220
 Asp Met Leu Ile Thr Gly Lys Asn Ala Asn Pro Glu Ile Leu Gln Gln
 225 230 235 240
 Leu Glu Ala Gln Gly Val Ser Ile Leu Arg Val
 245 250

<210> 306

<211> 274

<212> PRT

<213> Escherichia coli

<400> 306

Met Thr Glu Phe Thr Thr Leu Leu Gln Gln Gly Asn Ala Trp Phe Phe
 1 5 10 15
 Ile Pro Ser Ala Ile Leu Leu Gly Ala Leu His Gly Leu Glu Pro Gly
 20 25 30
 His Ser Lys Thr Met Met Ala Ala Phe Ile Ile Ala Ile Lys Gly Thr
 35 40 45
 Ile Lys Gln Ala Val Met Leu Gly Leu Ala Ala Thr Ile Ser His Thr
 50 55 60
 Ala Val Val Trp Leu Ile Ala Phe Gly Gly Met Val Ile Ser Lys Arg
 65 70 75 80
 Phe Thr Ala Gln Ser Ala Glu Pro Trp Leu Gln Leu Ile Ser Ala Val
 85 90 95
 Ile Ile Ile Ser Thr Ala Phe Trp Met Phe Trp Arg Thr Trp Arg Gly
 100 105 110
 Glu Arg Asn Trp Leu Glu Asn Met His Gly His Asp Tyr Glu His His
 115 120 125
 His His Asp His Glu His His His Asp His Gly His His His His
 130 135 140
 Glu His Gly Glu Tyr Gln Asp Ala His Ala Arg Ala His Ala Asn Asp
 145 150 155 160
 Ile Lys Arg Arg Phe Asp Gly Arg Glu Val Thr Asn Trp Gln Ile Leu
 165 170 175
 Leu Phe Gly Leu Thr Gly Gly Leu Ile Pro Cys Pro Ala Ala Ile Thr
 180 185 190
 Val Leu Leu Ile Cys Ile Gln Leu Lys Ala Leu Thr Leu Gly Ala Thr
 195 200 205
 Leu Val Val Ser Phe Ser Ile Gly Leu Ala Leu Thr Leu Val Thr Val
 210 215 220
 Gly Val Gly Ala Ala Ile Ser Val Gln Gln Val Ala Lys Arg Trp Ser
 225 230 235 240
 Gly Phe Asn Thr Leu Ala Lys Arg Ala Pro Tyr Phe Ser Ser Leu Leu
 245 250 255
 Ile Gly Leu Val Gly Val Tyr Met Gly Val His Gly Phe Met Gly Ile
 260 265 270
 Met Arg

<210> 307

<211> 172

<212> PRT

<213> Escherichia coli

<400> 307

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Met Ile Leu Lys Ser Ala Ile Ser Ala Asp Ser Leu Leu Ala Lys Asp
1      5      10      15
Ala Phe Arg Ala Ser Phe His Leu His Phe Leu Arg Asn His Gly Ile
20      25      30
Thr Asn Lys Ile Ser Leu Val Ser Tyr Ile Val Trp Gln Glu Arg Tyr
35      40      45
Ala Thr Asp Ile Thr Asp Pro Gln Ser Gly Glu Phe Met Thr Ile Lys
50      55      60
Asn Lys Met Leu Leu Gly Ala Leu Leu Leu Val Thr Ser Ala Ala Trp
65      70      75      80
Ala Ala Pro Ala Thr Ala Gly Ser Thr Asn Thr Ser Gly Ile Ser Lys
85      90      95
Tyr Glu Leu Ser Ser Phe Ile Ala Asp Phe Lys His Phe Lys Pro Gly
100     105     110
Asp Thr Val Pro Glu Met Tyr Arg Thr Asp Glu Tyr Asn Ile Lys Gln
115     120     125
Trp Gln Leu Arg Asn Leu Pro Ala Pro Asp Ala Gly Thr His Trp Thr
130     135     140
Tyr Met Gly Gly Ala Tyr Val Leu Ile Ser Asp Thr Asp Gly Lys Ile
145     150     155     160
Ile Lys Ala Tyr Asp Gly Glu Ile Phe Tyr His Arg
165     170

```

<210> 308

<211> 344

<212> PRT

<213> Escherichia coli

<400> 308

```

Met Glu Ile Arg Ile Met Leu Phe Ile Leu Met Met Met Val Met Pro
1      5      10      15
Val Ser Tyr Ala Cys Tyr Ser Glu Leu Ser Val Gln His Asn Leu
20      25      30
Val Val Gln Gly Asp Phe Ala Leu Thr Gln Thr Gln Met Ala Thr Tyr
35      40      45
Glu His Asn Phe Asn Asp Ser Ser Cys Val Ser Thr Asn Thr Ile Thr
50      55      60
Pro Met Ser Pro Ser Asp Ile Ile Val Gly Leu Tyr Asn Asp Thr Ile
65      70      75      80
Lys Leu Asn Leu His Phe Glu Trp Thr Asn Lys Asn Asn Ile Thr Leu
85      90      95
Ser Asn Asn Gln Thr Ser Phe Thr Ser Gly Tyr Ser Val Thr Val Thr
100     105     110
Pro Ala Ala Ser Asn Ala Lys Val Asn Val Ser Ala Gly Gly Gly Gly
115     120     125
Ser Val Met Ile Asn Gly Val Ala Thr Leu Ser Ser Ala Ser Ser Ser
130     135     140
Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly
145     150     155     160
Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln
165     170     175
Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile
180     185     190
Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile
195     200     205
Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser
210     215     220
Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln
225     230     235     240

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```
<210> 309
<211> 826
<212> PRT
<213> Escherichia coli
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Met 1	Leu	Arg	Met	Thr 5	Pro	Leu	Ala	Ser	Ala	Ile	Val	Ala	Leu	Leu	Leu
Gly	Ile	Glu	Ala	Tyr	Ala	Ala	Glu	Glu	Thr	Phe	Asp	Thr	His	Phe	Met
			20					25					30		
Ile	Gly	Gly	Met	Lys	Asp	Gln	Gln	Val	Ala	Asn	Ile	Arg	Leu	Asp	Asp
		35					40					45			
Asn	Gln	Pro	Leu	Pro	Gly	Gln	Tyr	Asp	Ile	Asp	Ile	Tyr	Val	Asn	Lys
	50					55					60				
Gln	Trp	Arg	Gly	Lys	Tyr	Glu	Ile	Ile	Val	Lys	Asp	Asn	Pro	Gln	Glu
65				70						75					80
Thr	Cys	Leu	Ser	Arg	Glu	Val	Ile	Lys	Arg	Leu	Gly	Ile	Asn	Ser	Asp
			85						90					95	
Asn	Phe	Ala	Ser	Gly	Lys	Gln	Cys	Leu	Thr	Phe	Glu	Gln	Leu	Val	Gln
		100						105					110		
Gly	Gly	Ser	Tyr	Thr	Trp	Asp	Ile	Gly	Val	Phe	Arg	Leu	Asp	Phe	Ser
		115					120					125			
Val	Pro	Gln	Ala	Trp	Val	Glu	Glu	Leu	Glu	Ser	Gly	Tyr	Val	Pro	Pro
		130				135					140				
Glu	Asn	Trp	Glu	Arg	Gly	Ile	Asn	Ala	Phe	Tyr	Thr	Ser	Tyr	Tyr	Leu
145				150						155					160
Ser	Gln	Tyr	Tyr	Ser	Asp	Tyr	Lys	Ala	Ser	Gly	Asn	Asn	Lys	Ser	Thr
			165						170					175	
Tyr	Val	Arg	Phe	Asn	Ser	Gly	Leu	Asn	Leu	Leu	Gly	Trp	Gln	Leu	His
			180					185					190		
Ser	Asp	Ala	Ser	Phe	Ser	Lys	Thr	Asn	Asn	Asn	Pro	Gly	Val	Trp	Lys
		195					200					205			
Ser	Asn	Thr	Leu	Tyr	Leu	Glu	Arg	Gly	Phe	Ala	Gln	Leu	Leu	Gly	Thr
		210				215					220				
Leu	Arg	Val	Gly	Asp	Met	Tyr	Thr	Ser	Ser	Asp	Ile	Phe	Asp	Ser	Val
225				230						235					240
Arg	Phe	Arg	Gly	Val	Arg	Leu	Phe	Arg	Asp	Met	Gln	Met	Leu	Pro	Asn
			245						250					255	
Ser	Lys	Gln	Asn	Phe	Thr	Pro	Arg	Val	Gln	Gly	Ile	Ala	Gln	Ser	Asn
			260					265					270		
Ala	Leu	Val	Thr	Ile	Glu	Gln	Asn	Gly	Phe	Val	Val	Tyr	Gln	Lys	Glu
		275					280					285			
Val	Pro	Pro	Gly	Pro	Phe	Ala	Ile	Thr	Asp	Leu	Gln	Leu	Ala	Gly	Gly
	290					295					300				
Gly	Ala	Asp	Leu	Asp	Val	Ser	Val	Lys	Glu	Ala	Asp	Gly	Ser	Val	Thr

305					310					315				320
Thr	Tyr	Leu	Val	Pro	Tyr	Ala	Ala	Val	Pro	Asn	Met	Leu	Gln	Pro
				325					330					335
Val	Ser	Lys	Tyr	Asp	Leu	Ala	Ala	Gly	Arg	Ser	His	Ile	Glu	Gly
			340					345					350	Ala
Ser	Lys	Gln	Ser	Asp	Phe	Val	Gln	Ala	Gly	Tyr	Gln	Tyr	Gly	Phe
		355					360					365		Asn
Asn	Leu	Leu	Thr	Leu	Tyr	Gly	Gly	Ser	Met	Val	Ala	Asn	Asn	Tyr
	370					375					380			Tyr
Ala	Phe	Thr	Leu	Gly	Ala	Gly	Trp	Asn	Thr	Arg	Ile	Gly	Ala	Ile
385					390					395				Ser
Val	Asp	Ala	Thr	Lys	Ser	His	Ser	Lys	Gln	Asp	Asn	Gly	Asp	Val
			405						410					Phe
Asp	Gly	Gln	Ser	Tyr	Gln	Ile	Ala	Tyr	Asn	Lys	Phe	Val	Ser	Gln
			420					425					430	Thr
Ser	Thr	Arg	Phe	Gly	Leu	Ala	Ala	Trp	Arg	Tyr	Ser	Ser	Arg	Asp
	435					440						445		Tyr
Arg	Thr	Phe	Asn	Asp	His	Val	Trp	Ala	Asn	Asn	Lys	Asp	Asn	Tyr
	450					455						460		Arg
Arg	Asp	Glu	Asn	Asp	Val	Tyr	Asp	Ile	Ala	Asp	Tyr	Tyr	Gln	Asn
465					470					475				Asp
Phe	Gly	Arg	Lys	Asn	Ser	Phe	Ser	Ala	Asn	Met	Ser	Gln	Ser	Leu
			485						490					Pro
Glu	Gly	Trp	Gly	Ser	Val	Ser	Leu	Ser	Thr	Leu	Trp	Arg	Asp	Tyr
			500					505					510	Trp
Gly	Arg	Ser	Gly	Ser	Ser	Lys	Asp	Tyr	Gln	Leu	Ser	Tyr	Ser	Asn
		515				520						525		Asn
Leu	Arg	Arg	Ile	Ser	Tyr	Thr	Leu	Ala	Ala	Ser	Gln	Ala	Tyr	Asp
	530					535					540			Glu
Asn	His	His	Glu	Glu	Lys	Arg	Phe	Asn	Ile	Phe	Ile	Ser	Ile	Pro
545					550					555				Phe
Asp	Trp	Gly	Asp	Asp	Val	Ser	Thr	Pro	Arg	Arg	Gln	Ile	Tyr	Met
			565						570					Ser
Asn	Ser	Thr	Thr	Phe	Asp	Asp	Gln	Gly	Phe	Ala	Ser	Asn	Asn	Thr
		580						585				590		Gly
Leu	Ser	Gly	Thr	Val	Gly	Ser	Arg	Asp	Gln	Phe	Asn	Tyr	Gly	Val
	595						600					605		Asn
Leu	Ser	His	Gln	His	Gln	Gly	Asn	Glu	Thr	Thr	Ala	Gly	Ala	Asn
	610					615					620			Leu
Thr	Trp	Asn	Ala	Pro	Val	Ala	Thr	Val	Asn	Gly	Ser	Tyr	Ser	Gln
625					630					635				Ser
Ser	Thr	Tyr	Arg	Gln	Ala	Gly	Ala	Ser	Val	Ser	Gly	Gly	Ile	Val
			645						650					Ala
Trp	Ser	Gly	Gly	Val	Asn	Leu	Ala	Asn	Arg	Leu	Ser	Glu	Thr	Phe
		660						665				670		Ala
Val	Met	Asn	Ala	Pro	Gly	Ile	Lys	Asp	Ala	Tyr	Val	Asn	Gly	Gln
	675						680					685		Lys
Tyr	Arg	Thr	Thr	Asn	Arg	Asn	Gly	Val	Val	Ile	Tyr	Asp	Gly	Met
	690					695					700			Thr
Pro	Tyr	Arg	Glu	Asn	His	Leu	Met	Leu	Asp	Val	Ser	Gln	Ser	Asp
705					710					715				Ser
Glu	Ala	Glu	Leu	Arg	Gly	Asn	Arg	Lys	Ile	Ala	Ala	Pro	Tyr	Arg
			725						730					Gly
Ala	Val	Val	Leu	Val	Asn	Phe	Asp	Thr	Asp	Gln	Arg	Lys	Pro	Trp
			740					745					750	Phe
Ile	Lys	Ala	Leu	Arg	Ala	Asp	Gly	Gln	Ser	Leu	Thr	Phe	Gly	Tyr
	755					760						765		Glu
Val	Asn	Asp	Ile	His	Gly	His	Asn	Ile	Gly	Val	Val	Gly	Gln	Gly
	770					775						780		Ser
Gln	Leu	Phe	Ile	Arg	Thr	Asn	Glu	Val	Pro	Pro	Ser	Val	Asn	Val
785					790					795				Ala
														800

Ile Asp Lys Gln Gln Gly Leu Ser Cys Thr Ile Thr Phe Gly Lys Glu
 805 810 815
 Ile Asp Glu Ser Arg Asn Tyr Ile Cys Gln
 820 825

<210> 310
 <211> 239
 <212> PRT
 <213> Escherichia coli

<400> 310
 Met Ala Ala Ile Pro Trp Arg Pro Phe Asn Leu Arg Gly Ile Lys Met
 1 5 10 15
 Lys Gly Leu Leu Ser Leu Leu Ile Phe Ser Met Val Leu Pro Ala His
 20 25 30
 Ala Gly Ile Val Ile Tyr Gly Thr Arg Ile Ile Tyr Pro Ala Glu Asn
 35 40 45
 Lys Glu Val Met Val Gln Leu Met Asn Gln Gly Asn Arg Ser Ser Leu
 50 55 60
 Leu Gln Ala Trp Ile Asp Asp Gly Asp Thr Ser Leu Pro Pro Glu Lys
 65 70 75 80
 Ile Gln Val Pro Phe Met Leu Thr Pro Pro Val Ala Lys Ile Gly Ala
 85 90 95
 Asn Ser Gly Gln Gln Val Lys Ile Lys Ile Met Pro Asn Lys Leu Pro
 100 105 110
 Thr Asn Lys Glu Ser Ile Phe Tyr Leu Asn Val Leu Asp Ile Pro Pro
 115 120 125
 Asn Ser Pro Glu Gln Glu Gly Lys Asn Ala Leu Lys Phe Ala Met Gln
 130 135 140
 Asn Arg Ile Lys Leu Phe Tyr Arg Pro Ala Gly Ile Ala Pro Val Asn
 145 150 155 160
 Lys Ala Thr Phe Lys Lys Leu Leu Val Asn Arg Ser Gly Asn Gly Leu
 165 170 175
 Val Ile Lys Asn Asp Ser Ala Asn Trp Val Thr Ile Ser Asp Val Lys
 180 185 190
 Ala Asn Asn Val Lys Val Asn Tyr Glu Thr Ile Met Ile Ala Pro Leu
 195 200 205
 Glu Ser Gln Ser Val Asn Val Lys Ser Asn Asn Ala Asn Asn Trp His
 210 215 220
 Leu Thr Ile Ile Asp Asp His Gly Asn Tyr Ile Ser Asp Lys Ile
 225 230 235

<210> 311
 <211> 180
 <212> PRT
 <213> Escherichia coli

<400> 311
 Met Lys Arg Ser Ile Ile Ala Ala Ala Val Phe Ser Ser Phe Phe Met
 1 5 10 15
 Ser Ala Gly Val Phe Ala Ala Asp Val Asp Thr Gly Thr Leu Thr Ile
 20 25 30
 Lys Gly Asn Ile Ala Glu Ser Pro Cys Lys Phe Glu Ala Gly Gly Asp
 35 40 45
 Ser Val Ser Ile Asn Met Pro Thr Val Pro Thr Ser Val Phe Glu Gly
 50 55 60
 Lys Ala Lys Tyr Ser Thr Tyr Asp Asp Ala Val Gly Val Thr Ser Ser
 65 70 75 80
 Met Leu Lys Ile Ser Cys Pro Lys Glu Val Ala Gly Val Lys Leu Ser

```

      85      90      95
Leu Ile Thr Asn Asp Lys Ile Thr Gly Asn Asp Lys Ala Ile Ala Ser
      100      105      110
Ser Asn Asp Thr Val Gly Tyr Tyr Leu Tyr Leu Gly Asp Asn Ser Asp
      115      120      125
Val Leu Asp Val Ser Ala Pro Phe Asn Ile Glu Ser Tyr Lys Thr Ala
      130      135      140
Glu Gly Gln Tyr Ala Ile Pro Phe Lys Ala Lys Tyr Leu Lys Leu Thr
      145      150      155      160
Asp Asn Ser Val Gln Ser Gly Asp Val Leu Ser Ser Leu Val Met Arg
      165      170      175
Val Ala Gln Asp
      180

```

<210> 312
 <211> 95
 <212> PRT
 <213> Escherichia coli

```

<400> 312
Met Leu His Thr Leu His Arg Ser Pro Trp Leu Thr Asp Phe Ala Ala
  1      5      10      15
Leu Leu Arg Leu Leu Ser Glu Gly Asp Glu Leu Leu Leu Leu Gln Asp
      20      25      30
Gly Val Thr Ala Ala Val Asp Gly Asn Arg Tyr Leu Glu Ser Leu Arg
      35      40      45
Asn Ala Pro Ile Lys Val Tyr Ala Leu Asn Glu Asp Leu Ile Ala Arg
      50      55      60
Gly Leu Thr Gly Gln Ile Ser Asn Asp Ile Ile Leu Ile Asp Tyr Thr
      65      70      75      80
Asp Phe Val Arg Leu Thr Val Lys His Pro Ser Gln Met Ala Trp
      85      90      95

```

<210> 313
 <211> 119
 <212> PRT
 <213> Escherichia coli

```

<400> 313
Met Lys Arg Ile Ala Phe Val Phe Ser Thr Ala Pro His Gly Thr Ala
  1      5      10      15
Ala Gly Arg Glu Gly Leu Asp Ala Leu Leu Ala Thr Ser Ala Leu Thr
      20      25      30
Asp Asp Leu Ala Val Phe Phe Ile Ala Asp Gly Val Phe Gln Leu Leu
      35      40      45
Pro Gly Gln Lys Pro Asp Ala Val Leu Ala Arg Asp Tyr Ile Ala Thr
      50      55      60
Phe Lys Leu Leu Gly Leu Tyr Asp Ile Glu Gln Cys Trp Val Cys Ala
      65      70      75      80
Ala Ser Leu Arg Glu Arg Gly Leu Asp Pro Gln Thr Pro Phe Val Val
      85      90      95
Glu Ala Thr Pro Leu Glu Ala Asp Ala Leu Arg Arg Glu Leu Ala Asn
      100      105      110
Tyr Asp Val Ile Leu Arg Phe
      115

```

<210> 314
 <211> 128

<212> PRT

<213> Escherichia coli

<400> 314

```

Met Arg Phe Ala Ile Val Val Thr Gly Pro Ala Tyr Gly Thr Gln Gln
 1           5           10           15
Ala Ser Ser Ala Phe Gln Phe Ala Gln Ala Leu Ile Ala Asp Gly His
      20           25           30
Glu Leu Ser Ser Val Phe Phe Tyr Arg Glu Gly Val Tyr Asn Ala Asn
      35           40           45
Gln Leu Thr Ser Pro Ala Ser Asp Glu Phe Asp Leu Val Arg Ala Trp
      50           55           60
Gln Gln Leu Asn Ala Gln His Gly Val Ala Leu Asn Ile Cys Val Ala
65           70           75           80
Ala Ala Leu Arg Arg Gly Val Val Asp Glu Thr Glu Ala Gly Arg Leu
      85           90           95
Gly Leu Ala Ser Ser Asn Leu Gln Gln Gly Phe Thr Leu Ser Gly Leu
      100          105          110
Gly Ala Leu Ala Glu Ala Ser Leu Thr Cys Asp Arg Val Val Gln Phe
      115          120          125

```

<210> 315

<211> 244

<212> PRT

<213> Escherichia coli

<400> 315

```

Met Phe Phe Phe Met Ser Arg Ser Leu Leu Thr Asn Glu Thr Ser Glu
 1           5           10           15
Leu Asp Leu Leu Asp Gln Arg Pro Phe Asp Gln Thr Asp Phe Asp Ile
      20           25           30
Leu Lys Ser Tyr Glu Ala Val Val Asp Gly Leu Ala Met Leu Ile Gly
      35           40           45
Ser His Cys Glu Ile Val Leu His Ser Leu Gln Asp Leu Lys Cys Ser
      50           55           60
Ala Ile Arg Ile Ala Asn Gly Glu His Thr Gly Arg Lys Ile Gly Ser
65           70           75           80
Pro Ile Thr Asp Leu Ala Leu Arg Met Leu His Asp Met Thr Gly Ala
      85           90           95
Asp Ser Ser Val Ser Lys Cys Tyr Phe Thr Arg Ala Lys Ser Gly Val
      100          105          110
Leu Met Lys Ser Leu Thr Ile Ala Ile Arg Asn Arg Glu Gln Arg Val
      115          120          125
Ile Gly Leu Leu Cys Ile Asn Met Asn Leu Asp Val Pro Phe Ser Gln
      130          135          140
Ile Met Ser Thr Phe Val Pro Pro Glu Thr Pro Asp Val Gly Ser Ser
145          150          155          160
Val Asn Phe Ala Ser Ser Val Glu Asp Leu Val Thr Gln Thr Leu Glu
      165          170          175
Phe Thr Ile Glu Glu Val Asn Ala Asp Arg Asn Val Ser Asn Asn Ala
      180          185          190
Lys Asn Arg Gln Ile Val Leu Asn Leu Tyr Glu Lys Gly Ile Phe Asp
      195          200          205
Ile Lys Asp Ala Ile Asn Gln Val Ala Asp Arg Leu Asn Ile Ser Lys
      210          215          220
His Thr Val Tyr Leu Tyr Ile Arg Gln Phe Lys Ser Gly Asp Phe Gln
225          230          235          240
Gly Gln Asp Lys

```

<210> 316
 <211> 84
 <212> PRT
 <213> Escherichia coli

<400> 316
 Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys
 1 5 10 15
 Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro
 20 25 30
 Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp
 35 40 45
 Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys
 50 55 60
 Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu
 65 70 75 80
 Lys Ala Val Leu

<210> 317
 <211> 63
 <212> PRT
 <213> Escherichia coli

<400> 317
 Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
 1 5 10 15
 Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
 20 25 30
 Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
 35 40 45
 Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala
 50 55 60

<210> 318
 <211> 136
 <212> PRT
 <213> Escherichia coli

<400> 318
 Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
 1 5 10 15
 Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
 20 25 30
 Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala
 35 40 45
 Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
 50 55 60
 Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val
 65 70 75 80
 Arg Met Gly Lys Gly Lys Gly Asn Val Glu Tyr Trp Val Ala Leu Ile
 85 90 95
 Gln Pro Gly Lys Val Leu Tyr Glu Met Asp Gly Val Pro Glu Glu Leu
 100 105 110
 Ala Arg Glu Ala Phe Lys Leu Ala Ala Lys Leu Pro Ile Lys Thr
 115 120 125
 Thr Phe Val Thr Lys Thr Val Met
 130 135

<210> 319
 <211> 233
 <212> PRT
 <213> Escherichia coli

<400> 319
 Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
 1 5 10 15
 Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
 20 25 30
 Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
 35 40 45
 Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
 50 55 60
 Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
 65 70 75 80
 Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly
 85 90 95
 Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp
 100 105 110
 Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
 115 120 125
 Met Phe Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
 130 135 140
 Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
 145 150 155 160
 Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
 165 170 175
 Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
 180 185 190
 Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
 195 200 205
 Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
 210 215 220
 Lys Lys Gln Gln Arg Lys Gly Arg Lys
 225 230

<210> 320
 <211> 110
 <212> PRT
 <213> Escherichia coli

<400> 320
 Met Glu Thr Ile Ala Lys His Arg His Ala Arg Ser Ser Ala Gln Lys
 1 5 10 15
 Val Arg Leu Val Ala Asp Leu Ile Arg Gly Lys Lys Val Ser Gln Ala
 20 25 30
 Leu Asp Ile Leu Thr Tyr Thr Asn Lys Lys Ala Ala Val Leu Val Lys
 35 40 45
 Lys Val Leu Glu Ser Ala Ile Ala Asn Ala Glu His Asn Asp Gly Ala
 50 55 60
 Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro
 65 70 75 80
 Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile
 85 90 95
 Leu Lys Arg Thr Ser His Ile Thr Val Val Val Ser Asp Arg
 100 105 110

<210> 321
 <211> 92
 <212> PRT
 <213> Escherichia coli

<400> 321
 Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu
 1 5 10 15
 Lys Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg
 20 25 30
 Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr
 35 40 45
 Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp
 50 55 60
 Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr
 65 70 75 80
 Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys Lys
 85 90

<210> 322
 <211> 273
 <212> PRT
 <213> Escherichia coli

<400> 322
 Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val
 1 5 10 15
 Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro
 20 25 30
 Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg
 35 40 45
 Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile
 50 55 60
 Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg
 65 70 75 80
 Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr
 85 90 95
 Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala
 100 105 110
 Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn
 115 120 125
 Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val
 130 135 140
 Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr
 145 150 155 160
 Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu
 165 170 175
 Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu
 180 185 190
 Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala
 195 200 205
 Gly Ala Ala Arg Trp Arg Gly Val Arg Pro Thr Val Arg Gly Thr Ala
 210 215 220
 Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Arg Asn Phe
 225 230 235 240
 Gly Lys His Pro Val Thr Pro Trp Gly Val Gln Thr Lys Gly Lys Lys
 245 250 255
 Thr Arg Ser Asn Lys Arg Thr Asp Lys Phe Ile Val Arg Arg Arg Ser
 260 265 270

Lys

<210> 323
 <211> 100
 <212> PRT
 <213> Escherichia coli

<400> 323
 Met Ile Arg Glu Glu Arg Leu Leu Lys Val Leu Arg Ala Pro His Val
 1 5 10 15
 Ser Glu Lys Ala Ser Thr Ala Met Glu Lys Ser Asn Thr Ile Val Leu
 20 25 30
 Lys Val Ala Lys Asp Ala Thr Lys Ala Glu Ile Lys Ala Ala Val Gln
 35 40 45
 Lys Leu Phe Glu Val Glu Val Glu Val Val Asn Thr Leu Val Val Lys
 50 55 60
 Gly Lys Val Lys Arg His Gly Gln Arg Ile Gly Arg Arg Ser Asp Trp
 65 70 75 80
 Lys Lys Ala Tyr Val Thr Leu Lys Glu Gly Gln Asn Leu Asp Phe Val
 85 90 95
 Gly Gly Ala Glu
 100

<210> 324
 <211> 201
 <212> PRT
 <213> Escherichia coli

<400> 324
 Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu
 1 5 10 15
 Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val
 20 25 30
 Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr
 35 40 45
 Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly
 50 55 60
 Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser
 65 70 75 80
 Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val
 85 90 95
 Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu
 100 105 110
 Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala
 115 120 125
 Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu
 130 135 140
 Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala
 145 150 155 160
 Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp
 165 170 175
 Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
 180 185 190
 Val Lys Gln Val Glu Glu Met Leu Ala
 195 200

<210> 325

<211> 209
 <212> PRT
 <213> Escherichia coli

<400> 325

```

Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr
 1           5           10           15
Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
           20           25           30
Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
           35           40           45
Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
           50           55           60
Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp
65           70           75           80
Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile
           85           90           95
Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr
           100          105          110
Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg
           115          120          125
Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly
           130          135          140
Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys
145          150          155          160
Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp
           165          170          175
Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala
           180          185          190
Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys
           195          200          205
Ala

```

<210> 326
 <211> 103
 <212> PRT
 <213> Escherichia coli

<400> 326

```

Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg
 1           5           10           15
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr
           20           25           30
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg
           35           40           45
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
           50           55           60
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
65           70           75           80
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
           85           90           95
Asp Val Gln Ile Ser Leu Gly
           100

```

<210> 327
 <211> 104
 <212> PRT
 <213> Escherichia coli

<400> 327

```

Met Ile Arg Lys Ala Phe Val Met Gln Val Asn Pro Asp Ala His Glu
 1           5           10           15
Glu Tyr Gln Arg Arg His Asn Pro Ile Trp Pro Glu Leu Glu Ala Val
          20           25           30
Leu Lys Ser His Gly Ala His Asn Tyr Ala Ile Tyr Leu Asp Lys Ala
          35           40           45
Arg Asn Leu Leu Phe Ala Met Val Glu Ile Glu Ser Glu Glu Arg Trp
          50           55           60
Asn Ala Val Ala Ser Thr Asp Val Cys Gln Arg Trp Trp Lys Tyr Met
65           70           75           80
Thr Asp Val Met Pro Ala Asn Pro Asp Asn Ser Pro Val Ser Ser Glu
          85           90           95
Leu Gln Glu Val Phe Tyr Leu Pro
          100

```

<210> 328

<211> 287

<212> PRT

<213> Escherichia coli

<400> 328

```

Met Ile Arg Ser Met Thr Ala Tyr Ala Arg Arg Glu Ile Lys Gly Glu
 1           5           10           15
Trp Gly Ser Ala Thr Trp Glu Met Arg Ser Val Asn Gln Arg Tyr Leu
          20           25           30
Glu Thr Tyr Phe Arg Leu Pro Glu Gln Phe Arg Ser Leu Glu Pro Val
          35           40           45
Val Arg Glu Arg Ile Arg Ser Arg Leu Thr Arg Gly Lys Val Glu Cys
          50           55           60
Thr Leu Arg Tyr Glu Pro Asp Val Ser Ala Gln Gly Glu Leu Ile Leu
65           70           75           80
Asn Glu Lys Leu Ala Lys Gln Leu Val Thr Ala Ala Asn Trp Val Lys
          85           90           95
Met Gln Ser Asp Glu Gly Glu Ile Asn Pro Val Asp Ile Leu Arg Trp
          100           105           110
Pro Gly Val Met Ala Ala Gln Glu Gln Asp Leu Asp Ala Ile Ala Ala
          115           120           125
Glu Ile Leu Ala Ala Leu Asp Gly Thr Leu Asp Asp Phe Ile Val Ala
          130           135           140
Arg Glu Thr Glu Gly Gln Ala Leu Lys Ala Leu Ile Glu Gln Arg Leu
145           150           155           160
Glu Gly Val Thr Ala Glu Val Val Lys Val Arg Ser His Met Pro Glu
          165           170           175
Ile Leu Gln Trp Gln Arg Glu Arg Leu Val Ala Lys Leu Glu Asp Ala
          180           185           190
Gln Val Gln Leu Glu Asn Asn Arg Leu Glu Gln Glu Leu Val Leu Leu
          195           200           205
Ala Gln Arg Ile Asp Val Ala Glu Glu Leu Asp Arg Leu Glu Ala His
          210           215           220
Val Lys Glu Thr Tyr Asn Ile Leu Lys Lys Lys Glu Ala Val Gly Arg
225           230           235           240
Arg Leu Asp Phe Met Met Gln Glu Phe Asn Arg Glu Ser Asn Thr Leu
          245           250           255
Ala Ser Lys Ser Ile Asn Ala Glu Val Thr Asn Ser Ala Ile Glu Leu
          260           265           270
Lys Val Leu Ile Glu Gln Met Arg Glu Gln Ile Gln Asn Ile Glu
          275           280           285

```

<210> 329
 <211> 163
 <212> PRT
 <213> Escherichia coli

<400> 329

```

Met Ser Thr Glu Thr Ile Glu Ile Phe Asn Asn Ser Asp Glu Trp Ala
 1           5           10           15
Asn Gln Leu Lys His Ala Leu Ser Lys Gly Glu Asn Leu Ala Leu Leu
      20           25           30
His Gly Leu Thr Pro Asp Ile Leu Asp Arg Ile Tyr Ala Tyr Ala Phe
      35           40           45
Asp Tyr His Glu Lys Gly Asn Ile Thr Asp Ala Glu Ile Tyr Tyr Lys
      50           55           60
Phe Leu Cys Ile Tyr Ala Phe Glu Asn His Glu Tyr Leu Lys Asp Phe
      65           70           75           80
Ala Ser Val Cys Gln Pro Lys Lys Lys Tyr Gln Gln Ala Tyr Asp Leu
      85           90           95
Tyr Lys Leu Ser Tyr Asn Tyr Phe Pro Tyr Asp Asp Tyr Ser Val Ile
      100          105          110
Tyr Arg Met Gly Gln Cys Gln Ile Gly Ala Lys Asn Ile Asp Asn Ala
      115          120          125
Met Gln Cys Phe Tyr His Ile Ile Asn Asn Cys Glu Asp Asp Ser Val
      130          135          140
Lys Ser Lys Ala Gln Ala Tyr Ile Glu Leu Leu Asn Asp Asn Ser Glu
      145          150          155          160
Asp Asn Gly
  
```

<210> 330
 <211> 648
 <212> PRT
 <213> Escherichia coli

<400> 330

```

Met Asn Ile Leu Gly Phe Phe Gln Arg Leu Gly Arg Ala Leu Gln Leu
 1           5           10           15
Pro Ile Ala Val Leu Pro Val Ala Ala Leu Leu Leu Arg Phe Gly Gln
      20           25           30
Pro Asp Leu Leu Asn Val Ala Phe Ile Ala Gln Ala Gly Gly Ala Ile
      35           40           45
Phe Asp Asn Leu Ala Leu Ile Phe Ala Ile Gly Val Ala Ser Ser Trp
      50           55           60
Ser Lys Asp Ser Ala Gly Ala Ala Ala Leu Ala Gly Ala Val Gly Tyr
      65           70           75           80
Phe Val Leu Thr Lys Ala Met Val Thr Ile Asn Pro Glu Ile Asn Met
      85           90           95
Gly Val Leu Ala Gly Ile Ile Thr Gly Leu Val Gly Gly Ala Ala Tyr
      100          105          110
Asn Arg Trp Ser Asp Ile Lys Leu Pro Asp Phe Leu Ser Phe Phe Gly
      115          120          125
Gly Lys Arg Phe Val Pro Ile Ala Thr Gly Phe Phe Cys Leu Val Leu
      130          135          140
Ala Ala Ile Phe Gly Tyr Val Trp Pro Pro Val Gln His Ala Ile His
      145          150          155          160
Ala Gly Gly Glu Trp Ile Val Ser Ala Gly Ala Leu Gly Ser Gly Ile
      165          170          175
Phe Gly Phe Ile Asn Arg Leu Leu Ile Pro Thr Gly Leu His Gln Val
      180          185          190
  
```

Leu Asn Thr Ile Ala Trp Phe Gln Ile Gly Glu Phe Thr Asn Ala Ala
 195 200 205
 Gly Thr Val Phe His Gly Asp Ile Asn Arg Phe Tyr Ala Gly Asp Gly
 210 215 220
 Thr Ala Gly Met Phe Met Ser Gly Phe Phe Pro Ile Met Met Phe Gly
 225 230 235 240
 Leu Pro Gly Ala Ala Leu Ala Met Tyr Phe Ala Ala Pro Lys Glu Arg
 245 250 255
 Arg Pro Met Val Gly Gly Met Leu Leu Ser Val Ala Val Thr Ala Phe
 260 265 270
 Leu Thr Gly Val Thr Glu Pro Leu Glu Phe Leu Phe Met Phe Leu Ala
 275 280 285
 Pro Leu Leu Tyr Leu Leu His Ala Leu Leu Thr Gly Ile Ser Leu Phe
 290 295 300
 Val Ala Thr Leu Leu Gly Ile His Ala Gly Phe Ser Phe Ser Ala Gly
 305 310 315 320
 Ala Ile Asp Tyr Ala Leu Met Tyr Asn Leu Pro Ala Ala Ser Gln Asn
 325 330 335
 Val Trp Met Leu Leu Val Met Gly Val Ile Phe Phe Ala Ile Tyr Phe
 340 345 350
 Val Val Phe Ser Leu Val Ile Arg Met Phe Asn Leu Lys Thr Pro Gly
 355 360 365
 Arg Glu Asp Lys Glu Asp Glu Ile Val Thr Glu Glu Ala Asn Ser Asn
 370 375 380
 Thr Glu Glu Gly Leu Thr Gln Leu Ala Thr Asn Tyr Ile Ala Ala Val
 385 390 395 400
 Gly Gly Thr Asp Asn Leu Lys Ala Ile Asp Ala Cys Ile Thr Arg Leu
 405 410 415
 Arg Leu Thr Val Ala Asp Ser Ala Arg Val Asn Asp Thr Met Cys Lys
 420 425 430
 Arg Leu Gly Ala Ser Gly Val Val Lys Leu Asn Lys Gln Thr Ile Gln
 435 440 445
 Val Ile Val Gly Ala Lys Ala Glu Ser Ile Gly Asp Ala Met Lys Lys
 450 455 460
 Val Val Ala Arg Gly Pro Val Ala Ala Ala Ser Ala Glu Ala Thr Pro
 465 470 475 480
 Ala Thr Ala Ala Pro Val Ala Lys Pro Gln Ala Val Pro Asn Ala Val
 485 490 495
 Ser Ile Ala Glu Leu Val Ser Pro Ile Thr Gly Asp Val Val Ala Leu
 500 505 510
 Asp Gln Val Pro Asp Glu Ala Phe Ala Ser Lys Ala Val Gly Asp Gly
 515 520 525
 Val Ala Val Lys Pro Thr Asp Lys Ile Val Val Ser Pro Ala Ala Gly
 530 535 540
 Thr Ile Val Lys Ile Phe Asn Thr Asn His Ala Phe Cys Leu Glu Thr
 545 550 555 560
 Glu Lys Gly Ala Glu Ile Val Val His Met Gly Ile Asp Thr Val Ala
 565 570 575
 Leu Glu Gly Lys Gly Phe Lys Arg Leu Val Glu Glu Gly Ala Gln Val
 580 585 590
 Ser Ala Gly Gln Pro Ile Leu Glu Met Asp Leu Asp Tyr Leu Asn Ala
 595 600 605
 Asn Ala Arg Ser Met Ile Ser Pro Val Val Cys Ser Asn Ile Asp Asp
 610 615 620
 Phe Ser Gly Leu Ile Ile Lys Ala Gln Gly His Ile Val Ala Gly Gln
 625 630 635 640
 Thr Pro Leu Tyr Glu Ile Lys Lys
 645

<210> 331

<211> 412

<212> PRT

<213> Escherichia coli

<400> 331

```

Met Lys Thr Ile Phe Arg Tyr Ile Leu Phe Leu Ala Leu Tyr Ser Cys
 1           5           10           15
Cys Asn Thr Val Ser Ala Tyr Thr Ser Phe Ile Val Gly Asn Asn Ala
 20           25           30
Gly Val Asp Asn Tyr Arg Gly Pro Ser Thr Ala Ala Gln Met Thr Phe
 35           40           45
Asn Tyr Thr Ser Thr Ala Ser Asn Leu Val Phe Tyr Lys Pro Thr Gln
 50           55           60
Leu Gly Pro Thr Gly Val Lys Met Tyr Trp Ser Tyr Leu Asp Thr Gly
 65           70           75           80
Thr Gly Gly Gly Ile Leu Tyr Cys Asn Thr Ser Gly Arg Ala Asn Pro
 85           90           95
Gly Pro Ile Thr Ile Glu Asn Ala Met Val Tyr Ser Gly Lys Asp Tyr
 100          105          110
Gly Gly His Lys Leu Phe Asn Thr Ser Val Pro Gly Leu Tyr Tyr Thr
 115          120          125
Met Leu Ile Ser Arg Val Trp Ser Ala Tyr Asp Thr Ile Thr Asp Ile
 130          135          140
Gln Ser Pro Gly Ile Tyr Ile Gly Asp Pro Ser Asn Gln Glu Phe Phe
 145          150          155          160
Phe Ser Val Thr Asp Ser Asp Leu Gln Thr Lys Gly Cys Asn Lys Ala
 165          170          175
Asp Asp Tyr Asp Lys Phe Trp Ala Ile Gly Gly Ile Val His Asn Ile
 180          185          190
Thr Val Glu Phe Tyr Thr Asp Thr Asn Phe Asp Pro Thr Leu Asn Gln
 195          200          205
Gln Val Gln Leu Ser Ser Ser Ser Asn Tyr Leu Tyr Ser Phe Lys Ala
 210          215          220
Tyr Ser Pro Gly Thr Lys Val Val Asp His Ser Asn His Ile Tyr Val
 225          230          235          240
Asn Phe Thr Leu Asn Asn Val Lys Leu Thr Leu Pro Thr Cys Phe Thr
 245          250          255
Ser Ile Leu Thr Gly Pro Ser Val Asn Gly Ser Thr Val Arg Met Gly
 260          265          270
Glu Tyr Ser Ser Gly Thr Ile Lys Asn Gly Ala Ser Pro Val Pro Phe
 275          280          285
Asp Ile Ser Leu Gln Asn Cys Ile Arg Val Arg Asn Ile Glu Thr Lys
 290          295          300
Leu Val Thr Gly Lys Val Gly Thr Gln Asn Thr Gln Leu Leu Gly Asn
 305          310          315          320
Thr Leu Thr Gly Ser Thr Ala Ala Lys Gly Val Gly Val Leu Ile Glu
 325          330          335
Gly Leu Ala Thr Ser Lys Asn Pro Leu Met Thr Leu Lys Pro Asn Asp
 340          345          350
Thr Asn Ser Val Tyr Ile Asp Tyr Glu Thr Glu Asp Asp Thr Ser Asp
 355          360          365
Gly Val Tyr Pro Asn Gln Gly Asn Gly Thr Ser Gln Pro Leu His Phe
 370          375          380
Gln Ala Thr Leu Lys Gln Asp Gly Asn Ile Ala Ile Glu Pro Gly Glu
 385          390          395          400
Phe Lys Ala Thr Ser Thr Phe Gln Val Thr Tyr Pro
 405          410

```

<210> 332

<211> 198

<212> PRT

<213> Escherichia coli

<400> 332

```

Met His Pro Thr Gln Arg Lys Leu Met Lys Arg Ile Ile Leu Phe Leu
 1          5          10          15
Ser Leu Leu Phe Cys Ile Ala Cys Pro Ala Ile Ala Gly Gln Asp Ile
      20          25          30
Asp Leu Val Ala Asn Val Lys Asn Ser Thr Cys Lys Ser Gly Ile Ser
      35          40          45
Asn Gln Gly Asn Ile Asp Leu Gly Val Val Gly Val Gly Tyr Phe Ser
      50          55          60
Gly Asn Val Thr Pro Glu Ser Tyr Gln Pro Gly Gly Lys Glu Phe Thr
      65          70          75          80
Ile Thr Val Ser Asp Cys Ala Leu Gln Gly Thr Gly Asp Val Leu Asn
      85          90          95
Gln Leu His Ile Asp Phe Arg Ala Leu Ser Gly Val Met Ala Ala Gly
      100          105          110
Ser Arg Gln Ile Phe Ala Asn Glu Ile Ser Ser Gly Ala Ser Asn Val
      115          120          125
Gly Val Val Ile Phe Ser Thr Gln Asp Ser Ala Asn Thr Phe Asn Val
      130          135          140
Leu Asn Ala Ser Gly Gly Ser Arg Ser Val Tyr Pro Val Met Ser Asp
      145          150          155          160
Asp Met Asn Gly Ser Ser Trp Lys Phe Ser Thr Arg Met Gln Lys Ile
      165          170          175
Asp Pro Ala Leu Ser Val Thr Ser Gly Gln Leu Met Ser His Val Leu
      180          185          190
Val Asp Ile Tyr Tyr Glu
      195

```

<210> 333

<211> 201

<212> PRT

<213> Escherichia coli

<400> 333

```

Met Met Thr Phe Lys Asn Leu Arg Tyr Gly Leu Ser Ser Ser Val Val
 1          5          10          15
Leu Ala Ala Ser Leu Phe Ser Val Leu Ser Tyr Ala Ala Thr Asp Ser
      20          25          30
Ile Gly Leu Thr Val Ile Thr Thr Val Glu Met Gly Thr Cys Thr Ala
      35          40          45
Thr Leu Val Asn Asp Ser Asp Gln Asp Ile Ser Val Val Asp Phe Gly
      50          55          60
Asp Val Tyr Ile Ser Glu Ile Asn Ala Lys Thr Lys Val Lys Thr Phe
      65          70          75          80
Lys Leu Lys Phe Lys Asp Cys Ala Gly Ile Pro Asn Lys Lys Ala Gln
      85          90          95
Ile Lys Leu Thr Lys Arg Ala Thr Cys Glu Gly Thr Ala Asn Asp Gly
      100          105          110
Ala Gly Phe Ala Asn Gly Ser Thr Ala Ala Asp Lys Ala Ser Ala Val
      115          120          125
Ala Val Glu Val Trp Ser Thr Val Thr Pro Ala Thr Gly Ser Ala Thr
      130          135          140
Gln Phe Ser Cys Val Thr Pro Ala Ser Gln Glu Val Thr Ile Ser Thr
      145          150          155          160
Ala Ala Asn Ala Val Val Tyr Tyr Pro Met Ser Ala Arg Leu Val Val
      165          170          175
Glu Lys Asn Lys Thr Val Asn Asn Val Thr Ala Gly Lys Phe Ser Ala

```

180 185 190
 Pro Ala Thr Phe Thr Val Thr Tyr Asn
 195 200

<210> 334
 <211> 203
 <212> PRT
 <213> Escherichia coli

<400> 334
 Met Glu Phe Gly Val Arg Phe Ser Asn Tyr Lys Gly Arg Gln Met Ile
 1 5 10 15
 Lys Thr Thr Pro His Lys Ile Val Ile Leu Met Gly Ile Leu Leu Ser
 20 25 30
 Pro Ser Val Phe Ala Thr Asp Ile Asn Val Glu Phe Thr Ala Thr Val
 35 40 45
 Lys Ala Thr Thr Cys Asn Ile Thr Leu Thr Gly Asn Asn Val Thr Asn
 50 55 60
 Asp Gly Asn Asn Asn Tyr Thr Leu Arg Ile Pro Lys Met Gly Leu Asp
 65 70 75 80
 Lys Ile Ala Asn Lys Thr Thr Glu Ser Gln Ala Asp Phe Lys Leu Val
 85 90 95
 Ala Ser Gly Cys Ser Ser Gly Ile Ser Trp Ile Asp Thr Thr Leu Thr
 100 105 110
 Gly Asn Ala Ser Ser Ser Ser Pro Lys Leu Ile Ile Pro Gln Ser Gly
 115 120 125
 Asp Ser Ser Ser Thr Thr Ser Asn Ile Gly Met Gly Phe Lys Lys Arg
 130 135 140
 Thr Thr Asp Asp Ala Thr Phe Leu Lys Pro Asn Ser Ala Glu Lys Ile
 145 150 155 160
 Arg Trp Ser Thr Asp Glu Met Gln Pro Asp Lys Gly Leu Glu Met Thr
 165 170 175
 Val Ala Leu Arg Glu Thr Asp Ala Gly Gln Gly Val Pro Gly Asn Phe
 180 185 190
 Arg Ala Leu Ala Thr Phe Asn Phe Ile Tyr Gln
 195 200

<210> 335
 <211> 139
 <212> PRT
 <213> Escherichia coli

<400> 335
 Met Ala Met Thr Tyr His Leu Asp Val Val Ser Ala Glu Gln Gln Met
 1 5 10 15
 Phe Ser Gly Leu Val Glu Lys Ile Gln Val Thr Gly Ser Glu Gly Glu
 20 25 30
 Leu Gly Ile Tyr Pro Gly His Ala Pro Leu Leu Thr Ala Ile Lys Pro
 35 40 45
 Gly Met Ile Arg Ile Val Lys Gln His Gly His Glu Glu Phe Ile Tyr
 50 55 60
 Leu Ser Gly Gly Ile Leu Glu Val Gln Pro Gly Asn Val Thr Val Leu
 65 70 75 80
 Ala Asp Thr Ala Ile Arg Gly Gln Asp Leu Asp Glu Ala Arg Ala Met
 85 90 95
 Glu Ala Lys Arg Lys Ala Glu Glu His Ile Ser Ser Ser His Gly Asp
 100 105 110
 Val Asp Tyr Ala Gln Ala Ser Ala Glu Leu Ala Lys Ala Ile Ala Gln
 115 120 125

Leu Arg Val Ile Glu Leu Thr Lys Lys Ala Met
130 135

<210> 336

<211> 460

<212> PRT

<213> Escherichia coli

<400> 336

Met Ala Thr Gly Lys Ile Val Gln Val Ile Gly Ala Val Val Asp Val
1 5 10 15
Glu Phe Pro Gln Asp Ala Val Pro Arg Val Tyr Asp Ala Leu Glu Val
20 25 30
Gln Asn Gly Asn Glu Arg Leu Val Leu Glu Val Gln Gln Gln Leu Gly
35 40 45
Gly Gly Ile Val Arg Thr Ile Ala Met Gly Ser Ser Asp Gly Leu Arg
50 55 60
Arg Gly Leu Asp Val Lys Asp Leu Glu His Pro Ile Glu Val Pro Val
65 70 75 80
Gly Lys Ala Thr Leu Gly Arg Ile Met Asn Val Leu Gly Glu Pro Val
85 90 95
Asp Met Lys Gly Glu Ile Gly Glu Glu Glu Arg Trp Ala Ile His Arg
100 105 110
Ala Ala Pro Ser Tyr Glu Glu Leu Ser Asn Ser Gln Glu Leu Leu Glu
115 120 125
Thr Gly Ile Lys Val Ile Asp Leu Met Cys Pro Phe Ala Lys Gly Gly
130 135 140
Lys Val Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Asn Met
145 150 155 160
Met Glu Leu Ile Arg Asn Ile Ala Ile Glu His Ser Gly Tyr Ser Val
165 170 175
Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Phe Tyr His
180 185 190
Glu Met Thr Asp Ser Asn Val Ile Asp Lys Val Ser Leu Val Tyr Gly
195 200 205
Gln Met Asn Glu Pro Pro Gly Asn Arg Leu Arg Val Ala Leu Thr Gly
210 215 220
Leu Thr Met Ala Glu Lys Phe Arg Asp Glu Gly Arg Asp Val Leu Leu
225 230 235 240
Phe Val Asp Asn Ile Tyr Arg Tyr Thr Leu Ala Gly Thr Glu Val Ser
245 250 255
Ala Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu
260 265 270
Ala Glu Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Thr
275 280 285
Gly Ser Ile Thr Ser Val Gln Ala Val Tyr Val Pro Ala Asp Asp Leu
290 295 300
Thr Asp Pro Ser Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Val
305 310 315 320
Val Leu Ser Arg Gln Ile Ala Ser Leu Gly Ile Tyr Pro Ala Val Asp
325 330 335
Pro Leu Asp Ser Thr Ser Arg Gln Leu Asp Pro Leu Val Val Gly Gln
340 345 350
Glu His Tyr Asp Thr Ala Arg Gly Val Gln Ser Ile Leu Gln Arg Tyr
355 360 365
Gln Glu Leu Lys Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser
370 375 380
Glu Glu Asp Lys Leu Val Val Ala Arg Ala Arg Lys Ile Gln Arg Phe
385 390 395 400
Leu Ser Gln Pro Phe Phe Val Ala Glu Val Phe Thr Gly Ser Pro Gly

				405					410				415				
Lys	Tyr	Val	Ser	Leu	Lys	Asp	Thr	Ile	Arg	Gly	Phe	Lys	Gly	Ile	Met		
			420					425					430				
Glu	Gly	Glu	Tyr	Asp	His	Leu	Pro	Glu	Gln	Ala	Phe	Tyr	Met	Val	Gly		
		435				440						445					
Ser	Ile	Glu	Glu	Ala	Val	Glu	Lys	Ala	Lys	Lys	Leu						
	450					455					460						

<210> 337

<211> 287

<212> PRT

<213> Escherichia coli

<400> 337

Met	Ala	Gly	Ala	Lys	Glu	Ile	Arg	Ser	Lys	Ile	Ala	Ser	Val	Gln	Asn		
1				5					10					15			
Thr	Gln	Lys	Ile	Thr	Lys	Ala	Met	Glu	Met	Val	Ala	Ala	Ser	Lys	Met		
			20					25					30				
Arg	Lys	Ser	Gln	Asp	Arg	Met	Ala	Ala	Ser	Arg	Pro	Tyr	Ala	Glu	Thr		
		35				40						45					
Met	Arg	Lys	Val	Ile	Gly	His	Leu	Ala	His	Gly	Asn	Leu	Glu	Tyr	Lys		
	50				55					60							
His	Pro	Tyr	Leu	Glu	Asp	Arg	Asp	Val	Lys	Arg	Val	Gly	Tyr	Leu	Val		
65				70					75					80			
Val	Ser	Thr	Asp	Arg	Gly	Leu	Cys	Gly	Gly	Leu	Asn	Ile	Asn	Leu	Phe		
			85					90					95				
Lys	Lys	Leu	Leu	Ala	Glu	Met	Lys	Thr	Trp	Thr	Asp	Lys	Gly	Val	Gln		
		100						105					110				
Cys	Asp	Leu	Ala	Met	Ile	Gly	Ser	Lys	Gly	Val	Ser	Phe	Phe	Asn	Ser		
	115					120					125						
Val	Gly	Gly	Asn	Val	Val	Ala	Gln	Val	Thr	Gly	Met	Gly	Asp	Asn	Pro		
	130				135					140							
Ser	Leu	Ser	Glu	Leu	Ile	Gly	Pro	Val	Lys	Val	Met	Leu	Gln	Ala	Tyr		
145				150					155						160		
Asp	Glu	Gly	Arg	Leu	Asp	Lys	Leu	Tyr	Ile	Val	Ser	Asn	Lys	Phe	Ile		
			165					170						175			
Asn	Thr	Met	Ser	Gln	Val	Pro	Thr	Ile	Ser	Gln	Leu	Leu	Pro	Leu	Pro		
		180						185					190				
Ala	Ser	Asp	Asp	Asp	Asp	Leu	Lys	His	Lys	Ser	Trp	Asp	Tyr	Leu	Tyr		
	195					200						205					
Glu	Pro	Asp	Pro	Lys	Ala	Leu	Leu	Asp	Thr	Leu	Leu	Arg	Arg	Tyr	Val		
	210				215					220							
Glu	Ser	Gln	Val	Tyr	Gln	Gly	Val	Val	Glu	Asn	Leu	Ala	Ser	Glu	Gln		
225				230					235					240			
Ala	Ala	Arg	Met	Val	Ala	Met	Lys	Ala	Ala	Thr	Asp	Asn	Gly	Gly	Ser		
		245						250					255				
Leu	Ile	Lys	Glu	Leu	Gln	Leu	Val	Tyr	Asn	Lys	Ala	Arg	Gln	Ala	Ser		
		260						265					270				
Ile	Thr	Gln	Glu	Leu	Thr	Glu	Ile	Val	Ser	Gly	Ala	Ala	Ala	Val			
	275					280						285					

<210> 338

<211> 513

<212> PRT

<213> Escherichia coli

<400> 338

Met	Gln	Leu	Asn	Ser	Thr	Glu	Ile	Ser	Glu	Leu	Ile	Lys	Gln	Arg	Ile		
1				5					10					15			

Ala Gln Phe Asn Val Val Ser Glu Ala His Asn Glu Gly Thr Ile Val
 20 25 30
 Ser Val Ser Asp Gly Val Ile Arg Ile His Gly Leu Ala Asp Cys Met
 35 40 45
 Gln Gly Glu Met Ile Ser Leu Pro Gly Asn Arg Tyr Ala Ile Ala Leu
 50 55 60
 Asn Leu Glu Arg Asp Ser Val Gly Ala Val Val Met Gly Pro Tyr Ala
 65 70 75 80
 Asp Leu Ala Glu Gly Met Lys Val Lys Cys Thr Gly Arg Ile Leu Glu
 85 90 95
 Val Pro Val Gly Arg Gly Leu Leu Gly Arg Val Val Asn Thr Leu Gly
 100 105 110
 Ala Pro Ile Asp Gly Lys Gly Pro Leu Asp His Asp Gly Phe Ser Ala
 115 120 125
 Val Glu Ala Ile Ala Pro Gly Val Ile Glu Arg Gln Ser Val Asp Gln
 130 135 140
 Pro Val Gln Thr Gly Tyr Lys Ala Val Asp Ser Met Ile Pro Ile Gly
 145 150 155 160
 Arg Gly Gln Arg Glu Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr
 165 170 175
 Ala Leu Ala Ile Asp Ala Ile Ile Asn Gln Arg Asp Ser Gly Ile Lys
 180 185 190
 Cys Ile Tyr Val Ala Ile Gly Gln Lys Ala Ser Thr Ile Ser Asn Val
 195 200 205
 Val Arg Lys Leu Glu Glu His Gly Ala Leu Ala Asn Thr Ile Val Val
 210 215 220
 Val Ala Thr Ala Ser Glu Ser Ala Ala Leu Gln Tyr Leu Ala Pro Tyr
 225 230 235 240
 Ala Gly Cys Ala Met Gly Glu Tyr Phe Arg Asp Arg Gly Glu Asp Ala
 245 250 255
 Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala Tyr Arg Gln
 260 265 270
 Ile Ser Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala Phe Pro Gly
 275 280 285
 Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala Ala Arg Val
 290 295 300
 Asn Ala Glu Tyr Val Glu Ala Phe Thr Lys Gly Glu Val Lys Gly Lys
 305 310 315 320
 Thr Gly Ser Leu Thr Ala Leu Pro Ile Ile Glu Thr Gln Ala Gly Asp
 325 330 335
 Val Ser Ala Phe Val Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln
 340 345 350
 Ile Phe Leu Glu Thr Asn Leu Phe Asn Ala Gly Ile Arg Pro Ala Val
 355 360 365
 Asn Pro Gly Ile Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys
 370 375 380
 Ile Met Lys Lys Leu Ser Gly Gly Ile Arg Thr Ala Leu Ala Gln Tyr
 385 390 395 400
 Arg Glu Leu Ala Ala Phe Ser Gln Phe Ala Ser Asp Leu Asp Asp Ala
 405 410 415
 Thr Arg Lys Gln Leu Asp His Gly Gln Lys Val Thr Glu Leu Leu Lys
 420 425 430
 Gln Lys Gln Tyr Ala Pro Met Ser Val Ala Gln Gln Ser Leu Val Leu
 435 440 445
 Phe Ala Ala Glu Arg Gly Tyr Leu Ala Asp Val Glu Leu Ser Lys Ile
 450 455 460
 Gly Ser Phe Glu Ala Ala Leu Leu Ala Tyr Val Asp Arg Asp His Ala
 465 470 475 480
 Pro Leu Met Gln Glu Ile Asn Gln Thr Gly Gly Tyr Asn Asp Glu Ile
 485 490 495
 Glu Gly Lys Leu Lys Gly Ile Leu Asp Ser Phe Lys Ala Thr Gln Ser

500 505 510

Trp

<210> 339
 <211> 177
 <212> PRT
 <213> Escherichia coli

<400> 339
 Met Ser Glu Phe Ile Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
 1 5 10 15
 Asp Phe Ala Val Glu His Gln Ser Val Glu Arg Trp Gln Asp Met Leu
 20 25 30
 Ala Phe Ala Ala Glu Val Thr Lys Asn Glu Gln Met Ala Glu Leu Leu
 35 40 45
 Ser Gly Ala Leu Ala Pro Glu Thr Leu Ala Glu Ser Phe Ile Ala Val
 50 55 60
 Cys Gly Glu Gln Leu Asp Glu Asn Gly Gln Asn Leu Ile Arg Val Met
 65 70 75 80
 Ala Glu Asn Gly Arg Leu Asn Ala Leu Pro Asp Val Leu Glu Gln Phe
 85 90 95
 Ile His Leu Arg Ala Val Ser Glu Ala Thr Ala Glu Val Asp Val Ile
 100 105 110
 Ser Ala Ala Ala Leu Ser Glu Gln Gln Leu Ala Lys Ile Ser Ala Ala
 115 120 125
 Met Glu Lys Arg Leu Ser Arg Lys Val Lys Leu Asn Cys Lys Ile Asp
 130 135 140
 Lys Ser Val Met Ala Gly Val Ile Ile Arg Ala Gly Asp Met Val Ile
 145 150 155 160
 Asp Gly Ser Val Arg Gly Arg Leu Glu Arg Leu Ala Asp Val Leu Gln
 165 170 175
 Ser

<210> 340
 <211> 156
 <212> PRT
 <213> Escherichia coli

<400> 340
 Met Asn Leu Asn Ala Thr Ile Leu Gly Gln Ala Ile Ala Phe Val Leu
 1 5 10 15
 Phe Val Leu Phe Cys Met Lys Tyr Val Trp Pro Pro Leu Met Ala Ala
 20 25 30
 Ile Glu Lys Arg Gln Lys Glu Ile Ala Asp Gly Leu Ala Ser Ala Glu
 35 40 45
 Arg Ala His Lys Asp Leu Asp Leu Ala Lys Ala Ser Ala Thr Asp Gln
 50 55 60
 Leu Lys Lys Ala Lys Ala Glu Ala Gln Val Ile Ile Glu Gln Ala Asn
 65 70 75 80
 Lys Arg Arg Ser Gln Ile Leu Asp Glu Ala Lys Ala Glu Ala Glu Gln
 85 90 95
 Glu Arg Thr Lys Ile Val Ala Gln Ala Gln Ala Glu Ile Glu Ala Glu
 100 105 110
 Arg Lys Arg Ala Arg Glu Glu Leu Arg Lys Gln Val Ala Ile Leu Ala
 115 120 125
 Val Ala Gly Ala Glu Lys Ile Ile Glu Arg Ser Val Asp Glu Ala Ala
 130 135 140

Asn Ser Asp Ile Val Asp Lys Leu Val Ala Glu Leu
 145 150 155

<210> 341
 <211> 79
 <212> PRT
 <213> Escherichia coli

<400> 341
 Met Glu Asn Leu Asn Met Asp Leu Leu Tyr Met Ala Ala Ala Val Met
 1 5 10 15
 Met Gly Leu Ala Ala Ile Gly Ala Ala Ile Gly Ile Gly Ile Leu Gly
 20 25 30
 Gly Lys Phe Leu Glu Gly Ala Ala Arg Gln Pro Asp Leu Ile Pro Leu
 35 40 45
 Leu Arg Thr Gln Phe Phe Ile Val Met Gly Leu Val Asp Ala Ile Pro
 50 55 60
 Met Ile Ala Val Gly Leu Gly Leu Tyr Val Met Phe Ala Val Ala
 65 70 75

<210> 342
 <211> 271
 <212> PRT
 <213> Escherichia coli

<400> 342
 Met Ala Ser Glu Asn Met Thr Pro Gln Asp Tyr Ile Gly His His Leu
 1 5 10 15
 Asn Asn Leu Gln Leu Asp Leu Arg Thr Phe Ser Leu Val Asp Pro Gln
 20 25 30
 Asn Pro Pro Ala Thr Phe Trp Thr Ile Asn Ile Asp Ser Met Phe Phe
 35 40 45
 Ser Val Val Leu Gly Leu Leu Phe Leu Val Leu Phe Arg Ser Val Ala
 50 55 60
 Lys Lys Ala Thr Ser Gly Val Pro Gly Lys Phe Gln Thr Ala Ile Glu
 65 70 75 80
 Leu Val Ile Gly Phe Val Asn Gly Ser Val Lys Asp Met Tyr His Gly
 85 90 95
 Lys Ser Lys Leu Ile Ala Pro Leu Ala Leu Thr Ile Phe Val Trp Val
 100 105 110
 Phe Leu Met Asn Leu Met Asp Leu Leu Pro Ile Asp Leu Leu Pro Tyr
 115 120 125
 Ile Ala Glu His Val Leu Gly Leu Pro Ala Leu Arg Val Val Pro Ser
 130 135 140
 Ala Asp Val Asn Val Thr Leu Ser Met Ala Leu Gly Val Phe Ile Leu
 145 150 155 160
 Ile Leu Phe Tyr Ser Ile Lys Met Lys Gly Ile Gly Gly Phe Thr Lys
 165 170 175
 Glu Leu Thr Leu Gln Pro Phe Asn His Trp Ala Phe Ile Pro Val Asn
 180 185 190
 Leu Ile Leu Glu Gly Val Ser Leu Leu Ser Lys Pro Val Ser Leu Gly
 195 200 205
 Leu Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile Leu
 210 215 220
 Ile Ala Gly Leu Leu Pro Trp Trp Ser Gln Trp Ile Leu Asn Val Pro
 225 230 235 240
 Trp Ala Ile Phe His Ile Leu Ile Ile Thr Leu Gln Ala Phe Ile Phe
 245 250 255
 Met Val Leu Thr Ile Val Tyr Leu Ser Met Ala Ser Glu Glu His

260

265

270

<210> 343
 <211> 130
 <212> PRT
 <213> Escherichia coli

<400> 343
 Met Lys Asn Val Met Ser Val Ser Leu Val Ser Arg Asn Val Ala Arg
 1 5 10 15
 Lys Leu Leu Leu Val Gln Leu Leu Val Val Ile Ala Ser Gly Leu Leu
 20 25 30
 Phe Ser Leu Lys Asp Pro Phe Trp Gly Val Ser Ala Ile Ser Gly Gly
 35 40 45
 Leu Ala Val Phe Leu Pro Asn Val Leu Phe Met Ile Phe Ala Trp Arg
 50 55 60
 His Gln Ala His Thr Pro Ala Lys Gly Arg Val Ala Trp Thr Phe Ala
 65 70 75 80
 Phe Gly Glu Ala Phe Lys Val Leu Ala Met Leu Val Leu Leu Val Val
 85 90 95
 Ala Leu Ala Val Leu Lys Ala Val Phe Leu Pro Leu Ile Val Thr Trp
 100 105 110
 Val Leu Val Leu Val Val Gln Ile Leu Ala Pro Ala Val Ile Asn Asn
 115 120 125
 Lys Gly
 130

<210> 344
 <211> 413
 <212> PRT
 <213> Escherichia coli

<400> 344
 Met Gln Lys His Gly Asp Arg Tyr Val Trp Ile Asn Pro Pro Ala Ile
 1 5 10 15
 Pro Leu Ser Thr Glu Glu Met Asp Ser Val Phe Ala Leu Pro Tyr Lys
 20 25 30
 Arg Val Pro His Pro Ala Tyr Gly Asn Ala Arg Ile Pro Ala Tyr Glu
 35 40 45
 Met Ile Arg Phe Ser Val Asn Ile Met Arg Gly Cys Phe Gly Gly Cys
 50 55 60
 Ser Phe Cys Ser Ile Thr Glu His Glu Gly Arg Ile Ile Gln Ser Arg
 65 70 75 80
 Ser Glu Asp Ser Ile Ile Asn Glu Ile Glu Ala Ile Arg Asp Thr Val
 85 90 95
 Pro Gly Phe Thr Gly Val Ile Ser Asp Leu Gly Gly Pro Thr Ala Asn
 100 105 110
 Met Tyr Met Leu Arg Cys Lys Ser Pro Arg Ala Glu Gln Thr Cys Arg
 115 120 125
 Arg Leu Ser Cys Val Tyr Pro Asp Ile Cys Pro His Met Asp Thr Asn
 130 135 140
 His Glu Pro Thr Ile Asn Leu Tyr Arg Arg Ala Arg Asp Leu Lys Gly
 145 150 155 160
 Ile Lys Lys Ile Leu Ile Ala Ser Gly Val Arg Tyr Asp Ile Ala Val
 165 170 175
 Glu Asp Pro Arg Tyr Ile Lys Glu Leu Ala Thr His His Val Gly Gly
 180 185 190
 Tyr Leu Lys Ile Ala Pro Glu His Thr Glu Glu Gly Pro Leu Ser Lys
 195 200 205

```

Met Met Lys Pro Gly Met Gly Ser Tyr Asp Arg Phe Lys Glu Leu Phe
  210          215          220
Asp Thr Tyr Ser Lys Gln Ala Gly Lys Glu Gln Tyr Leu Ile Pro Tyr
225          230          235          240
Phe Ile Ser Ala His Pro Gly Thr Arg Asp Glu Asp Met Val Asn Leu
          245          250          255
Ala Leu Trp Leu Lys Lys His Arg Phe Arg Leu Asp Gln Val Gln Asn
          260          265          270
Phe Tyr Pro Ser Pro Leu Ala Asn Ser Thr Thr Met Tyr Tyr Thr Gly
          275          280          285
Lys Asn Pro Leu Ala Lys Ile Gly Tyr Lys Ser Glu Asp Val Phe Val
          290          295          300
Pro Lys Gly Asp Lys Gln Arg Arg Leu His Lys Ala Leu Leu Arg Tyr
305          310          315          320
His Asp Pro Ala Asn Trp Pro Leu Ile Arg Gln Ala Leu Glu Ala Met
          325          330          335
Gly Lys Lys His Leu Ile Gly Ser Arg Arg Asp Cys Leu Val Pro Ala
          340          345          350
Pro Thr Ile Glu Glu Met Arg Glu Ala Arg Arg Gln Asn Arg Asn Thr
          355          360          365
Arg Pro Ala Leu Thr Lys His Thr Pro Met Ala Thr Gln Arg Gln Thr
          370          375          380
Pro Ala Thr Ala Lys Lys Ala Ser Ser Thr Gln Ser Arg Pro Val Asn
385          390          395          400
Ala Gly Ala Lys Lys Arg Pro Lys Ala Ala Val Gly Arg
          405          410

```

<210> 345

<211> 325

<212> PRT

<213> Escherichia coli

<400> 345

```

Met Ser Ser Ile Ser Leu Ile Gln Pro Asp Arg Asp Leu Phe Ser Trp
  1          5          10          15
Pro Gln Tyr Trp Ala Ala Cys Phe Gly Pro Ala Pro Phe Leu Pro Met
          20          25          30
Ser Arg Glu Glu Met Asp Gln Leu Gly Trp Asp Ser Cys Asp Ile Ile
          35          40          45
Leu Val Thr Gly Asp Ala Tyr Val Asp His Pro Ser Phe Gly Met Ala
          50          55          60
Ile Cys Gly Arg Met Leu Glu Ala Gln Gly Phe Arg Val Gly Ile Ile
65          70          75          80
Ala Gln Pro Asp Trp Ser Ser Lys Asp Asp Phe Met Arg Leu Gly Lys
          85          90          95
Pro Asn Leu Phe Phe Gly Val Thr Ala Gly Asn Met Asp Ser Met Ile
          100          105          110
Asn Arg Tyr Thr Ala Asp Arg Arg Leu Arg His Asp Asp Ala Tyr Thr
          115          120          125
Pro Asp Asn Val Ala Gly Lys Arg Pro Asp Arg Ala Thr Leu Val Tyr
          130          135          140
Thr Gln Arg Cys Lys Glu Ala Trp Lys Asp Val Pro Val Ile Leu Gly
145          150          155          160
Gly Ile Glu Ala Ser Leu Arg Arg Thr Ala His Tyr Asp Tyr Trp Ser
          165          170          175
Asp Thr Val Arg Arg Ser Val Leu Val Asp Ser Lys Ala Asp Met Leu
          180          185          190
Met Phe Gly Asn Gly Glu Arg Pro Leu Val Glu Val Ala His Arg Leu
          195          200          205
Ala Met Gly Glu Pro Ile Ser Glu Ile Arg Asp Val Arg Asn Thr Ala

```

210		215		220
Ile Ile Val Lys Glu Ala Leu Pro Gly Trp Ser Gly Val Asp Ser Thr				
225		230		235
Arg Leu Asp Thr Pro Gly Lys Ile Asp Pro Ile Pro His Pro Tyr Gly				
	245		250	255
Glu Asp Leu Pro Cys Ala Asp Asn Lys Pro Val Ala Pro Lys Lys Gln				
	260		265	270
Glu Ala Lys Ala Val Thr Val Gln Pro Pro Arg Pro Lys Pro Trp Glu				
	275		280	285
Lys Thr Tyr Val Leu Leu Pro Ser Phe Glu Lys Val Lys Gly Asp Lys				
	290		295	300
Val Leu Tyr Ala His Ala Ser Arg Ile Leu His His Glu Thr Asn Pro				
305		310		315
Ala Val Pro Ala His				320
	325			

<210> 346

<211> 226

<212> PRT

<213> Escherichia coli

<400> 346

Met Ile Gln Tyr Leu Asn Val Phe Phe Tyr Asp Ile Tyr Pro Tyr Ile				
1	5		10	15
Cys Ala Thr Val Phe Phe Leu Gly Ser Trp Leu Arg Tyr Asp Tyr Gly				
	20		25	30
Gln Tyr Thr Trp Arg Ala Ser Ser Ser Gln Met Leu Asp Lys Arg Gly				
	35		40	45
Met Val Ile Trp Ser Asn Leu Phe His Ile Gly Ile Leu Gly Ile Phe				
	50		55	60
Phe Gly His Leu Phe Gly Met Leu Thr Pro His Trp Met Tyr Ala Trp				
65		70	75	80
Phe Leu Pro Val Ala Lys Gln Leu Met Ala Met Val Leu Gly Gly				
	85		90	95
Ile Cys Gly Val Leu Thr Leu Ile Gly Gly Ala Gly Leu Leu Trp Arg				
	100		105	110
Arg Leu Thr Asn Gln Arg Val Arg Ala Thr Ser Thr Thr Pro Asp Ile				
	115		120	125
Ile Ile Met Ser Ile Leu Leu Ile Gln Cys Leu Leu Gly Leu Ser Thr				
	130		135	140
Ile Pro Phe Ser Ala Gln Tyr Pro Asp Gly Ser Glu Met Met Lys Leu				
145		150	155	160
Val Gly Trp Ala Gln Ser Ile Val Thr Phe Arg Gly Gly Ser Ser Glu				
	165		170	175
Met Leu Asn Gly Val Ala Phe Val Phe Arg Leu His Leu Val Leu Gly				
	180		185	190
Met Thr Ile Phe Leu Leu Phe Pro Phe Thr Arg Leu Val His Val Trp				
	195		200	205
Ser Ala Pro Phe Glu Tyr Phe Thr Arg Arg Tyr Gln Ile Val Arg Ser				
	210		215	220
Arg Arg				
225				

<210> 347

<211> 231

<212> PRT

<213> Escherichia coli

<400> 347

```

Met Gln Ile Leu Lys Val Ile Gly Leu Leu Met Glu Tyr Pro Asp Glu
 1      5      10      15
Leu Leu Trp Glu Cys Lys Glu Asp Ala Leu Ala Leu Ile Arg Arg Asp
 20      25      30
Ala Pro Met Leu Thr Asp Phe Thr His Asn Leu Leu Asn Ala Pro Leu
 35      40      45
Leu Asp Lys Gln Ala Glu Trp Cys Glu Val Phe Asp Arg Gly Arg Thr
 50      55      60
Thr Ser Leu Leu Leu Phe Glu His Val His Ala Glu Ser Arg Asp Arg
 65      70      75      80
Gly Gln Ala Met Val Asp Leu Leu Ala Glu Tyr Glu Lys Val Gly Leu
 85      90      95
Gln Leu Asp Cys Arg Glu Leu Pro Asp Tyr Leu Pro Leu Tyr Leu Glu
100      105      110
Tyr Leu Ser Val Leu Pro Asp Asp Gln Ala Lys Glu Gly Leu Leu Asn
115      120      125
Val Ala Pro Ile Leu Ala Leu Gly Gly Arg Leu Lys Gln Arg Glu
130      135      140
Ala Pro Trp Tyr Ala Leu Phe Asp Ala Leu Leu Gln Leu Ala Gly Ser
145      150      155      160
Ser Leu Ser Ser Asp Ser Val Thr Lys Gln Val Asn Ser Glu Glu Arg
165      170      175
Asp Asp Thr Arg Gln Ala Leu Asp Ala Val Trp Glu Glu Glu Gln Val
180      185      190
Lys Phe Ile Glu Asp Asn Ala Thr Ala Cys Asp Ser Ser Pro Leu Asn
195      200      205
Gln Tyr Gln Arg Arg Phe Ser Gln Asp Val Ala Pro Gln Tyr Val Asp
210      215      220
Ile Ser Ala Gly Gly Gly Lys
225      230

```

<210> 348

<211> 514

<212> PRT

<213> Escherichia coli

<400> 348

```

Met Lys Ile Arg Ser Gln Val Gly Met Val Leu Asn Leu Asp Lys Cys
 1      5      10      15
Ile Gly Cys His Thr Cys Ser Val Thr Cys Lys Asn Val Trp Thr Gly
 20      25      30
Arg Glu Gly Met Glu Tyr Ala Trp Phe Asn Asn Val Glu Thr Lys Pro
 35      40      45
Gly Ile Gly Tyr Pro Lys Asn Trp Glu Asp Gln Glu Glu Trp Gln Gly
 50      55      60
Gly Trp Val Arg Asp Val Asn Gly Lys Ile Arg Pro Arg Leu Gly Asn
 65      70      75      80
Lys Met Gly Val Ile Thr Lys Ile Phe Ala Asn Pro Val Val Pro Gln
 85      90      95
Ile Asp Asp Tyr Tyr Glu Pro Phe Thr Phe Asp Tyr Glu His Leu His
100      105      110
Ser Ala Pro Glu Gly Lys His Ile Pro Thr Ala Arg Pro Arg Ser Leu
115      120      125
Ile Asp Gly Lys Arg Met Asp Lys Val Ile Trp Gly Pro Asn Trp Glu
130      135      140
Glu Leu Leu Gly Gly Glu Phe Glu Lys Arg Ala Arg Asp Arg Asn Phe
145      150      155      160
Glu Ala Met Gln Lys Glu Met Tyr Gly Gln Phe Glu Asn Thr Phe Met
165      170      175
Met Tyr Leu Pro Arg Leu Cys Glu His Cys Leu Asn Pro Ser Cys Val

```

```
<210> 349
<211> 1246
<212> PRT
<213> Escherichia coli
```

-366-

Thr	Arg	Pro	Asp	Leu	Pro	Asn	His	Glu	Pro	Arg	Gly	Cys	Pro	Arg	Gly
				85					90					95	
Ala	Ser	Tyr	Ser	Trp	Tyr	Leu	Tyr	Ser	Ala	Asn	Arg	Leu	Lys	Tyr	Pro
			100					105					110		
Leu	Ile	Arg	Lys	Arg	Leu	Ile	Glu	Leu	Trp	Arg	Glu	Ala	Leu	Lys	Gln
			115				120					125			
His	Ser	Asp	Pro	Val	Leu	Ala	Trp	Ala	Ser	Ile	Met	Asn	Asp	Pro	Gln
			130				135				140				
Lys	Cys	Leu	Ser	Tyr	Lys	Gln	Val	Arg	Gly	Arg	Gly	Gly	Phe	Ile	Arg
145					150					155					160
Ser	Asn	Trp	Gln	Glu	Leu	Asn	Gln	Leu	Ile	Ala	Ala	Ala	Asn	Val	Trp
			165						170					175	
Thr	Ile	Lys	Thr	Tyr	Gly	Pro	Asp	Arg	Val	Ala	Gly	Phe	Ser	Pro	Ile
			180					185					190		
Pro	Ala	Met	Ser	Met	Val	Ser	Tyr	Ala	Ala	Gly	Thr	Arg	Tyr	Leu	Ser
			195				200					205			
Leu	Leu	Gly	Gly	Thr	Cys	Leu	Ser	Phe	Tyr	Asp	Trp	Tyr	Cys	Asp	Leu
210						215					220				
Pro	Pro	Ala	Ser	Pro	Met	Thr	Trp	Gly	Glu	Gln	Thr	Asp	Val	Pro	Glu
225					230					235					240
Ser	Ala	Asp	Trp	Tyr	Asn	Ser	Ser	Tyr	Ile	Ile	Ala	Trp	Gly	Ser	Asn
			245						250					255	
Val	Pro	Gln	Thr	Arg	Thr	Pro	Asp	Ala	His	Phe	Phe	Thr	Glu	Val	Arg
			260					265					270		
Tyr	Lys	Gly	Thr	Lys	Thr	Ile	Ala	Ile	Thr	Pro	Asp	Tyr	Ser	Glu	Val
			275				280					285			
Ala	Lys	Leu	Cys	Asp	Gln	Trp	Leu	Ala	Pro	Lys	Gln	Gly	Thr	Asp	Ser
290					295						300				
Ala	Leu	Ala	Met	Ala	Met	Gly	His	Val	Ile	Leu	Lys	Glu	Phe	His	Leu
305					310					315					320
Asp	Asn	Pro	Ser	Asp	Tyr	Phe	Ile	Asn	Tyr	Cys	Arg	Arg	Tyr	Ser	Asp
			325						330					335	
Met	Pro	Met	Leu	Val	Met	Leu	Glu	Pro	Arg	Asp	Asp	Gly	Ser	Tyr	Val
			340					345					350		
Pro	Gly	Arg	Met	Ile	Arg	Ala	Ser	Asp	Leu	Val	Asp	Gly	Leu	Gly	Glu
			355				360					365			
Ser	Asn	Asn	Pro	Gln	Trp	Lys	Thr	Val	Ala	Val	Asn	Thr	Ala	Gly	Glu
370						375					380				
Leu	Val	Val	Pro	Asn	Gly	Ser	Ile	Gly	Phe	Arg	Trp	Gly	Glu	Lys	Gly
385					390					395					400
Lys	Trp	Asn	Leu	Glu	Ser	Ile	Ala	Ala	Gly	Thr	Glu	Thr	Glu	Leu	Ser
			405						410				415		
Leu	Thr	Leu	Leu	Gly	Gln	His	Asp	Ala	Val	Ala	Gly	Val	Ala	Phe	Pro
			420					425					430		
Tyr	Phe	Gly	Gly	Ile	Glu	Asn	Pro	His	Phe	Arg	Ser	Val	Lys	His	Asn
			435				440					445			
Pro	Val	Leu	Val	Arg	Gln	Leu	Pro	Val	Lys	Asn	Leu	Thr	Leu	Val	Asp
450					455						460				
Gly	Asn	Thr	Cys	Pro	Val	Val	Ser	Val	Tyr	Asp	Leu	Val	Leu	Ala	Asn
465					470					475					480
Tyr	Gly	Leu	Asp	Arg	Gly	Leu	Glu	Asp	Glu	Asn	Ser	Ala	Lys	Asp	Tyr
			485						490				495		
Ala	Glu	Ile	Lys	Pro	Tyr	Thr	Pro	Ala	Trp	Gly	Glu	Gln	Ile	Thr	Gly
			500					505					510		
Val	Pro	Arg	Gln	Tyr	Ile	Glu	Thr	Ile	Ala	Arg	Glu	Phe	Ala	Asp	Thr
			515				520					525			
Ala	His	Lys	Thr	His	Gly	Arg	Ser	Met	Ile	Ile	Leu	Gly	Ala	Gly	Val
530					535						540				
Asn	His	Trp	Tyr	His	Met	Asp	Met	Asn	Tyr	Arg	Gly	Met	Ile	Asn	Met
545					550					555					560
Leu	Ile	Phe	Cys	Gly	Cys	Val	Gly	Gln	Ser	Gly	Gly	Gly	Trp	Ala	His

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Ser Leu Val Ala Tyr Arg Pro Pro Ile Asp Thr Arg Ser Val Ser Glu
 1060 1065 1070
 Met Arg Gln Ile Pro Pro Asn Gly Phe Pro Glu Lys Ala Leu Asn Phe
 1075 1080 1085
 Leu Thr Pro His Gln Lys Trp Gly Ile His Ser Thr Tyr Ser Glu Asn
 1090 1095 1100
 Leu Leu Met Leu Thr Leu Ser Arg Gly Gly Pro Ile Val Trp Ile Ser
 1105 1110 1115 1120
 Glu Thr Asp Ala Arg Glu Leu Thr Ile Val Asp Asn Asp Trp Val Glu
 1125 1130 1135
 Val Phe Asn Ala Asn Gly Ala Leu Thr Ala Arg Ala Val Val Ser Gln
 1140 1145 1150
 Arg Val Pro Pro Gly Met Thr Met Met Tyr His Ala Gln Glu Arg Ile
 1155 1160 1165
 Met Asn Ile Pro Gly Ser Glu Val Thr Gly Met Arg Gly Gly Ile His
 1170 1175 1180
 Asn Ser Val Thr Arg Val Cys Pro Lys Pro Thr His Met Ile Gly Gly
 1185 1190 1195 1200
 Tyr Ala Gln Leu Ala Trp Gly Phe Asn Tyr Tyr Gly Thr Val Gly Ser
 1205 1210 1215
 Asn Arg Asp Glu Phe Ile Met Ile Arg Lys Met Lys Asn Val Asn Trp
 1220 1225 1230
 Leu Asp Asp Glu Gly Arg Asp Gln Val Gln Glu Ala Lys Lys
 1235 1240 1245

<210> 350
 <211> 165
 <212> PRT
 <213> Escherichia coli

<400> 350
 Met Asp Leu Ser Gln Leu Thr Pro Arg Arg Pro Tyr Leu Leu Arg Ala
 1 5 10 15
 Phe Tyr Glu Trp Leu Leu Asp Asn Gln Leu Thr Pro His Leu Val Val
 20 25 30
 Asp Val Thr Leu Pro Gly Val Gln Val Pro Met Glu Tyr Ala Arg Asp
 35 40 45
 Gly Gln Ile Val Leu Asn Ile Ala Pro Arg Ala Val Gly Asn Leu Glu
 50 55 60
 Leu Ala Asn Asp Glu Val Arg Phe Asn Ala Arg Phe Gly Gly Ile Pro
 65 70 75 80
 Arg Gln Val Ser Val Pro Leu Ala Ala Val Leu Ala Ile Tyr Ala Arg
 85 90 95
 Glu Asn Gly Ala Gly Thr Met Phe Glu Pro Glu Ala Ala Tyr Asp Glu
 100 105 110
 Asp Thr Ser Ile Met Asn Asp Glu Glu Ala Ser Ala Asp Asn Glu Thr
 115 120 125
 Val Met Ser Val Ile Asp Gly Asp Lys Pro Asp His Asp Asp Asp Thr
 130 135 140
 His Pro Asp Asp Glu Pro Pro Gln Pro Pro Arg Gly Gly Arg Pro Ala
 145 150 155 160
 Leu Arg Val Val Lys
 165

<210> 351
 <211> 212
 <212> PRT
 <213> Escherichia coli

<400> 351

```

Met Ala Val Ala Ala Asn Lys Arg Ser Val Met Thr Leu Phe Ser Gly
 1          5      10      15
Pro Thr Asp Ile Tyr Ser His Gln Val Arg Ile Val Leu Ala Glu Lys
 20      25      30
Gly Val Ser Phe Glu Ile Glu His Val Glu Lys Asp Asn Pro Pro Gln
 35      40      45
Asp Leu Ile Asp Leu Asn Pro Asn Gln Ser Val Pro Thr Leu Val Asp
 50      55      60
Arg Glu Leu Thr Leu Trp Glu Ser Arg Ile Ile Met Glu Tyr Leu Asp
 65      70      75      80
Glu Arg Phe Pro His Pro Pro Leu Met Pro Val Tyr Pro Val Ala Arg
 85      90      95
Gly Glu Ser Arg Leu Tyr Met His Arg Ile Glu Lys Asp Trp Tyr Thr
 100      105      110
Leu Met Asn Thr Ile Ile Asn Gly Ser Ala Ser Glu Ala Asp Ala Ala
 115      120      125
Arg Lys Gln Leu Arg Glu Glu Leu Leu Ala Ile Ala Pro Val Phe Gly
 130      135      140
Gln Lys Pro Tyr Phe Leu Ser Asp Glu Phe Ser Leu Val Asp Cys Tyr
 145      150      155      160
Leu Ala Pro Leu Leu Trp Arg Leu Pro Gln Leu Gly Ile Glu Phe Ser
 165      170      175
Gly Pro Gly Ala Lys Glu Leu Lys Gly Tyr Met Thr Arg Val Phe Glu
 180      185      190
Arg Asp Ser Phe Leu Ala Ser Leu Thr Glu Ala Glu Arg Glu Met Arg
 195      200      205
Leu Gly Arg Ser
 210

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<210> 352

<211> 505

<212> PRT

<213> Escherichia coli

<400> 352

```

Met Ser Glu Gln His Ala Gln Gly Ala Asp Ala Val Val Asp Leu Asn
 1          5      10      15
Asn Glu Leu Lys Thr Arg Arg Glu Lys Leu Ala Asn Leu Arg Glu Gln
 20      25      30
Gly Ile Ala Phe Pro Asn Asp Phe Arg Arg Asp His Thr Ser Asp Gln
 35      40      45
Leu His Ala Glu Phe Asp Gly Lys Glu Asn Glu Glu Leu Glu Ala Leu
 50      55      60
Asn Ile Glu Val Ala Val Ala Gly Arg Met Met Thr Arg Arg Ile Met
 65      70      75      80
Gly Lys Ala Ser Phe Val Thr Leu Gln Asp Val Gly Gly Arg Ile Gln
 85      90      95
Leu Tyr Val Ala Arg Asp Asp Leu Pro Glu Gly Val Tyr Asn Glu Gln
 100      105      110
Phe Lys Lys Trp Asp Leu Gly Asp Ile Leu Gly Ala Lys Gly Lys Leu
 115      120      125
Phe Lys Thr Lys Thr Gly Glu Leu Ser Ile His Cys Thr Glu Leu Arg
 130      135      140
Leu Leu Thr Lys Ala Leu Arg Pro Leu Pro Asp Lys Phe His Gly Leu
 145      150      155      160
Gln Asp Gln Glu Ala Arg Tyr Arg Gln Arg Tyr Leu Asp Leu Ile Ser
 165      170      175
Asn Asp Glu Ser Arg Asn Thr Phe Lys Val Arg Ser Gln Ile Leu Ser
 180      185      190

```

Gly Ile Arg Gln Phe Met Val Asn Arg Gly Phe Met Glu Val Glu Thr
 195 200 205
 Pro Met Met Gln Val Ile Pro Gly Gly Ala Ala Ala Arg Pro Phe Ile
 210 215 220
 Thr His His Asn Ala Leu Asp Leu Asp Met Tyr Leu Arg Ile Ala Pro
 225 230 235 240
 Glu Leu Tyr Leu Lys Arg Leu Val Val Gly Gly Phe Glu Arg Val Phe
 245 250 255
 Glu Ile Asn Arg Asn Phe Arg Asn Glu Gly Ile Ser Val Arg His Asn
 260 265 270
 Pro Glu Phe Thr Met Met Glu Leu Tyr Met Ala Tyr Ala Asp Tyr Lys
 275 280 285
 Asp Leu Ile Glu Leu Thr Glu Ser Leu Phe Arg Thr Leu Ala Gln Asp
 290 295 300
 Ile Leu Gly Lys Thr Glu Val Thr Tyr Gly Asp Val Thr Leu Asp Phe
 305 310 315 320
 Gly Lys Pro Phe Glu Lys Leu Thr Met Arg Glu Ala Ile Lys Lys Tyr
 325 330 335
 Arg Pro Glu Thr Asp Met Ala Asp Leu Asp Asn Phe Asp Ser Ala Lys
 340 345 350
 Ala Ile Ala Glu Ser Ile Gly Ile His Val Glu Lys Ser Trp Gly Leu
 355 360 365
 Gly Arg Ile Val Thr Glu Ile Phe Glu Glu Val Ala Glu Ala His Leu
 370 375 380
 Ile Gln Pro Thr Phe Ile Thr Glu Tyr Pro Ala Glu Val Ser Pro Leu
 385 390 395 400
 Ala Arg Arg Asn Asp Val Asn Pro Glu Ile Thr Asp Arg Phe Glu Phe
 405 410 415
 Phe Ile Gly Gly Arg Glu Ile Gly Asn Gly Phe Ser Glu Leu Asn Asp
 420 425 430
 Ala Glu Asp Gln Ala Gln Arg Phe Leu Asp Gln Val Ala Ala Lys Asp
 435 440 445
 Ala Gly Asp Asp Glu Ala Met Phe Tyr Asp Glu Asp Tyr Val Thr Ala
 450 455 460
 Leu Glu His Gly Leu Pro Pro Thr Ala Gly Leu Gly Ile Gly Ile Asp
 465 470 475 480
 Arg Met Val Met Leu Phe Thr Asn Ser His Thr Ile Arg Asp Val Ile
 485 490 495
 Leu Phe Pro Ala Met Arg Pro Val Lys
 500 505

<210> 353

<211> 365

<212> PRT

<213> Escherichia coli

<400> 353

Met Phe Glu Ile Asn Pro Val Asn Asn Arg Ile Gln Asp Leu Thr Glu
 1 5 10 15
 Arg Ser Asp Val Leu Arg Gly Tyr Leu Asp Tyr Asp Ala Lys Lys Glu
 20 25 30
 Arg Leu Glu Glu Val Asn Ala Glu Leu Glu Gln Pro Asp Val Trp Asn
 35 40 45
 Glu Pro Glu Arg Ala Gln Ala Leu Gly Lys Glu Arg Ser Ser Leu Glu
 50 55 60
 Ala Val Val Asp Thr Leu Asp Gln Met Lys Gln Gly Leu Glu Asp Val
 65 70 75 80
 Ser Gly Leu Leu Glu Leu Ala Val Glu Ala Asp Asp Glu Glu Thr Phe
 85 90 95
 Asn Glu Ala Val Ala Glu Leu Asp Ala Leu Glu Glu Lys Leu Ala Gln

100	105	110
Leu Glu Phe Arg Arg Met Phe Ser Gly Glu Tyr Asp Ser Ala Asp Cys		
115	120	125
Tyr Leu Asp Ile Gln Ala Gly Ser Gly Gly Thr Glu Ala Gln Asp Trp		
130	135	140
Ala Ser Met Leu Glu Arg Met Tyr Leu Arg Trp Ala Glu Ser Arg Gly		
145	150	155
Phe Lys Thr Glu Ile Ile Glu Glu Ser Glu Gly Glu Val Ala Gly Ile		
165	170	175
Lys Ser Val Thr Ile Lys Ile Ser Gly Asp Tyr Ala Tyr Gly Trp Leu		
180	185	190
Arg Thr Glu Thr Gly Val His Arg Leu Val Arg Lys Ser Pro Phe Asp		
195	200	205
Ser Gly Gly Arg Arg His Thr Ser Phe Ser Ser Ala Phe Val Tyr Pro		
210	215	220
Glu Val Asp Asp Asp Ile Asp Ile Glu Ile Asn Pro Ala Asp Leu Arg		
225	230	235
Ile Asp Val Tyr Arg Thr Ser Gly Ala Gly Gly Gln His Val Asn Arg		
245	250	255
Thr Glu Ser Ala Val Arg Ile Thr His Ile Pro Thr Gly Ile Val Thr		
260	265	270
Gln Cys Gln Asn Asp Arg Ser Gln His Lys Asn Lys Asp Gln Ala Met		
275	280	285
Lys Gln Met Lys Ala Lys Leu Tyr Glu Leu Glu Met Gln Lys Lys Asn		
290	295	300
Ala Glu Lys Gln Ala Met Glu Asp Asn Lys Ser Asp Ile Gly Trp Gly		
305	310	315
Ser Gln Ile Arg Ser Tyr Val Leu Asp Asp Ser Arg Ile Lys Asp Leu		
325	330	335
Arg Thr Gly Val Glu Thr Arg Asn Thr Gln Ala Val Leu Asp Gly Ser		
340	345	350
Leu Asp Gln Phe Ile Glu Ala Ser Leu Lys Ala Gly Leu		
355	360	365

<210> 354

<211> 577

<212> PRT

<213> Escherichia coli

<400> 354

Met Lys Gln Gln Ile Gln Leu Arg Arg Arg Glu Val Asp Glu Thr Ala	
1	5
Asp Leu Pro Ala Glu Leu Pro Pro Leu Leu Arg Arg Leu Tyr Ala Ser	
20	25
Arg Gly Val Arg Ser Ala Gln Glu Leu Glu Arg Ser Val Lys Gly Met	
35	40
Leu Pro Trp Gln Gln Leu Ser Gly Val Glu Lys Ala Val Glu Ile Leu	
50	55
Tyr Asn Ala Phe Arg Glu Gly Thr Arg Ile Ile Val Val Gly Asp Phe	
65	70
Asp Ala Asp Gly Ala Thr Ser Thr Ala Leu Ser Val Leu Ala Met Arg	
85	90
Ser Leu Gly Cys Ser Asn Ile Asp Tyr Leu Val Pro Asn Arg Phe Glu	
100	105
Asp Gly Tyr Gly Leu Ser Pro Glu Val Val Asp Gln Ala His Ala Arg	
115	120
Gly Ala Gln Leu Ile Val Thr Val Asp Asn Gly Ile Ser Ser His Ala	
130	135
Gly Val Glu His Ala Arg Ser Leu Gly Ile Pro Val Ile Val Thr Asp	
145	150
	155
	160

His His Leu Pro Gly Asp Thr Leu Pro Ala Ala Glu Ala Ile Ile Asn
 165 170 175
 Pro Asn Leu Arg Asp Cys Asn Phe Pro Ser Lys Ser Leu Ala Gly Val
 180 185 190
 Gly Val Ala Phe Tyr Leu Met Leu Ala Leu Arg Thr Phe Leu Arg Asp
 195 200 205
 Gln Gly Trp Phe Asp Glu Arg Asn Ile Ala Ile Pro Asn Leu Ala Glu
 210 215 220
 Leu Leu Asp Leu Val Ala Leu Gly Thr Val Ala Asp Val Val Pro Leu
 225 230 235 240
 Asp Ala Asn Asn Arg Ile Leu Thr Trp Gln Gly Met Ser Arg Ile Arg
 245 250 255
 Ala Gly Lys Cys Arg Pro Gly Ile Lys Ala Leu Leu Glu Val Ala Asn
 260 265 270
 Arg Asp Ala Gln Lys Leu Ala Ala Ser Asp Leu Gly Phe Ala Leu Gly
 275 280 285
 Pro Arg Leu Asn Ala Ala Gly Arg Leu Asp Asp Met Ser Val Gly Val
 290 295 300
 Ala Leu Leu Leu Cys Asp Asn Ile Gly Glu Ala Arg Val Leu Ala Asn
 305 310 315 320
 Glu Leu Asp Ala Leu Asn Gln Thr Arg Lys Glu Ile Glu Gln Gly Met
 325 330 335
 Gln Ile Glu Ala Leu Thr Leu Cys Glu Lys Leu Glu Arg Ser Arg Asp
 340 345 350
 Thr Leu Pro Gly Gly Leu Ala Met Tyr His Pro Glu Trp His Gln Gly
 355 360 365
 Val Val Gly Ile Leu Ala Ser Arg Ile Lys Glu Arg Phe His Arg Pro
 370 375 380
 Val Ile Ala Phe Ala Pro Ala Gly Asp Gly Thr Leu Lys Gly Ser Gly
 385 390 395 400
 Arg Ser Ile Gln Gly Leu His Met Arg Asp Ala Leu Glu Arg Leu Asp
 405 410 415
 Thr Leu Tyr Pro Gly Met Met Leu Lys Phe Gly Gly His Ala Met Ala
 420 425 430
 Ala Gly Leu Ser Leu Glu Glu Asp Lys Phe Lys Leu Phe Gln Gln Arg
 435 440 445
 Phe Gly Glu Leu Val Thr Glu Trp Leu Asp Pro Ser Leu Leu Gln Gly
 450 455 460
 Glu Val Val Ser Asp Gly Pro Leu Ser Pro Ala Glu Met Thr Met Glu
 465 470 475 480
 Val Ala Gln Leu Leu Arg Asp Ala Gly Pro Trp Gly Gln Met Phe Pro
 485 490 495
 Glu Pro Leu Phe Asp Gly His Phe Arg Leu Leu Gln Gln Arg Leu Val
 500 505 510
 Gly Glu Arg His Leu Lys Val Met Val Glu Pro Val Gly Gly Gly Pro
 515 520 525
 Leu Leu Asp Gly Ile Ala Phe Asn Val Asp Thr Ala Leu Trp Pro Asp
 530 535 540
 Asn Gly Val Arg Glu Val Gln Leu Ala Tyr Lys Leu Asp Ile Asn Glu
 545 550 555 560
 Phe Arg Gly Asn Arg Ser Leu Gln Ile Ile Ile Asp Asn Ile Trp Pro
 565 570 575
 Ile

<210> 355

<211> 236

<212> PRT

<213> Escherichia coli

<400> 355

```

Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
 1          5          10          15
Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
          20          25          30
Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
          35          40          45
Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
          50          55          60
His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
65          70          75          80
Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
          85          90          95
Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
          100          105          110
Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
          115          120          125
Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
130          135          140
Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
145          150          155          160
Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
          165          170          175
Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
          180          185          190
Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
195          200          205
Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
210          215          220
Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys
225          230          235

```

<210> 356

<211> 298

<212> PRT

<213> Escherichia coli

<400> 356

```

Met Lys Gln Asp Leu Ala Arg Ile Glu Gln Phe Leu Asp Ala Leu Trp
 1          5          10          15
Leu Glu Lys Asn Leu Ala Glu Asn Thr Leu Asn Ala Tyr Arg Arg Asp
          20          25          30
Leu Ser Met Met Val Glu Trp Leu His His Arg Gly Leu Thr Leu Ala
          35          40          45
Thr Ala Gln Ser Asp Asp Leu Gln Ala Leu Leu Ala Glu Arg Leu Glu
          50          55          60
Gly Gly Tyr Lys Ala Thr Ser Ser Ala Arg Leu Leu Ser Ala Val Arg
65          70          75          80
Arg Leu Phe Gln Tyr Leu Tyr Arg Glu Lys Phe Arg Glu Asp Asp Pro
          85          90          95
Ser Ala His Leu Ala Ser Pro Lys Leu Pro Gln Arg Leu Pro Lys Asp
          100          105          110
Leu Ser Glu Ala Gln Val Glu Arg Leu Leu Gln Ala Pro Leu Ile Asp
          115          120          125
Gln Pro Leu Glu Leu Arg Asp Lys Ala Met Leu Glu Val Leu Tyr Ala
130          135          140
Thr Gly Leu Arg Val Ser Glu Leu Val Gly Leu Thr Met Ser Asp Ile
145          150          155          160
Ser Leu Arg Gln Gly Val Val Arg Val Ile Gly Lys Gly Asn Lys Glu
          165          170          175

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Arg Leu Val Pro Leu Gly Glu Glu Ala Val Tyr Trp Leu Glu Thr Tyr
 180 185 190
 Leu Glu His Gly Arg Pro Trp Leu Leu Asn Gly Val Ser Ile Asp Val
 195 200 205
 Leu Phe Pro Ser Gln Arg Ala Gln Gln Met Thr Arg Gln Thr Phe Trp
 210 215 220
 His Arg Ile Lys His Tyr Ala Val Leu Ala Gly Ile Asp Ser Glu Lys
 225 230 235 240
 Leu Ser Pro His Val Leu Arg His Ala Phe Ala Thr His Leu Leu Asn
 245 250 255
 His Gly Ala Asp Leu Arg Val Val Gln Met Leu Leu Gly His Ser Asp
 260 265 270
 Leu Ser Thr Thr Gln Ile Tyr Thr His Val Ala Thr Glu Arg Leu Arg
 275 280 285
 Gln Leu His Gln Gln His His Pro Arg Ala
 290 295

<210> 357

<211> 367

<212> PRT

<213> Escherichia coli

<400> 357

Met Ser Asp Ser Gln Thr Leu Val Val Lys Leu Gly Thr Ser Val Leu
 1 5 10 15
 Thr Gly Gly Ser Arg Arg Leu Asn Arg Ala His Ile Val Glu Leu Val
 20 25 30
 Arg Gln Cys Ala Gln Leu His Ala Ala Gly His Arg Ile Val Ile Val
 35 40 45
 Thr Ser Gly Ala Ile Ala Ala Gly Arg Glu His Leu Gly Tyr Pro Glu
 50 55 60
 Leu Pro Ala Thr Ile Ala Ser Lys Gln Leu Leu Ala Ala Val Gly Gln
 65 70 75 80
 Ser Arg Leu Ile Gln Leu Trp Glu Gln Leu Phe Ser Ile Tyr Gly Ile
 85 90 95
 His Val Gly Gln Met Leu Leu Thr Arg Ala Asp Met Glu Asp Arg Glu
 100 105 110
 Arg Phe Leu Asn Ala Arg Asp Thr Leu Arg Ala Leu Leu Asp Asn Asn
 115 120 125
 Ile Val Pro Val Ile Asn Glu Asn Asp Ala Val Ala Thr Ala Glu Ile
 130 135 140
 Lys Val Gly Asp Asn Asp Asn Leu Ser Ala Leu Ala Ala Ile Leu Ala
 145 150 155 160
 Gly Ala Asp Lys Leu Leu Leu Leu Thr Asp Gln Lys Gly Leu Tyr Thr
 165 170 175
 Ala Asp Pro Arg Ser Asn Pro Gln Ala Glu Leu Ile Lys Asp Val Tyr
 180 185 190
 Gly Ile Asp Asp Ala Leu Arg Ala Ile Ala Gly Asp Ser Val Ser Gly
 195 200 205
 Leu Gly Thr Gly Gly Met Ser Thr Lys Leu Gln Ala Ala Asp Val Ala
 210 215 220
 Cys Arg Ala Gly Ile Asp Thr Ile Ile Ala Ala Gly Ser Lys Pro Gly
 225 230 235 240
 Val Ile Gly Asp Val Met Glu Gly Ile Ser Val Gly Thr Leu Phe His
 245 250 255
 Ala Gln Ala Thr Pro Leu Glu Asn Arg Lys Arg Trp Ile Phe Gly Ala
 260 265 270
 Pro Pro Ala Gly Glu Ile Thr Val Asp Glu Gly Ala Thr Ala Ala Ile
 275 280 285
 Leu Glu Arg Gly Ser Ser Leu Leu Pro Lys Gly Ile Lys Ser Val Thr

290		295		300
Gly Asn Phe Ser Arg	Gly Glu Val Ile Arg	Ile Cys Asn Leu Glu Gly		
305	310	315		320
Arg Asp Ile Ala His	Gly Val Ser Arg Tyr	Asn Ser Asp Ala Leu Arg		
	325	330		335
Arg Ile Ala Gly His	His Ser Gln Glu Ile	Asp Ala Ile Leu Gly Tyr		
	340	345		350
Glu Tyr Gly Pro Val	Ala Val His Arg Asp	Asp Met Ile Thr Arg		
	355	360		365

<210> 358

<211> 417

<212> PRT

<213> Escherichia coli

<400> 358

Met Leu Glu Gln Met Gly	Ile Ala Ala Lys Gln	Ala Ser Tyr Lys Leu
1	5	10
Ala Gln Leu Ser Arg	Glu Lys Asn Arg Val	Leu Glu Lys Ile Ala
	20	25
Asp Glu Leu Glu Ala Gln	Ser Glu Ile Ile Leu	Asn Ala Asn Ala Gln
	35	40
Asp Val Ala Asp Ala Arg	Ala Asn Gly Leu Ser	Glu Ala Met Leu Asp
	50	55
Arg Leu Ala Leu Thr Pro	Ala Arg Leu Lys Gly	Ile Ala Asp Asp Val
	65	70
Arg Gln Val Cys Asn Leu	Ala Asp Pro Val Gly	Gln Val Ile Asp Gly
	85	90
Gly Val Leu Asp Ser Gly	Leu Arg Leu Glu Arg	Arg Arg Val Pro Leu
	100	105
Gly Val Ile Gly Val Ile	Tyr Glu Ala Arg Pro	Asn Val Thr Val Asp
	115	120
Val Ala Ser Leu Cys Leu	Lys Thr Gly Asn Ala	Val Ile Leu Arg Gly
	130	135
Gly Lys Glu Thr Cys Arg	Thr Asn Ala Ala Thr	Val Ala Val Ile Gln
	145	150
Asp Ala Leu Lys Ser Cys	Gly Leu Pro Ala Gly	Ala Val Gln Ala Ile
	165	170
Asp Asn Pro Asp Arg Ala	Leu Val Ser Glu Met	Leu Arg Met Asp Lys
	180	185
Tyr Ile Asp Met Leu Ile	Pro Arg Gly Gly Ala	Gly Leu His Lys Leu
	195	200
Cys Arg Glu Gln Ser Thr	Ile Pro Val Ile Thr	Gly Gly Ile Gly Val
	210	215
Cys His Ile Tyr Val Asp	Glu Ser Val Glu Ile	Ala Glu Ala Leu Lys
	225	230
Val Ile Val Asn Ala Lys	Thr Gln Arg Pro Ser	Thr Cys Asn Thr Val
	245	250
Glu Thr Leu Leu Val Asn	Lys Asn Ile Ala Asp	Ser Phe Leu Pro Ala
	260	265
Leu Ser Lys Gln Met Ala	Glu Ser Gly Val Thr	Leu His Ala Asp Ala
	275	280
Ala Ala Leu Ala Gln Leu	Gln Ala Gly Pro Ala	Lys Val Val Ala Val
	290	295
Lys Ala Glu Glu Tyr Asp	Asp Glu Phe Leu Ser	Leu Asp Leu Asn Val
	305	310
Lys Ile Val Ser Asp Leu	Asp Asp Ala Ile Ala	His Ile Arg Glu His
	325	330
Gly Thr Gln His Ser Asp	Ala Ile Leu Thr Arg	Asp Met Arg Asn Ala
	340	345

Gln Arg Phe Val Asn Glu Val Asp Ser Ser Ala Val Tyr Val Asn Ala
 355 360 365
 Ser Thr Arg Phe Thr Asp Gly Gly Gln Phe Gly Leu Gly Ala Glu Val
 370 375 380
 Ala Val Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Gly Leu Glu
 385 390 395 400
 Ala Leu Thr Thr Tyr Lys Trp Ile Gly Ile Gly Asp Tyr Thr Ile Arg
 405 410 415
 Ala

<210> 359
 <211> 186
 <212> PRT
 <213> Escherichia coli

<400> 359
 Met Met Thr Arg Gln Ala Ser Met Lys Gly Phe Pro Ile Ala His Ile
 1 5 10 15
 Phe His Pro Ser Ile Pro Pro Met His Ala Val Val Asn Asn His Asn
 20 25 30
 Arg Asn Ile Asp Tyr Trp Thr Val Lys Arg Lys Phe Ala Glu Ile Val
 35 40 45
 Ser Thr Asn Asp Val Asn Lys Ile Tyr Ser Ile Ser Asn Glu Leu Arg
 50 55 60
 Arg Val Leu Ser Ala Ile Thr Ala Leu Asn Phe Tyr His Gly Asp Val
 65 70 75 80
 Pro Ser Val Met Ile Arg Ile Gln Pro Glu Asn Met Ser Pro Phe Ile
 85 90 95
 Ile Asp Ile Ser Thr Gly Glu His Asp Asp Tyr Ile Ile Gln Thr Leu
 100 105 110
 Asp Val Gly Thr Phe Ala Pro Phe Gly Glu Gln Cys Thr Cys Ser Ala
 115 120 125
 Val Asn Lys Lys Glu Leu Glu Cys Ile Lys Glu Thr Ile Ser Lys Tyr
 130 135 140
 Cys Ala Lys Phe Thr Arg Lys Glu Ala Ile Leu Thr Pro Leu Val His
 145 150 155 160
 Phe Asn Lys Thr Ser Ile Thr Ser Asp Cys Trp Gln Ile Leu Phe Phe
 165 170 175
 Ser Pro Asp His Phe Asn Asn Asp Phe Tyr
 180 185

<210> 360
 <211> 395
 <212> PRT
 <213> Escherichia coli

<400> 360
 Met Phe Pro Val Ser Ser Ile Gly Asn Asp Ile Ser Ser Asp Leu Val
 1 5 10 15
 Arg Arg Lys Met Asn Asp Leu Pro Glu Ser Pro Thr Gly Asn Asn Leu
 20 25 30
 Glu Ala Leu Ala Pro Gly Ile Glu Lys Leu Lys Gln Thr Ser Ile Glu
 35 40 45
 Met Val Thr Leu Leu Asn Thr Leu Gln Pro Gly Gly Lys Cys Ile Ile
 50 55 60
 Thr Gly Asp Phe Gln Lys Glu Leu Ala Tyr Leu Gln Asn Val Ile Leu
 65 70 75 80
 Tyr Asn Val Ser Ser Leu Arg Leu Asp Phe Leu Gly Tyr Asn Ala Gln

				85				90				95				
Ile	Ile	Gln	Arg	Ser	Asp	Asn	Thr	Cys	Glu	Leu	Thr	Ile	Asn	Glu	Pro	
100				105				110								
Leu	Lys	Asn	Gln	Glu	Ile	Ser	Thr	Gly	Asn	Ile	Asn	Ile	Asn	Cys	Pro	
115				120				125								
Leu	Lys	Asp	Ile	Tyr	Asn	Glu	Ile	Arg	Arg	Leu	Asn	Val	Ile	Phe	Ser	
130				135				140								
Cys	Gly	Thr	Gly	Asp	Ile	Val	Asp	Leu	Ser	Ser	Leu	Asp	Leu	Arg	Asn	
145					150				155				160			
Val	Asp	Leu	Asp	Tyr	Tyr	Asp	Phe	Thr	Asp	Lys	His	Met	Ala	Asn	Thr	
				165				170				175				
Ile	Leu	Asn	Pro	Phe	Lys	Leu	Asn	Ser	Thr	Asn	Phe	Thr	Asn	Ala	Asn	
180				185				190								
Met	Phe	Gln	Val	Asn	Phe	Val	Ser	Ser	Thr	Gln	Asn	Ala	Thr	Ile	Ser	
195				200				205								
Trp	Asp	Tyr	Leu	Leu	Lys	Ile	Thr	Pro	Val	Leu	Ile	Ser	Ile	Ser	Asp	
210				215				220								
Met	Tyr	Ser	Glu	Glu	Lys	Ile	Lys	Phe	Val	Glu	Ser	Cys	Leu	Asn	Glu	
225					230				235				240			
Pro	Gly	Asp	Ile	Thr	Glu	Glu	Gln	Leu	Lys	Ile	Met	Arg	Phe	Ala	Ile	
				245				250				255				
Ile	Lys	Ser	Ile	Pro	Arg	Ala	Thr	Leu	Thr	Asp	Lys	Leu	Glu	Asn	Glu	
260				265				270								
Leu	Thr	Lys	Glu	Ile	Tyr	Lys	Ser	Ser	Ser	Lys	Ile	Ile	Asn	Cys	Leu	
275				280				285								
Asn	Arg	Ile	Lys	Leu	Thr	Glu	Met	Lys	Glu	Phe	Ser	Ser	Glu	Lys	Ile	
290				295				300								
Tyr	Asp	Tyr	Ile	Asp	Ile	Ile	Ile	Glu	Asp	Tyr	Glu	Asn	Thr	Lys	Glu	
305					310				315				320			
Asn	Ala	Tyr	Leu	Val	Val	Pro	Gln	Ile	Asn	Tyr	Thr	Met	Asp	Leu	Asn	
				325				330				335				
Ile	Glu	Asp	Ser	Ser	Ser	Glu	Glu	Leu	Leu	Ser	Asp	Asn	Thr	Leu	Glu	
340				345				350								
Lys	Asp	Glu	Asn	Ser	Pro	Asp	Asn	Gly	Phe	Glu	Val	Gly	Glu	Tyr	Asn	
355				360				365								
Thr	Tyr	Glu	Ala	Tyr	Asn	Ser	Glu	Lys	Gln	Tyr	Phe	Thr	Arg	Glu	Asp	
370				375				380								
Tyr	Thr	Tyr	Asp	Tyr	Asp	Leu	Leu	Asn	Ala	Ile						
385					390				395							

<210> 361

<211> 315

<212> PRT

<213> Escherichia coli

<400> 361

Met	Cys	His	Arg	Ala	Phe	Arg	Leu	His	Leu	Cys	Lys	Asp	Trp	Val	Phe
1				5					10					15	
Met	Phe	Ser	Gly	Leu	Leu	Ile	Ile	Leu	Val	Pro	Leu	Ile	Val	Gly	Tyr
			20					25					30		
Leu	Ile	Pro	Leu	Arg	Gln	Gln	Ala	Leu	Lys	Val	Ile	Asn	Gln	Leu	
			35				40					45			
Leu	Ser	Trp	Met	Val	Tyr	Leu	Ile	Leu	Phe	Phe	Met	Gly	Ile	Ser	Leu
	50					55					60				
Ala	Phe	Leu	Asp	Asn	Leu	Ala	Ser	Asn	Leu	Leu	Ala	Ile	Leu	His	Tyr
65					70					75				80	
Ser	Ala	Val	Ser	Ile	Thr	Val	Ile	Leu	Leu	Cys	Asn	Ile	Ala	Ala	Leu
				85					90					95	
Met	Trp	Leu	Glu	Arg	Gly	Leu	Pro	Trp	Arg	Asn	His	His	Gln	Gln	Glu
			100					105					110		

Lys Leu Pro Ser Arg Ile Ala Met Ala Leu Glu Ser Leu Lys Leu Cys
 115 120 125
 Gly Val Val Val Ile Gly Phe Ala Ile Gly Leu Ser Gly Leu Ala Phe
 130 135 140
 Leu Gln His Ala Thr Glu Ala Ser Glu Tyr Thr Leu Ile Leu Leu Leu
 145 150 155 160
 Phe Leu Val Gly Ile Gln Leu Arg Asn Asn Gly Met Thr Leu Lys Gln
 165 170 175
 Ile Val Leu Asn Arg Arg Gly Met Ile Val Ala Val Val Val Val
 180 185 190
 Ser Ser Leu Ile Gly Gly Leu Ile Asn Ala Phe Ile Leu Asp Leu Pro
 195 200 205
 Ile Asn Thr Ala Leu Ala Met Ala Ser Gly Phe Gly Trp Tyr Ser Leu
 210 215 220
 Ser Gly Ile Leu Leu Thr Glu Ser Phe Gly Pro Val Ile Gly Ser Ala
 225 230 235 240
 Ala Phe Phe Asn Asp Leu Ala Arg Glu Leu Ile Ala Ile Met Leu Ile
 245 250 255
 Pro Gly Leu Ile Arg Arg Ser Arg Ser Thr Ala Leu Gly Leu Cys Gly
 260 265 270
 Ala Thr Ser Met Asp Phe Thr Leu Pro Val Leu Gln Arg Thr Gly Gly
 275 280 285
 Leu Asp Met Val Pro Ala Ala Ile Val His Gly Phe Ile Leu Ser Leu
 290 295 300
 Leu Val Pro Ile Leu Ile Ala Phe Phe Ser Ala
 305 310 315

<210> 362

<211> 96

<212> PRT

<213> Escherichia coli

<400> 362

Met Gln Asn Thr Thr His Asp Asn Val Ile Leu Glu Leu Thr Val Arg
 1 5 10 15
 Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg
 20 25 30
 Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp
 35 40 45
 Lys Ser His Ile Trp Leu Leu Val Asn Asp Asp Gln Arg Leu Glu Gln
 50 55 60
 Met Ile Ser Gln Ile Asp Lys Leu Glu Asp Val Val Lys Val Gln Arg
 65 70 75 80
 Asn Gln Ser Asp Pro Thr Met Phe Asn Lys Ile Ala Val Phe Phe Gln
 85 90 95

<210> 363

<211> 562

<212> PRT

<213> Escherichia coli

<400> 363

Met Ala Ser Ser Gly Thr Thr Ser Thr Arg Lys Arg Phe Thr Gly Ala
 1 5 10 15
 Glu Phe Ile Val His Phe Leu Glu Gln Gly Ile Lys Ile Val Thr
 20 25 30
 Gly Ile Pro Gly Gly Ser Ile Leu Pro Val Tyr Asp Ala Leu Ser Gln
 35 40 45
 Ser Thr Gln Ile Arg His Ile Leu Ala Arg His Glu Gln Gly Ala Gly

50	55	60
Phe Ile Ala Gln Gly Met	Ala Arg Thr Asp Gly Lys Pro Ala Val Cys	
65	70	75
Met Ala Cys Ser Gly Pro	Gly Ala Thr Asn Leu Val Thr Ala Ile Ala	80
	85	90
Asp Ala Arg Leu Asp Ser	Ile Pro Leu Ile Cys Ile Thr Gly Gln Val	95
	100	105
Pro Ala Ser Met Ile Gly	Thr Asp Ala Phe Gln Glu Val Asp Thr Tyr	110
	115	120
Gly Ile Ser Ile Pro Ile	Thr Lys His Asn Tyr Leu Val Arg His Ile	125
	130	135
Glu Glu Leu Pro Gln Val	Met Ser Asp Ala Phe Arg Ile Ala Gln Ser	140
145	150	155
Gly Arg Pro Gly Pro Val	Trp Ile Asp Ile Pro Lys Asp Val Gln Thr	160
	165	170
Ala Val Phe Glu Ile Glu	Thr Gln Pro Ala Met Ala Glu Lys Ala Ala	175
	180	185
Ala Pro Ala Phe Ser Glu	Glu Ser Ile Arg Asp Ala Ala Met Ile	190
	195	200
Asn Ala Ala Lys Arg Pro	Val Leu Tyr Leu Gly Gly Val Ile Asn	205
	210	215
Ala Pro Ala Arg Val Arg	Glu Leu Ala Glu Lys Ala Gln Leu Pro Thr	220
225	230	235
Thr Met Thr Leu Met Ala	Leu Gly Met Leu Pro Lys Ala His Pro Leu	240
	245	250
Ser Leu Gly Met Leu Gly	Met His Gly Val Arg Ser Thr Asn Tyr Ile	255
	260	265
Leu Gln Glu Ala Asp Leu	Leu Ile Val Leu Gly Ala Arg Phe Asp Asp	270
	275	280
Arg Ala Ile Gly Lys Thr	Glu Gln Phe Cys Pro Asn Ala Lys Ile Ile	285
	290	295
His Val Asp Ile Asp Arg	Ala Glu Leu Gly Lys Ile Lys Gln Pro His	300
305	310	315
Val Ala Ile Gln Ala Asp	Val Asp Asp Val Leu Ala Gln Leu Ile Pro	320
	325	330
Leu Val Glu Ala Gln Pro	Arg Ala Glu Trp His Gln Leu Val Ala Asp	335
	340	345
Leu Gln Arg Glu Phe Pro	Cys Pro Ile Pro Lys Ala Cys Asp Pro Leu	350
	355	360
Ser His Tyr Gly Leu Ile	Asn Ala Val Ala Ala Cys Val Asp Asp Asn	365
	370	375
Ala Ile Ile Thr Thr Asp	Val Gly Gln His Gln Met Trp Thr Ala Gln	380
385	390	395
Ala Tyr Pro Leu Asn Arg	Pro Arg Gln Trp Leu Thr Ser Gly Gly Leu	400
	405	410
Gly Thr Met Gly Phe Gly	Leu Pro Ala Ala Ile Gly Ala Ala Leu Ala	415
	420	425
Asn Pro Asp Arg Lys Val	Leu Cys Phe Ser Gly Asp Gly Ser Leu Met	430
	435	440
Met Asn Ile Gln Glu Met	Ala Thr Ala Ser Glu Asn Gln Leu Asp Val	445
	450	455
Lys Ile Ile Leu Met Asn	Asn Glu Ala Leu Gly Leu Val His Gln Gln	460
465	470	475
Gln Ser Leu Phe Tyr Glu	Gln Gly Val Phe Ala Ala Thr Tyr Pro Gly	480
	485	490
Lys Ile Asn Phe Met Gln	Ile Ala Ala Gly Phe Gly Leu Glu Thr Cys	495
	500	505
Asp Leu Asn Asn Glu Ala	Asp Pro Gln Ala Ser Leu Gln Glu Ile Ile	510
	515	520
Asn Arg Pro Gly Pro Ala	Leu Ile His Val Arg Ile Asp Ala Glu Glu	525
	530	535
		540

Lys Val Tyr Pro Met Val Pro Pro Gly Ala Ala Asn Thr Glu Met Val
 545 550 555 560
 Gly Glu

<210> 364
 <211> 32
 <212> PRT
 <213> Escherichia coli

<400> 364
 Met Thr Thr Ser Met Leu Asn Ala Lys Leu Leu Pro Thr Ala Pro Ser
 1 5 10 15
 Ala Ala Val Val Val Arg Val Val Val Val Gly Asn Ala Pro
 20 25 30

<210> 365
 <211> 338
 <212> PRT
 <213> Escherichia coli

<400> 365
 Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln
 1 5 10 15
 Leu Thr Phe Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg
 20 25 30
 Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn
 35 40 45
 Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg
 50 55 60
 Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His
 65 70 75 80
 Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile
 85 90 95
 Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro
 100 105 110
 Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln
 115 120 125
 Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala
 130 135 140
 Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu
 145 150 155 160
 Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met
 165 170 175
 His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His
 180 185 190
 Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr
 195 200 205
 Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly
 210 215 220
 Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln
 225 230 235 240
 Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg
 245 250 255
 Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr
 260 265 270
 Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu
 275 280 285
 His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg

290 295 300
 Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr
 305 310 315 320
 Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg
 325 330 335
 Ser His

<210> 366
 <211> 157
 <212> PRT
 <213> Escherichia coli

<400> 366
 Met Val Tyr Ile Ile Ile Val Ser His Gly His Glu Asp Tyr Ile Lys
 1 5 10 15
 Lys Leu Leu Glu Asn Leu Asn Ala Asp Asp Glu His Tyr Lys Ile Ile
 20 25 30
 Val Arg Asp Asn Lys Asp Ser Leu Leu Lys Gln Ile Cys Gln His
 35 40 45
 Tyr Ala Gly Leu Asp Tyr Ile Ser Gly Gly Val Tyr Gly Phe Gly His
 50 55 60
 Asn Asn Asn Ile Ala Val Ala Tyr Val Lys Glu Lys Tyr Arg Pro Ala
 65 70 75 80
 Asp Asp Asp Tyr Ile Leu Phe Leu Asn Pro Asp Ile Ile Met Lys His
 85 90 95
 Asp Asp Leu Leu Thr Tyr Ile Lys Tyr Val Glu Ser Lys Arg Tyr Ala
 100 105 110
 Phe Ser Thr Leu Cys Leu Phe Arg Asp Glu Ala Lys Ser Leu His Asp
 115 120 125
 Tyr Ser Val Arg Lys Phe Pro Val Leu Ser Asp Phe Ile Val Ser Phe
 130 135 140
 Met Leu Gly Ile Lys Glu Gly Ala Asn Lys Ser Leu Ile
 145 150 155

<210> 367
 <211> 372
 <212> PRT
 <213> Escherichia coli

<400> 367
 Met Gly Lys Ser Ile Val Val Val Ser Ala Val Asn Phe Thr Thr Gly
 1 5 10 15
 Gly Pro Phe Thr Ile Leu Lys Lys Phe Leu Ala Ala Thr Asn Asn Lys
 20 25 30
 Glu Asn Val Ser Phe Ile Ala Leu Val His Ser Ala Lys Glu Leu Lys
 35 40 45
 Glu Ser Tyr Pro Trp Val Lys Phe Ile Glu Phe Pro Glu Val Lys Gly
 50 55 60
 Ser Trp Leu Lys Arg Leu His Phe Glu Tyr Val Val Cys Lys Lys Leu
 65 70 75 80
 Ser Lys Glu Leu Asn Ala Thr His Trp Ile Cys Leu His Asp Ile Thr
 85 90 95
 Ala Asn Val Val Thr Lys Lys Arg Tyr Val Tyr Cys His Asn Pro Ala
 100 105 110
 Pro Phe Tyr Lys Gly Ile Leu Phe Arg Glu Ile Leu Met Glu Pro Ser
 115 120 125
 Phe Phe Leu Phe Lys Met Leu Tyr Gly Leu Ile Tyr Lys Ile Asn Ile
 130 135 140

Lys Lys Asn Thr Ala Val Phe Val Gln Gln Phe Trp Met Lys Glu Lys
 145 150 155 160
 Phe Ile Lys Lys Tyr Ser Ile Asn Asn Ile Ile Val Ser Arg Pro Glu
 165 170 175
 Ile Lys Leu Ser Asp Lys Ser Gln Leu Thr Asp Asp Asp Ser Gln Phe
 180 185 190
 Lys Asn Asn Pro Ser Glu Leu Thr Ile Phe Tyr Pro Ala Val Pro Arg
 195 200 205
 Val Phe Lys Asn Tyr Glu Leu Ile Ile Ser Ala Ala Arg Lys Leu Lys
 210 215 220
 Glu Gln Ser Asn Ile Lys Phe Leu Leu Thr Ile Ser Gly Thr Glu Asn
 225 230 235 240
 Ala Tyr Ala Lys Tyr Ile Ile Ser Leu Ala Glu Gly Leu Asp Asn Val
 245 250 255
 His Phe Leu Gly Tyr Leu Asp Lys Glu Lys Ile Asp His Cys Tyr Asn
 260 265 270
 Ile Ser Asp Ile Val Cys Phe Pro Ser Arg Leu Glu Thr Trp Gly Leu
 275 280 285
 Pro Leu Ser Glu Ala Lys Glu Arg Gly Lys Trp Val Leu Ala Ser Asp
 290 295 300
 Phe Pro Phe Thr Arg Glu Thr Leu Gly Ser Tyr Glu Lys Lys Ala Phe
 305 310 315 320
 Phe Asp Ser Asn Asn Asp Asp Met Leu Val Lys Leu Ile Ile Asp Phe
 325 330 335
 Lys Lys Gly Asn Leu Lys Lys Asp Ile Ser Asp Ala Asn Phe Ile Tyr
 340 345 350
 Arg Asn Glu Asn Val Leu Val Gly Phe Asp Glu Leu Val Asn Phe Ile
 355 360 365
 Thr Glu Glu His
 370

<210> 368

<211> 196

<212> PRT

<213> Escherichia coli

<400> 368

Met Ile Leu Lys Leu Ala Lys Arg Tyr Gly Leu Cys Gly Phe Ile Arg
 1 5 10 15
 Leu Val Arg Asp Val Leu Leu Thr Arg Val Phe Tyr Arg Asn Cys Arg
 20 25 30
 Ile Ile Arg Phe Pro Cys Tyr Ile Arg Asn Asp Gly Ser Ile Asn Phe
 35 40 45
 Gly Glu Asn Phe Thr Ser Gly Val Gly Leu Arg Leu Asp Ala Phe Gly
 50 55 60
 Arg Gly Val Ile Phe Phe Ser Asp Asn Val Gln Val Asn Asp Tyr Val
 65 70 75 80
 His Ile Ala Ser Ile Glu Ser Val Thr Ile Gly Arg Asp Thr Leu Ile
 85 90 95
 Ala Ser Lys Val Phe Ile Thr Asp His Asn His Gly Ser Phe Lys His
 100 105 110
 Ser Asp Pro Met Ser Ser Pro Asn Ile Pro Pro Asp Met Arg Thr Leu
 115 120 125
 Glu Ser Ser Ala Val Val Ile Gly Gln Arg Val Trp Leu Gly Glu Asn
 130 135 140
 Val Thr Val Leu Pro Gly Thr Ile Ile Gly Asn Gly Val Val Val Gly
 145 150 155 160
 Ala Asn Ser Val Val Arg Gly Ser Ile Pro Glu Asn Thr Val Ile Ala
 165 170 175
 Gly Val Pro Ala Lys Ile Ile Lys Lys Tyr Asn His Glu Thr Lys Leu

180
Trp Glu Lys Ala
195

185

190

<210> 369
<211> 330
<212> PRT
<213> Escherichia coli

<400> 369
Met Tyr Phe Leu Asn Asp Leu Asn Phe Ser Arg Arg Asp Ala Gly Phe
1 5 10 15
Lys Ala Arg Lys Asp Ala Leu Asp Ile Ala Ser Asp Tyr Glu Asn Ile
20 25 30
Ser Val Val Asn Ile Pro Leu Trp Gly Gly Val Val Gln Arg Ile Ile
35 40 45
Ser Ser Val Lys Leu Ser Thr Phe Leu Cys Gly Leu Glu Asn Lys Asp
50 55 60
Val Leu Ile Phe Asn Phe Pro Met Ala Lys Pro Phe Trp His Ile Leu
65 70 75 80
Ser Phe Phe His Arg Leu Leu Lys Phe Arg Ile Val Pro Leu Ile His
85 90 95
Asp Ile Asp Glu Leu Arg Gly Gly Gly Gly Ser Asp Ser Val Arg Leu
100 105 110
Ala Thr Cys Asp Met Val Ile Ser His Asn Pro Gln Met Thr Lys Tyr
115 120 125
Leu Ser Lys Tyr Met Ser Gln Asp Lys Ile Lys Asp Ile Lys Ile Phe
130 135 140
Asp Tyr Leu Val Ser Ser Asp Val Glu His Arg Asp Val Thr Asp Lys
145 150 155 160
Gln Arg Gly Val Ile Tyr Ala Gly Asn Leu Ser Arg His Lys Cys Ser
165 170 175
Phe Ile Tyr Thr Glu Gly Cys Asp Phe Thr Leu Phe Gly Val Asn Tyr
180 185 190
Glu Asn Lys Asp Asn Pro Lys Tyr Leu Gly Ser Phe Asp Ala Gln Ser
195 200 205
Pro Glu Lys Ile Asn Leu Pro Gly Met Gln Phe Gly Leu Ile Trp Asp
210 215 220
Gly Asp Ser Val Glu Thr Cys Ser Gly Ala Phe Gly Asp Tyr Leu Lys
225 230 235 240
Phe Asn Asn Pro His Lys Thr Ser Leu Tyr Leu Ser Met Glu Leu Pro
245 250 255
Val Phe Ile Trp Asp Lys Ala Ala Leu Ala Asp Phe Ile Val Asp Asn
260 265 270
Arg Ile Gly Tyr Ala Val Gly Ser Ile Lys Glu Met Gln Glu Ile Val
275 280 285
Asp Ser Met Thr Ile Glu Thr Tyr Lys Gln Ile Ser Glu Asn Thr Lys
290 295 300
Ile Ile Ser Gln Lys Ile Arg Thr Gly Ser Tyr Phe Arg Asp Val Leu
305 310 315 320
Glu Glu Val Ile Asp Asp Leu Lys Thr Arg
325 330

<210> 370
<211> 388
<212> PRT
<213> Escherichia coli

<400> 370

Met Ile Tyr Leu Val Ile Ser Val Phe Leu Ile Thr Ala Phe Ile Cys
 1 5 10 15
 Leu Tyr Leu Lys Lys Asp Ile Phe Tyr Pro Ala Val Cys Val Asn Ile
 20 25 30
 Ile Phe Ala Leu Val Leu Leu Gly Tyr Glu Ile Thr Ser Asp Ile Tyr
 35 40 45
 Ala Phe Gln Leu Asn Asp Ala Thr Leu Ile Phe Leu Leu Cys Asn Val
 50 55 60
 Leu Thr Phe Thr Leu Ser Cys Leu Leu Thr Glu Ser Val Leu Asp Leu
 65 70 75 80
 Asn Ile Arg Lys Val Asn Asn Ala Ile Tyr Ser Ile Pro Ser Lys Lys
 85 90 95
 Val His Asn Val Gly Leu Leu Val Ile Ser Phe Ser Met Ile Tyr Ile
 100 105 110
 Cys Met Arg Leu Ser Asn Tyr Gln Phe Gly Thr Ser Leu Leu Ser Tyr
 115 120 125
 Met Asn Leu Ile Arg Asp Ala Asp Val Glu Asp Thr Ser Arg Asn Phe
 130 135 140
 Ser Ala Tyr Met Gln Pro Ile Ile Leu Thr Thr Phe Ala Leu Phe Ile
 145 150 155 160
 Trp Ser Lys Lys Phe Thr Asn Thr Lys Val Ser Lys Thr Phe Thr Leu
 165 170 175
 Leu Val Phe Ile Val Phe Ile Phe Ala Ile Ile Leu Asn Thr Gly Lys
 180 185 190
 Gln Ile Val Phe Met Val Ile Ile Ser Tyr Ala Phe Ile Val Gly Val
 195 200 205
 Asn Arg Val Lys His Tyr Val Tyr Leu Ile Thr Ala Val Gly Val Leu
 210 215 220
 Phe Ser Leu Tyr Met Leu Phe Leu Arg Gly Leu Pro Gly Gly Met Ala
 225 230 235 240
 Tyr Tyr Leu Ser Met Tyr Leu Val Ser Pro Ile Ile Ala Phe Gln Glu
 245 250 255
 Phe Tyr Phe Gln Val Ser Asn Ser Ala Ser Ser His Val Phe Trp
 260 265 270
 Phe Phe Glu Arg Leu Met Gly Leu Leu Thr Gly Gly Val Ser Met Ser
 275 280 285
 Leu His Lys Glu Phe Val Trp Val Gly Leu Pro Thr Asn Val Tyr Thr
 290 295 300
 Ala Phe Ser Asp Tyr Val Tyr Ile Ser Ala Glu Leu Ser Tyr Leu Met
 305 310 315 320
 Met Val Ile His Gly Cys Ile Ser Gly Val Leu Trp Arg Leu Ser Arg
 325 330 335
 Asn Tyr Ile Ser Val Lys Ile Phe Tyr Ser Tyr Phe Ile Tyr Thr Phe
 340 345 350
 Ser Phe Ile Phe Tyr His Glu Ser Phe Met Thr Asn Ile Ser Ser Trp
 355 360 365
 Ile Gln Ile Thr Leu Cys Ile Ile Val Phe Ser Gln Phe Leu Lys Ala
 370 375 380
 Gln Lys Ile Lys
 385

<210> 371

<211> 367

<212> PRT

<213> Escherichia coli

<400> 371

Met Tyr Asp Tyr Ile Ile Val Gly Ser Gly Leu Phe Gly Ala Val Cys
 1 5 10 15
 Ala Asn Glu Leu Lys Lys Leu Asn Lys Lys Val Leu Val Ile Glu Lys

```
<210> 372
<211> 230
<212> PRT
<213> Escherichia coli
```

<400> 372																
Met	Thr	Ser	Ser	Ile	Thr	Asn	Glu	Ile	Met	Gln	Leu	Tyr	Thr	Asp	Arg	
1	4			5					10					15		
Glu	Val	Leu	Asn	Met	Gly	Leu	Cys	Ser	Arg	Tyr	Lys	Ser	Leu	Thr	Cys	
			20					25					30			
Asn	Ser	Cys	Ser	Met	His	Cys	Gln	Ile	Met	Pro	Glu	Glu	Ser	Pro	Arg	
		35					40					45				
Leu	Gln	Tyr	Cys	Ala	Asn	Ser	Cys	Phe	Cys	Met	Trp	Pro	Glu	Glu	Ser	
	50					55					60					
Ser	Tyr	Phe	Asn	Arg	Gly	Val	Val	Glu	Gly	Ile	Leu	Thr	Lys	Asn	His	
65					70					75					80	

```

Asn Ala Arg Leu Ser Gly Tyr Ile Phe Val Asp Phe Ser Val Ser Phe
      85                      90                      95
Leu Arg Leu Phe Leu Glu Lys Asp Trp Ile Asp Tyr Leu Ala Ser Thr
      100                    105                    110
Asp Met Gly Ile Val Leu Val Ser Asp Arg Asn Met Gln Ser Leu Ala
      115                    120                    125
Asn Tyr Trp Arg Lys His Asn Ser Ala Ile Ser Ala Val Ile Tyr Asn
      130                    135                    140
Asp Asp Gly Leu Asp Val Ala Asn Glu Lys Ile Arg Gln Leu Phe Ile
      145                    150                    155                    160
Gly Arg Tyr Leu Ser Phe Thr Gly Gly Asn Thr Leu Thr Gln Met Glu
      165                    170                    175
Phe Thr Ile Met Gly Tyr Met Val Ser Gly Tyr Asn Pro Tyr Gln Ile
      180                    185                    190
Ala Glu Val Leu Asp Met Asp Ile Arg Ser Ile Tyr Ala Tyr Lys Gln
      195                    200                    205
Arg Ile Glu Lys Arg Met Gly Gly Lys Ile Asn Glu Leu Phe Ile Arg
      210                    215                    220
Ser His Ser Val Gln His
      225                    230

```

<210> 373

<211> 391

<212> PRT

<213> Escherichia coli

<400> 373

```

Met Gln Lys Leu Ile Asn Ser Val Gln Asn Tyr Ala Trp Gly Ser Lys
  1                      5                      10                      15
Thr Ala Leu Thr Glu Leu Tyr Gly Met Glu Asn Pro Ser Ser Gln Pro
      20                    25
Met Ala Glu Leu Trp Met Gly Ala His Pro Lys Ser Ser Arg Val
      35                    40                    45
Gln Asn Ala Ala Gly Asp Ile Val Ser Leu Arg Asp Val Ile Glu Ser
      50                    55                    60
Asp Lys Ser Thr Leu Leu Gly Glu Ala Val Ala Lys Arg Phe Gly Glu
      65                    70                    75                    80
Leu Pro Phe Leu Phe Lys Val Leu Cys Ala Ala Gln Pro Leu Ser Ile
      85                    90                    95
Gln Val His Pro Asn Lys His Asn Ser Glu Ile Gly Phe Ala Lys Glu
      100                   105                   110
Asn Ala Ala Gly Ile Pro Met Asp Ala Ala Glu Arg Asn Tyr Lys Asp
      115                   120                   125
Pro Asn His Lys Pro Glu Leu Val Phe Ala Leu Thr Pro Phe Leu Ala
      130                   135                   140
Met Asn Ala Phe Arg Glu Phe Ser Glu Ile Val Ser Leu Leu Gln Pro
      145                   150                   155                    160
Val Ala Gly Ala His Pro Ala Ile Ala His Phe Leu Gln Gln Pro Asp
      165                   170                   175
Ala Glu Arg Leu Ser Glu Leu Phe Ala Ser Leu Leu Asn Met Gln Gly
      180                   185                   190
Glu Glu Lys Ser Arg Ala Leu Ala Ile Leu Lys Ser Ala Leu Asp Ser
      195                   200                   205
Gln Gln Gly Glu Pro Trp Gln Thr Ile Arg Leu Ile Ser Glu Phe Tyr
      210                   215                   220
Pro Glu Asp Ser Gly Leu Phe Ser Pro Leu Leu Asn Val Val Lys
      225                   230                   235                    240
Leu Asn Pro Gly Glu Ala Met Phe Leu Phe Ala Glu Thr Pro His Ala
      245                   250                   255
Tyr Leu Gln Gly Val Ala Leu Glu Val Met Ala Asn Ser Asp Asn Val

```

```

      260      265      270
Leu Arg Ala Gly Leu Thr Pro Lys Tyr Ile Asp Ile Pro Glu Leu Val
      275      280      285
Ala Asn Val Lys Phe Glu Ala Lys Pro Ala Asn Gln Leu Leu Thr Gln
      290      295      300
Pro Val Lys Gln Gly Ala Glu Leu Asp Phe Pro Ile Pro Val Asp Asp
      305      310      315      320
Phe Ala Phe Ser Leu His Asp Leu Ser Asp Lys Glu Thr Thr Ile Ser
      325      330      335
Gln Gln Ser Ala Ala Ile Leu Phe Cys Val Glu Gly Asp Ala Thr Leu
      340      345      350
Trp Lys Gly Ser Gln Gln Leu Gln Leu Lys Pro Gly Glu Ser Ala Phe
      355      360      365
Ile Ala Ala Asn Glu Ser Pro Val Thr Val Lys Gly His Gly Arg Leu
      370      375      380
Ala Arg Val Tyr Asn Lys Leu
      385      390

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<210> 374

<211> 264

<212> PRT

<213> Escherichia coli

<400> 374

```

Met Lys Gln Tyr Leu Glu Leu Met Gln Lys Val Leu Asp Glu Gly Thr
  1      5      10      15
Gln Lys Asn Asp Arg Thr Gly Thr Gly Thr Leu Ser Ile Phe Gly His
      20      25      30
Gln Met Arg Phe Asn Leu Gln Asp Gly Phe Pro Leu Val Thr Thr Lys
      35      40      45
Arg Cys His Leu Arg Ser Ile Ile His Glu Leu Leu Trp Phe Leu Gln
      50      55      60
Gly Asp Thr Asn Ile Ala Tyr Leu His Glu Asn Asn Val Thr Ile Trp
      65      70      75      80
Asp Glu Trp Ala Asp Glu Asn Gly Asp Leu Gly Pro Val Tyr Gly Lys
      85      90      95
Gln Trp Arg Ala Trp Pro Thr Pro Asp Gly Arg His Ile Asp Gln Ile
      100      105      110
Thr Thr Val Leu Asn Gln Leu Lys Asn Asp Pro Asp Ser Arg Arg Ile
      115      120      125
Ile Val Ser Ala Trp Asn Val Gly Glu Leu Asp Lys Met Ala Leu Ala
      130      135      140
Pro Cys His Ala Phe Phe Gln Phe Tyr Val Ala Asp Gly Lys Leu Ser
      145      150      155      160
Cys Gln Leu Tyr Gln Arg Ser Cys Asp Val Phe Leu Gly Leu Pro Phe
      165      170      175
Asn Ile Ala Ser Tyr Ala Leu Leu Val His Met Met Ala Gln Gln Cys
      180      185      190
Asp Leu Glu Val Gly Asp Phe Val Trp Thr Gly Gly Asp Thr His Leu
      195      200      205
Tyr Ser Asn His Met Asp Gln Thr His Leu Gln Leu Ser Arg Glu Pro
      210      215      220
Arg Pro Leu Pro Lys Leu Ile Ile Lys Arg Lys Pro Glu Ser Ile Phe
      225      230      235      240
Asp Tyr Arg Phe Glu Asp Phe Glu Ile Glu Gly Tyr Asp Pro His Pro
      245      250      255
Gly Ile Lys Ala Pro Val Ala Ile
      260

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<210> 375
 <211> 291
 <212> PRT
 <213> Escherichia coli

<400> 375
 Met Thr Ser Ser Tyr Leu His Phe Pro Glu Phe Asp Pro Val Ile Phe
 1 5 10 15
 Ser Ile Gly Pro Val Ala Leu His Trp Tyr Gly Leu Met Tyr Leu Val
 20 25 30
 Gly Phe Ile Phe Ala Met Trp Leu Ala Thr Arg Arg Ala Asn Arg Pro
 35 40 45
 Gly Ser Gly Trp Thr Lys Asn Glu Val Glu Asn Leu Leu Tyr Ala Gly
 50 55 60
 Phe Leu Gly Val Phe Leu Gly Gly Arg Ile Gly Tyr Val Leu Phe Tyr
 65 70 75 80
 Asn Phe Pro Gln Phe Met Ala Asp Pro Leu Tyr Leu Phe Arg Val Trp
 85 90 95
 Asp Gly Gly Met Ser Phe His Gly Gly Leu Ile Gly Val Ile Val Val
 100 105 110
 Met Ile Ile Phe Ala Arg Arg Thr Lys Arg Ser Phe Phe Gln Val Ser
 115 120 125
 Asp Phe Ile Ala Pro Leu Ile Pro Phe Gly Leu Gly Ala Gly Arg Leu
 130 135 140
 Gly Asn Phe Ile Asn Gly Glu Leu Trp Gly Arg Val Asp Pro Asn Phe
 145 150 155 160
 Pro Phe Ala Met Leu Phe Pro Gly Ser Arg Thr Glu Asp Ile Leu Leu
 165 170 175
 Leu Gln Thr Asn Pro Gln Trp Gln Ser Ile Phe Asp Thr Tyr Gly Val
 180 185 190
 Leu Pro Arg His Pro Ser Gln Leu Tyr Glu Leu Leu Leu Glu Gly Val
 195 200 205
 Val Leu Phe Ile Ile Leu Asn Leu Tyr Ile Arg Lys Pro Arg Pro Met
 210 215 220
 Gly Ala Val Ser Gly Leu Phe Leu Ile Gly Tyr Gly Ala Phe Arg Ile
 225 230 235 240
 Ile Val Glu Phe Phe Arg Gln Pro Asp Ala Gln Phe Thr Gly Ala Trp
 245 250 255
 Val Gln Tyr Ile Ser Met Gly Gln Ile Leu Ser Ile Pro Met Ile Val
 260 265 270
 Ala Gly Val Ile Met Met Val Trp Ala Tyr Arg Arg Ser Pro Gln Gln
 275 280 285
 His Val Ser
 290

<210> 376
 <211> 241
 <212> PRT
 <213> Escherichia coli

<400> 376
 Met Asp Ser Leu Asn Leu Asn Lys His Ile Ser Gly Gln Phe Asn Ala
 1 5 10 15
 Glu Leu Glu Ser Ile Arg Thr Gln Val Met Thr Met Gly Gly Met Val
 20 25 30
 Glu Gln Gln Leu Ser Asp Ala Ile Thr Ala Met His Asn Gln Asp Ser
 35 40 45
 Asp Leu Ala Lys Arg Val Ile Glu Gly Asp Lys Asn Val Asn Met Met
 50 55 60
 Glu Val Ala Ile Asp Glu Ala Cys Val Arg Ile Ile Ala Lys Arg Gln

```

65          70          75          80
Pro Thr Ala Ser Asp Leu Arg Leu Val Met Val Ile Ser Lys Thr Ile
          85          90          95
Ala Glu Leu Glu Arg Ile Gly Asp Val Ala Asp Lys Ile Cys Arg Thr
          100          105          110
Ala Leu Glu Lys Phe Ser Gln Gln His Gln Pro Leu Leu Val Ser Leu
          115          120          125
Glu Ser Leu Gly Arg His Thr Ile Gln Met Leu His Asp Val Leu Asp
          130          135          140
Ala Phe Ala Arg Met Asp Ile Asp Glu Ala Val Arg Ile Tyr Arg Glu
          145          150          155          160
Asp Lys Lys Val Asp Gln Glu Tyr Glu Gly Ile Val Arg Gln Leu Met
          165          170          175
Thr Tyr Met Met Glu Asp Ser Arg Thr Ile Pro Ser Val Leu Thr Ala
          180          185          190
Leu Phe Cys Ala Arg Ser Ile Glu Arg Ile Gly Asp Arg Cys Gln Asn
          195          200          205
Ile Cys Glu Phe Ile Phe Tyr Tyr Val Lys Gly Gln Asp Phe Arg His
          210          215          220
Val Gly Gly Asp Glu Leu Asp Lys Leu Leu Ala Gly Lys Asp Ser Asp
          225          230          235          240
Lys

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<210> 377

<211> 257

<212> PRT

<213> Escherichia coli

<400> 377

```

Met Ser Met Val Glu Thr Ala Pro Ser Lys Ile Gln Val Arg Asn Leu
1          5          10          15
Asn Phe Tyr Tyr Gly Lys Phe His Ala Leu Lys Asn Ile Asn Leu Asp
          20          25          30
Ile Ala Lys Asn Gln Val Thr Ala Phe Ile Gly Pro Ser Gly Cys Gly
          35          40          45
Lys Ser Thr Leu Leu Arg Thr Phe Asn Lys Met Phe Glu Leu Tyr Pro
          50          55          60
Glu Gln Arg Ala Glu Gly Glu Ile Leu Leu Asp Gly Asp Asn Ile Leu
65          70          75          80
Thr Asn Ser Gln Asp Ile Ala Leu Leu Arg Ala Lys Val Gly Met Val
          85          90          95
Phe Gln Lys Pro Thr Pro Phe Pro Met Ser Ile Tyr Asp Asn Ile Ala
          100          105          110
Phe Gly Val Arg Leu Phe Glu Lys Leu Ser Arg Ala Asp Met Asp Glu
          115          120          125
Arg Val Gln Trp Ala Leu Thr Lys Ala Ala Leu Trp Asn Glu Thr Lys
          130          135          140
Asp Lys Leu His Gln Ser Gly Tyr Ser Leu Ser Gly Gly Gln Gln Gln
          145          150          155          160
Arg Leu Cys Ile Ala Arg Gly Ile Ala Ile Arg Pro Glu Val Leu Leu
          165          170          175
Leu Asp Glu Pro Cys Ser Ala Leu Asp Pro Ile Ser Thr Gly Arg Ile
          180          185          190
Glu Glu Leu Ile Thr Glu Leu Lys Gln Asp Tyr Thr Val Val Ile Val
          195          200          205
Thr His Asn Met Gln Gln Ala Ala Arg Cys Ser Asp His Thr Ala Phe
          210          215          220
Met Tyr Leu Gly Glu Leu Ile Glu Phe Ser Asn Thr Asp Asp Leu Phe
          225          230          235          240

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Thr Lys Pro Ala Lys Lys Gln Thr Glu Asp Tyr Ile Thr Gly Arg Tyr
 245 250 255
 Gly

<210> 378

<211> 296

<212> PRT

<213> Escherichia coli

<400> 378

Met Ala Met Val Glu Met Gln Thr Thr Ala Ala Leu Ala Glu Ser Arg
 1 5 10 15
 Arg Lys Met Gln Ala Arg Arg Arg Leu Lys Asn Arg Ile Ala Leu Thr
 20 25 30
 Leu Ser Met Ala Thr Met Ala Phe Gly Leu Phe Trp Leu Ile Trp Ile
 35 40 45
 Leu Met Ser Thr Ile Thr Arg Gly Ile Asp Gly Met Ser Leu Ala Leu
 50 55 60
 Phe Thr Glu Met Thr Pro Pro Pro Asn Thr Glu Gly Gly Gly Leu Ala
 65 70 75 80
 Asn Ala Leu Ala Gly Ser Gly Leu Leu Ile Leu Trp Ala Thr Val Phe
 85 90 95
 Gly Thr Pro Leu Gly Ile Met Ala Gly Ile Tyr Leu Ala Glu Tyr Gly
 100 105 110
 Arg Lys Ser Trp Leu Ala Glu Val Ile Arg Phe Ile Asn Asp Ile Leu
 115 120 125
 Leu Ser Ala Pro Ser Ile Val Val Gly Leu Phe Val Tyr Thr Ile Val
 130 135 140
 Val Ala Gln Met Glu His Phe Ser Gly Trp Ala Gly Val Ile Ala Leu
 145 150 155 160
 Ala Leu Leu Gln Val Pro Ile Val Ile Arg Thr Thr Glu Asn Met Leu
 165 170 175
 Lys Leu Val Pro Tyr Ser Leu Arg Glu Ala Ala Tyr Ala Leu Gly Thr
 180 185 190
 Pro Lys Trp Lys Met Ile Ser Ala Ile Thr Leu Lys Ala Ser Val Ser
 195 200 205
 Gly Ile Met Thr Gly Ile Leu Leu Ala Ile Ala Arg Ile Ala Gly Glu
 210 215 220
 Thr Ala Pro Leu Leu Phe Thr Ala Leu Ser Asn Gln Phe Trp Ser Thr
 225 230 235 240
 Asp Met Met Gln Pro Ile Ala Asn Leu Pro Val Thr Ile Phe Lys Phe
 245 250 255
 Ala Met Ser Pro Phe Ala Glu Trp Gln Gln Leu Ala Trp Ala Gly Val
 260 265 270
 Leu Ile Ile Thr Leu Cys Val Leu Leu Leu Asn Ile Leu Ala Arg Val
 275 280 285
 Val Phe Ala Lys Asn Lys His Gly
 290 295

<210> 379

<211> 319

<212> PRT

<213> Escherichia coli

<400> 379

Met Ala Ala Thr Lys Pro Ala Phe Asn Pro Pro Gly Lys Lys Gly Asp
 1 5 10 15
 Ile Ile Phe Ser Val Leu Val Lys Leu Ala Ala Leu Ile Val Leu Leu

```

      20      25      30
Met Leu Gly Gly Ile Ile Val Ser Leu Ile Ile Ser Ser Trp Pro Ser
  35      40      45
Ile Gln Lys Phe Gly Leu Ala Phe Leu Trp Thr Lys Glu Trp Asp Ala
  50      55      60
Pro Asn Asp Ile Tyr Gly Ala Leu Val Pro Ile Tyr Gly Thr Leu Val
  65      70      75      80
Thr Ser Phe Ile Ala Leu Leu Ile Ala Val Pro Val Ser Phe Gly Ile
      85      90      95
Ala Leu Phe Leu Thr Glu Leu Ala Pro Gly Trp Leu Lys Arg Pro Leu
      100      105      110
Gly Ile Ala Ile Glu Leu Leu Ala Ala Ile Pro Ser Ile Val Tyr Gly
      115      120      125
Met Trp Gly Leu Phe Ile Phe Ala Pro Leu Phe Ala Val Tyr Phe Gln
      130      135      140
Glu Pro Val Gly Asn Ile Met Ser Asn Ile Pro Ile Val Gly Ala Leu
      145      150      155      160
Phe Ser Gly Pro Ala Phe Gly Ile Gly Ile Leu Ala Ala Gly Val Ile
      165      170      175
Leu Ala Ile Met Ile Ile Pro Tyr Ile Ala Ala Val Met Arg Asp Val
      180      185      190
Phe Glu Gln Thr Pro Val Met Met Lys Glu Ser Ala Tyr Gly Ile Gly
      195      200      205
Cys Thr Thr Trp Glu Val Ile Trp Arg Ile Val Leu Pro Phe Thr Lys
      210      215      220
Asn Gly Val Ile Gly Gly Ile Met Leu Gly Leu Gly Arg Ala Leu Gly
      225      230      235      240
Glu Thr Met Ala Val Thr Phe Ile Ile Gly Asn Thr Tyr Gln Leu Asp
      245      250      255
Ser Ala Ser Leu Tyr Met Pro Gly Asn Ser Ile Thr Ser Ala Leu Ala
      260      265      270
Asn Glu Phe Ala Glu Ala Glu Ser Gly Leu His Val Ala Ala Leu Met
      275      280      285
Glu Leu Gly Leu Ile Leu Phe Val Ile Thr Phe Ile Val Leu Ala Ala
      290      295      300
Ser Lys Phe Met Ile Met Arg Leu Ala Lys Asn Glu Gly Ala Arg
      305      310      315

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<210> 380

<211> 346

<212> PRT

<213> Escherichia coli

<400> 380

```

Met Lys Val Met Arg Thr Thr Val Ala Thr Val Val Ala Ala Thr Leu
  1      5      10      15
Ser Met Ser Ala Phe Ser Val Phe Ala Glu Ala Ser Leu Thr Gly Ala
      20      25      30
Gly Ala Thr Phe Pro Ala Pro Val Tyr Ala Lys Trp Ala Asp Thr Tyr
      35      40      45
Gln Lys Glu Thr Gly Asn Lys Val Asn Tyr Gln Gly Ile Gly Ser Ser
      50      55      60
Gly Gly Val Lys Gln Ile Ile Ala Asn Thr Val Asp Phe Gly Ala Ser
      65      70      75      80
Asp Ala Pro Leu Ser Asp Glu Lys Leu Ala Gln Glu Gly Leu Phe Gln
      85      90      95
Phe Pro Thr Val Ile Gly Gly Val Val Leu Ala Val Asn Ile Pro Gly
      100      105      110
Leu Lys Ser Gly Glu Leu Val Leu Asp Gly Lys Thr Leu Gly Asp Ile
      115      120      125

```

Tyr Leu Gly Lys Ile Lys Lys Trp Asp Asp Glu Ala Ile Ala Lys Leu
 130 135 140
 Asn Pro Gly Leu Lys Leu Pro Ser Gln Asn Ile Ala Val Val Arg Arg
 145 150 155 160
 Ala Asp Gly Ser Gly Thr Ser Phe Val Phe Thr Ser Tyr Leu Ala Lys
 165 170 175
 Val Asn Glu Glu Trp Lys Asn Asn Val Gly Thr Gly Ser Thr Val Lys
 180 185 190
 Trp Pro Ile Gly Leu Gly Gly Lys Gly Asn Asp Gly Ile Ala Ala Phe
 195 200 205
 Val Gln Arg Leu Pro Gly Ala Ile Gly Tyr Val Glu Tyr Ala Tyr Ala
 210 215 220
 Lys Gln Asn Asn Leu Ala Tyr Thr Lys Leu Ile Ser Ala Asp Gly Lys
 225 230 235 240
 Pro Val Ser Pro Thr Glu Glu Asn Phe Ala Asn Ala Ala Lys Gly Ala
 245 250 255
 Asp Trp Ser Lys Thr Phe Ala Gln Asp Leu Thr Asn Gln Lys Gly Glu
 260 265 270
 Asp Ala Trp Pro Ile Thr Ser Thr Thr Phe Ile Leu Ile His Lys Asp
 275 280 285
 Gln Lys Lys Pro Glu Gln Gly Thr Glu Val Leu Lys Phe Phe Asp Trp
 290 295 300
 Ala Tyr Lys Thr Gly Ala Lys Gln Ala Asn Asp Leu Asp Tyr Ala Ser
 305 310 315 320
 Leu Pro Asp Ser Val Val Glu Gln Val Arg Ala Ala Trp Lys Thr Asn
 325 330 335
 Ile Lys Asp Ser Ser Gly Lys Pro Leu Tyr
 340 345

<210> 381

<211> 236

<212> PRT

<213> Escherichia coli

<400> 381

Met Gly Ser Gly Leu Val Asn Gly Gly Asp Tyr Phe Tyr Asn Asn Leu
 1 5 10 15
 Ser Phe Thr Val Thr Arg Tyr Asn Gly Ile Met Ala Thr Asp Ser Thr
 20 25 30
 Gln Cys Val Lys Lys Ser Arg Gly Arg Pro Lys Val Phe Asp Arg Asp
 35 40 45
 Ala Ala Leu Asp Lys Ala Met Lys Leu Phe Trp Gln His Gly Tyr Glu
 50 55 60
 Ala Thr Ser Leu Ala Asp Leu Val Glu Ala Thr Gly Ala Lys Ala Pro
 65 70 75 80
 Thr Leu Tyr Ala Glu Phe Thr Asn Lys Glu Gly Leu Phe Arg Ala Val
 85 90 95
 Leu Asp Arg Tyr Ile Asp Arg Phe Ala Ala Lys His Glu Ala Gln Leu
 100 105 110
 Phe Cys Glu Glu Lys Ser Val Glu Ser Ala Leu Ala Asp Tyr Phe Ala
 115 120 125
 Ala Ile Ala Asn Cys Phe Thr Ser Lys Asp Thr Pro Ala Gly Cys Phe
 130 135 140
 Met Ile Asn Asn Cys Thr Thr Leu Ser Pro Asp Ser Gly Asp Ile Ala
 145 150 155 160
 Asn Thr Leu Lys Ser Arg His Ala Met Gln Glu Arg Thr Leu Gln Gln
 165 170 175
 Phe Leu Cys Gln Arg Gln Ala Arg Gly Glu Ile Pro Pro His Cys Asp
 180 185 190
 Val Thr His Leu Ala Glu Phe Leu Asn Cys Ile Ile Gln Gly Met Ser

195	200	205
Ile Ser Ala Arg Glu Gly	Ala Ser Leu Glu Lys	Leu Met Gln Ile Ala
210	215	220
Gly Thr Thr Leu Arg Leu Trp	Pro Glu Leu Val Lys	
225	230	235

<210> 382

<211> 181

<212> PRT

<213> Escherichia coli

<400> 382

Met Gln Ala Lys	Ile Ala Ala	Ser Asn Thr	Gly Glu Leu	Asp Ala Leu
1	5	10	15	
Gln Gln Leu Gly	Phe Ser Leu Val	Glu Gly Glu Val	Asp Leu Ala Leu	
20	25	30		
Pro Val Asn Asn	Ala Ser Asp	Ser Gly Ala Val	Val Ala Gln Glu Thr	
35	40	45		
Asp Ile Pro Ala	Leu Arg Gln	Leu Ala Ser Ala	Ala Phe Ala Gln Ser	
50	55	60		
Arg Phe Arg Ala	Pro Trp Tyr	Ala Pro Asp Ala	Ser Ser Arg Phe Tyr	
65	70	75	80	
Ala Gln Trp Ile	Glu Asn Ala Val	Arg Gly Thr Phe	Asp His Gln Cys	
85	90	95		
Leu Ile Leu Arg	Ala Ala Ser Gly	Asp Ile Arg Gly	Tyr Val Ser Leu	
100	105	110		
Arg Glu Leu Asn	Ala Thr Asp	Ala Arg Ile Gly	Leu Leu Ala Gly Arg	
115	120	125		
Gly Ala Gly Ala	Glu Leu Met Gln	Thr Ala Leu Asn	Trp Ala Tyr Arg	
130	135	140		
Arg Gly Lys Thr	Thr Leu Arg Val	Ala Thr Gln Met	Gly Asn Thr Ala	
145	150	155	160	
Ala Leu Lys Arg	Tyr Ile Gln Ser	Gly Ala Asn Val	Glu Ser Thr Ala	
165	170	175		
Tyr Trp Leu Tyr	Arg			
180				

<210> 383

<211> 376

<212> PRT

<213> Escherichia coli

<400> 383

Met Ile Pro Phe	Asn Ala Pro	Pro Val Val	Gly Thr Glu	Leu Asp Tyr
1	5	10	15	
Met Gln Ser Ala	Met Gly Ser Gly	Lys Leu Cys Gly	Asp Gly Gly Phe	
20	25	30		
Thr Arg Arg Cys	Gln Gln Trp	Leu Glu Gln Arg	Phe Gly Ser Ala Lys	
35	40	45		
Val Leu Leu Thr	Pro Ser Cys Thr	Ala Ser Leu Glu	Met Ala Ala Leu	
50	55	60		
Leu Leu Asp Ile	Gln Pro Gly Asp	Glu Val Ile Met	Pro Ser Tyr Thr	
65	70	75	80	
Phe Val Ser Thr	Ala Asn Ala Phe	Val Leu Arg Gly	Ala Lys Ile Val	
85	90	95		
Phe Val Asp Val	Arg Pro Asp Thr	Met Asn Ile Asp	Glu Thr Leu Ile	
100	105	110		
Glu Ala Ala Ile	Thr Asp Lys Thr	Arg Val Ile Val	Pro Val His Tyr	
115	120	125		

Ala Gly Val Ala Cys Glu Met Asp Thr Ile Met Ala Leu Ala Lys Lys
 130 135 140
 His Asn Leu Phe Val Val Glu Asp Ala Ala Gln Gly Val Met Ser Thr
 145 150 155 160
 Tyr Lys Gly Arg Ala Leu Gly Thr Ile Gly His Ile Gly Cys Phe Ser
 165 170 175
 Phe His Glu Thr Lys Asn Tyr Thr Ala Gly Gly Glu Gly Gly Ala Thr
 180 185 190
 Leu Ile Asn Asp Lys Ala Leu Ile Glu Arg Ala Glu Ile Ile Arg Glu
 195 200 205
 Lys Gly Thr Asn Arg Ser Gln Phe Phe Arg Gly Gln Val Asp Lys Tyr
 210 215 220
 Thr Trp Arg Asp Ile Gly Ser Ser Tyr Leu Met Ser Asp Leu Gln Ala
 225 230 235 240
 Ala Tyr Leu Trp Ala Gln Leu Glu Ala Ala Asp Arg Ile Asn Gln Gln
 245 250 255
 Arg Leu Ala Leu Trp Gln Asn Tyr Tyr Asp Ala Leu Ala Pro Leu Ala
 260 265 270
 Lys Ala Gly Arg Ile Glu Leu Pro Ser Ile Pro Asp Gly Cys Val Gln
 275 280 285
 Asn Ala His Met Phe Tyr Ile Lys Leu Arg Asp Ile Asp Asp Arg Ser
 290 295 300
 Ala Leu Ile Asn Phe Leu Lys Glu Ala Glu Ile Met Ala Val Phe His
 305 310 315 320
 Tyr Ile Pro Leu His Gly Cys Pro Ala Gly Glu His Phe Gly Glu Phe
 325 330 335
 His Gly Glu Asp Arg Tyr Thr Thr Lys Glu Ser Glu Arg Leu Leu Arg
 340 345 350
 Leu Pro Leu Phe Tyr Asn Leu Ser Pro Val Asn Gln Arg Thr Val Ile
 355 360 365
 Ala Thr Leu Leu Asn Tyr Phe Ser
 370 375

<210> 384

<211> 416

<212> PRT

<213> Escherichia coli

<400> 384

Met Ser Leu Ala Lys Ala Ser Leu Trp Thr Ala Ala Ser Thr Leu Val
 1 5 10 15
 Lys Ile Gly Ala Gly Leu Leu Val Gly Lys Leu Leu Ala Val Ser Phe
 20 25 30
 Gly Pro Ala Gly Leu Gly Leu Ala Ala Asn Phe Arg Gln Leu Ile Thr
 35 40 45
 Val Leu Gly Val Leu Ala Gly Ala Gly Ile Phe Asn Gly Val Thr Lys
 50 55 60
 Tyr Val Ala Gln Tyr His Asp Asn Pro Gln Gln Leu Arg Arg Val Val
 65 70 75 80
 Gly Thr Ser Ser Ala Met Val Leu Gly Phe Ser Thr Leu Met Ala Leu
 85 90 95
 Val Phe Val Leu Ala Ala Ala Pro Ile Ser Gln Gly Leu Phe Gly Asn
 100 105 110
 Thr Asp Tyr Gln Gly Leu Val Arg Leu Val Ala Leu Val Gln Met Gly
 115 120 125
 Ile Ala Trp Gly Asn Leu Leu Leu Ala Leu Met Lys Gly Phe Arg Asp
 130 135 140
 Ala Ala Gly Asn Ala Leu Ser Leu Ile Val Gly Ser Leu Ile Gly Val
 145 150 155 160
 Leu Ala Tyr Tyr Val Ser Tyr Arg Leu Gly Gly Tyr Glu Gly Ala Leu

```

      165      170      175
Leu Gly Leu Ala Leu Ile Pro Ala Leu Val Val Ile Pro Ala Ala Ile
      180      185      190
Met Leu Ile Lys Arg Gly Val Ile Pro Leu Ser Tyr Leu Lys Pro Ser
      195      200      205
Trp Asp Asn Gly Leu Ala Gly Gln Leu Ser Lys Phe Thr Leu Met Ala
      210      215      220
Leu Ile Thr Ser Val Thr Leu Pro Val Ala Tyr Ile Met Met Arg Lys
      225      230      235      240
Leu Leu Ala Ala Gln Tyr Ser Trp Asp Glu Val Gly Ile Trp Gln Gly
      245      250      255
Val Ser Ser Ile Ser Asp Ala Tyr Leu Gln Phe Ile Thr Ala Ser Phe
      260      265      270
Ser Val Tyr Leu Leu Pro Thr Leu Ser Arg Leu Thr Glu Lys Arg Asp
      275      280      285
Ile Thr Arg Glu Val Val Lys Ser Leu Lys Phe Val Leu Pro Ala Val
      290      295      300
Ala Ala Ala Ser Phe Thr Val Trp Leu Leu Arg Asp Phe Ala Ile Trp
      305      310      315      320
Leu Leu Leu Ser Asn Lys Phe Thr Ala Met Arg Asp Leu Phe Ala Trp
      325      330      335
Gln Leu Val Gly Asp Val Leu Lys Val Gly Ala Tyr Val Phe Gly Tyr
      340      345      350
Leu Val Ile Ala Lys Ala Ser Leu Arg Phe Tyr Ile Leu Ala Glu Val
      355      360      365
Ser Gln Phe Thr Leu Leu Met Val Phe Ala His Trp Leu Ile Pro Ala
      370      375      380
His Gly Ala Leu Gly Ala Ala Gln Ala Tyr Met Ala Thr Tyr Ile Val
      385      390      395      400
Tyr Phe Ser Leu Cys Cys Gly Val Phe Leu Leu Trp Arg Arg Arg Ala
      405      410      415

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<210> 385

<211> 450

<212> PRT

<213> Escherichia coli

<400> 385

```

Met Ser Leu Leu Gln Phe Ser Gly Leu Phe Val Val Trp Leu Leu Cys
  1      5      10      15
Thr Leu Phe Ile Ala Thr Leu Thr Trp Phe Glu Phe Arg Arg Val Arg
      20      25      30
Phe Asn Phe Asn Val Phe Phe Ser Leu Leu Phe Leu Thr Phe Phe
      35      40      45
Phe Gly Phe Pro Leu Thr Ser Val Leu Val Phe Arg Phe Asp Val Gly
      50      55      60
Val Ala Pro Pro Glu Ile Leu Leu Gln Ala Leu Leu Ser Ala Gly Cys
      65      70      75      80
Phe Tyr Ala Val Tyr Thr Val Thr Tyr Lys Thr Arg Leu Arg Lys Arg
      85      90      95
Val Ala Asp Val Pro Arg Arg Pro Leu Phe Thr Met Asn Arg Val Glu
      100      105      110
Thr Asn Leu Thr Trp Val Ile Leu Met Gly Ile Ala Leu Val Ser Val
      115      120      125
Gly Ile Phe Phe Met His Asn Gly Phe Leu Leu Phe Arg Leu Asn Ser
      130      135      140
Tyr Ser Gln Ile Phe Ser Ser Glu Val Ser Gly Val Ala Leu Lys Arg
      145      150      155      160
Phe Phe Tyr Phe Phe Ile Pro Ala Met Leu Val Val Tyr Phe Leu Arg
      165      170      175

```

Gln Asp Ser Lys Ala Trp Leu Phe Phe Leu Val Ser Thr Val Ala Phe
 180 185 190
 Gly Leu Leu Thr Tyr Met Ile Val Gly Gly Thr Arg Ala Asn Ile Ile
 195 200 205
 Ile Ala Phe Ala Ile Phe Leu Phe Ile Gly Ile Ile Arg Gly Trp Ile
 210 215 220
 Ser Leu Trp Met Leu Ala Ala Ala Gly Val Leu Gly Ile Val Gly Met
 225 230 235 240
 Phe Trp Leu Ala Leu Lys Arg Tyr Gly Met Asn Val Ser Gly Asp Glu
 245 250 255
 Ala Phe Tyr Thr Phe Leu Tyr Leu Thr Arg Asp Thr Phe Ser Pro Trp
 260 265 270
 Glu Asn Leu Ala Leu Leu Leu Gln Asn Tyr Asp Asn Ile Asp Phe Gln
 275 280 285
 Gly Leu Ala Pro Ile Val Arg Asp Phe Tyr Val Phe Ile Pro Ser Trp
 290 295 300
 Leu Trp Pro Gly Arg Pro Ser Met Val Leu Asn Ser Ala Asn Tyr Phe
 305 310 315 320
 Thr Trp Glu Val Leu Asn Asn His Ser Gly Leu Ala Ile Ser Pro Thr
 325 330 335
 Leu Ile Gly Ser Leu Val Val Met Gly Gly Ala Leu Phe Ile Pro Leu
 340 345 350
 Gly Ala Ile Val Val Gly Leu Ile Ile Lys Trp Phe Asp Trp Leu Tyr
 355 360 365
 Glu Leu Gly Asn Arg Glu Pro Asn Arg Tyr Lys Ala Ala Ile Leu His
 370 375 380
 Ser Phe Cys Phe Gly Ala Ile Phe Asn Met Ile Val Leu Ala Arg Glu
 385 390 395 400
 Gly Leu Asp Ser Phe Val Ser Arg Val Val Phe Phe Ile Val Val Phe
 405 410 415
 Gly Ala Cys Leu Met Ile Ala Lys Leu Leu Tyr Trp Leu Phe Glu Ser
 420 425 430
 Ala Gly Leu Ile His Lys Arg Thr Lys Ser Ser Leu Arg Thr Gln Val
 435 440 445
 Glu Gly
 450

<210> 386

<211> 246

<212> PRT

<213> Escherichia coli

<400> 386

Met Asn Asn Asn Thr Thr Ala Pro Thr Tyr Thr Leu Arg Gly Leu Gln
 1 5 10 15
 Leu Ile Gly Trp Arg Asp Met Gln His Ala Leu Asp Tyr Leu Phe Ala
 20 25 30
 Asp Gly Gln Leu Lys Gln Gly Thr Leu Val Ala Ile Asn Ala Glu Lys
 35 40 45
 Met Leu Thr Ile Glu Asp Asn Ala Glu Val Arg Glu Leu Ile Asn Ala
 50 55 60
 Ala Glu Phe Lys Tyr Ala Asp Gly Ile Ser Val Val Arg Ser Val Arg
 65 70 75 80
 Lys Lys Tyr Pro Gln Ala Gln Val Ser Arg Val Ala Gly Ala Asp Leu
 85 90 95
 Trp Glu Glu Leu Met Ala Arg Ala Gly Lys Glu Gly Thr Pro Val Phe
 100 105 110
 Leu Val Gly Gly Lys Pro Glu Val Leu Ala Gln Thr Glu Ala Lys Leu
 115 120 125
 Arg Asn Gln Trp Asn Val Asn Ile Val Gly Ser Gln Asp Gly Tyr Phe

```

      130              135              140
Lys Pro Glu Gln Arg Gln Ala Leu Phe Glu Arg Ile His Ala Ser Gly
145              150              155              160
Ala Gln Ile Val Thr Val Ala Met Gly Ser Pro Lys Gln Glu Ile Ile
      165              170              175
Met Arg Asp Cys Arg Leu Val His Pro Asp Ala Leu Tyr Met Gly Val
      180              185              190
Gly Gly Thr Tyr Asp Val Phe Thr Gly His Val Lys Arg Ala Pro Lys
      195              200              205
Ile Trp Gln Thr Leu Gly Leu Glu Trp Leu Tyr Arg Leu Leu Ser Gln
      210              215              220
Pro Ser Arg Ile Lys Arg Gln Leu Arg Leu Leu Arg Tyr Leu Arg Trp
225              230              235              240
His Tyr Thr Gly Asn Leu
      245

```

<210> 387
 <211> 74
 <212> PRT
 <213> Escherichia coli

```

<400> 387
Met Thr Val Leu Ile His Val Leu Gly Ser Asp Ile Pro His His Asn
 1              5              10              15
Arg Thr Val Leu Arg Phe Phe Asn Asp Ala Leu Ala Ala Thr Ser Glu
      20              25              30
His Ala Arg Glu Phe Met Val Val Gly Lys Asp Asp Gly Leu Ser Asp
      35              40              45
Ser Cys Pro Ala Leu Ser Val Gln Phe Phe Pro Trp Glu Lys Ile Ala
 50              55              60
Gly Gly Ser Gly His Arg Glu Ser Lys Ser
65              70

```

<210> 388
 <211> 204
 <212> PRT
 <213> Escherichia coli

```

<400> 388
Met Arg Gly Glu Leu Leu Phe Phe Pro Thr Arg Met Asp Pro Ser Leu
 1              5              10              15
Asn Thr Met Ala Asn Asp Arg Gln Arg Glu Gly Lys Met Thr Ile Leu
      20              25              30
Val Gly Asn Ser Gly Asp Arg Ser Asn Glu His Ile Ala Ala Leu Arg
      35              40              45
Ala Val His Gln Gln Phe Gly Asp Thr Val Lys Val Val Val Pro Met
 50              55              60
Gly Tyr Pro Pro Asn Asn Glu Ala Tyr Ile Glu Glu Val Arg Gln Ala
65              70              75              80
Gly Leu Glu Leu Phe Ser Glu Glu Asn Leu Gln Ile Leu Ser Glu Lys
      85              90              95
Leu Glu Phe Asp Ala Tyr Leu Ala Leu Leu Arg Gln Cys Asp Leu Gly
      100              105              110
Tyr Phe Ile Phe Ala Arg Gln Gln Gly Ile Gly Thr Leu Cys Leu Leu
      115              120              125
Ile Gln Ala Gly Ile Pro Cys Val Leu Asn Arg Glu Asn Pro Phe Trp
      130              135              140
Gln Asp Met Thr Glu Gln His Leu Pro Val Leu Phe Thr Thr Asp Asp
145              150              155              160

```


Leu Asn Glu Asp Ile Val Arg Glu Ala Gln Arg Gln Leu Ala Ser Val
 165 170 175
 Asp Lys Asn Thr Ile Ala Phe Phe Ser Pro Asn Tyr Leu Gln Gly Trp
 180 185 190
 Gln Arg Ala Leu Ala Ile Ala Ala Arg Glu Val Ala
 195 200

<210> 389

<211> 182

<212> PRT

<213> Escherichia coli

<400> 389

Met Ile Arg Gln Arg Arg Arg Ala Leu Thr Pro Glu Gln Gln Gln Glu
 1 5 10 15
 Met Gly Gln Gln Ala Ala Thr Arg Met Met Thr Tyr Pro Pro Val Val
 20 25 30
 Met Ala His Thr Val Ala Val Phe Leu Ser Phe Asp Gly Glu Leu Asp
 35 40 45
 Thr Gln Pro Leu Ile Glu Gln Leu Trp Arg Ala Gly Lys Arg Val Tyr
 50 55 60
 Leu Pro Val Leu His Pro Phe Ser Ala Gly Asn Leu Leu Phe Leu Asn
 65 70 75 80
 Tyr His Pro Gln Ser Glu Leu Val Met Asn Arg Leu Lys Ile His Glu
 85 90 95
 Pro Lys Leu Asp Val Arg Asp Val Leu Pro Leu Ser Arg Leu Asp Val
 100 105 110
 Leu Ile Thr Pro Leu Val Ala Phe Asp Glu Tyr Gly Gln Arg Leu Gly
 115 120 125
 Met Gly Gly Gly Phe Tyr Asp Arg Thr Leu Gln Asn Trp Gln His Tyr
 130 135 140
 Lys Thr Gln Pro Val Gly Tyr Ala His Asp Cys Gln Leu Val Glu Lys
 145 150 155 160
 Leu Pro Val Glu Glu Trp Asp Ile Pro Leu Pro Ala Val Val Thr Pro
 165 170 175
 Ser Lys Val Trp Glu Trp
 180

<210> 390

<211> 91

<212> PRT

<213> Escherichia coli

<400> 390

Met Ala Arg Val Thr Val Gln Asp Ala Val Glu Lys Ile Gly Asn Arg
 1 5 10 15
 Phe Asp Leu Val Leu Val Ala Ala Arg Arg Ala Arg Gln Met Gln Val
 20 25 30
 Gly Gly Lys Asp Pro Leu Val Pro Glu Glu Asn Asp Lys Thr Thr Val
 35 40 45
 Ile Ala Leu Arg Glu Ile Glu Glu Gly Leu Ile Asn Asn Gln Ile Leu
 50 55 60
 Asp Val Arg Glu Arg Gln Glu Gln Gln Glu Gln Glu Ala Ala Glu Leu
 65 70 75 80
 Gln Ala Val Thr Ala Ile Ala Glu Gly Arg Arg
 85 90

<210> 391

<211> 702

<212> PRT

<213> Escherichia coli

<400> 391

```

Met Tyr Leu Phe Glu Ser Leu Asn Gln Leu Ile Gln Thr Tyr Leu Pro
 1          5          10          15
Glu Asp Gln Ile Lys Arg Leu Arg Gln Ala Tyr Leu Val Ala Arg Asp
          20          25          30
Ala His Glu Gly Gln Thr Arg Ser Gly Glu Pro Tyr Ile Thr His
          35          40          45
Pro Val Ala Val Ala Cys Ile Leu Ala Glu Met Lys Leu Asp Tyr Glu
          50          55          60
Thr Leu Met Ala Ala Leu Leu His Asp Val Ile Glu Asp Thr Pro Ala
          65          70          75          80
Thr Tyr Gln Asp Met Glu Gln Leu Phe Gly Lys Ser Val Ala Glu Leu
          85          90          95
Val Glu Gly Val Ser Lys Leu Asp Lys Leu Lys Phe Arg Asp Lys Lys
          100          105          110
Glu Ala Gln Ala Glu Asn Phe Arg Lys Met Ile Met Ala Met Val Gln
          115          120          125
Asp Ile Arg Val Ile Leu Ile Lys Leu Ala Asp Arg Thr His Asn Met
          130          135          140
Arg Thr Leu Gly Ser Leu Arg Pro Asp Lys Arg Arg Arg Ile Ala Arg
          145          150          155          160
Glu Thr Leu Glu Ile Tyr Ser Pro Leu Ala His Arg Leu Gly Ile His
          165          170          175
His Ile Lys Thr Glu Leu Glu Glu Leu Gly Phe Glu Ala Leu Tyr Pro
          180          185          190
Asn Arg Tyr Arg Val Ile Lys Glu Val Val Lys Ala Ala Arg Gly Asn
          195          200          205
Arg Lys Glu Met Ile Gln Lys Ile Leu Ser Glu Ile Glu Gly Arg Leu
          210          215          220
Gln Glu Ala Gly Ile Pro Cys Arg Val Ser Gly Arg Glu Lys His Leu
          225          230          235          240
Tyr Ser Ile Tyr Cys Lys Met Val Leu Lys Glu Gln Arg Phe His Ser
          245          250          255
Ile Met Asp Ile Tyr Ala Phe Arg Val Ile Val Asn Asp Ser Asp Thr
          260          265          270
Cys Tyr Arg Val Leu Gly Gln Met His Ser Leu Tyr Lys Pro Arg Pro
          275          280          285
Gly Arg Val Lys Asp Tyr Ile Ala Ile Pro Lys Ala Asn Gly Tyr Gln
          290          295          300
Ser Leu His Thr Ser Met Ile Gly Pro His Gly Val Pro Val Glu Val
          305          310          315          320
Gln Ile Arg Thr Glu Asp Met Asp Gln Met Ala Glu Met Gly Val Ala
          325          330          335
Ala His Trp Ala Tyr Lys Glu His Gly Glu Thr Ser Thr Thr Ala Gln
          340          345          350
Ile Arg Ala Gln Arg Trp Met Gln Ser Leu Leu Glu Leu Gln Gln Ser
          355          360          365
Ala Gly Ser Ser Phe Glu Phe Ile Glu Ser Val Lys Ser Asp Leu Phe
          370          375          380
Pro Asp Glu Ile Tyr Val Phe Thr Pro Glu Gly Arg Ile Val Glu Leu
          385          390          395          400
Pro Ala Gly Ala Thr Pro Val Asp Phe Ala Tyr Ala Val His Thr Asp
          405          410          415
Ile Gly His Ala Cys Val Gly Ala Arg Val Asp Arg Gln Pro Tyr Pro
          420          425          430
Leu Ser Gln Pro Leu Thr Ser Gly Gln Thr Val Glu Ile Ile Thr Ala
          435          440          445

```

Pro Gly Ala Arg Pro Asn Ala Ala Trp Leu Asn Phe Val Val Ser Ser
 450 455 460
 Lys Ala Arg Ala Lys Ile Arg Gln Leu Leu Lys Asn Leu Lys Arg Asp
 465 470 475 480
 Asp Ser Val Ser Leu Gly Arg Arg Leu Leu Asn His Ala Leu Gly Gly
 485 490 495
 Ser Arg Lys Leu Asn Glu Ile Pro Gln Glu Asn Ile Gln Arg Glu Leu
 500 505 510
 Asp Arg Met Lys Leu Ala Thr Leu Asp Asp Leu Leu Ala Glu Ile Gly
 515 520 525
 Leu Gly Asn Ala Met Ser Val Val Val Ala Lys Asn Leu Gln His Gly
 530 535 540
 Asp Ala Ser Ile Pro Pro Ala Thr Gln Ser His Gly His Leu Pro Ile
 545 550 555 560
 Lys Gly Ala Asp Gly Val Leu Ile Thr Phe Ala Lys Cys Cys Arg Pro
 565 570 575
 Ile Pro Gly Asp Pro Ile Ile Ala His Val Ser Pro Gly Lys Gly Leu
 580 585 590
 Val Ile His His Glu Ser Cys Arg Asn Ile Arg Gly Tyr Gln Lys Glu
 595 600 605
 Pro Glu Lys Phe Met Ala Val Glu Trp Asp Lys Glu Thr Ala Gln Glu
 610 615 620
 Phe Ile Thr Glu Ile Lys Val Glu Met Phe Asn His Gln Gly Ala Leu
 625 630 635 640
 Ala Asn Leu Thr Ala Ala Ile Asn Thr Thr Thr Ser Asn Ile Gln Ser
 645 650 655
 Leu Asn Thr Glu Glu Lys Asp Gly Arg Val Tyr Ser Ala Phe Ile Arg
 660 665 670
 Leu Thr Ala Arg Asp Arg Val His Leu Ala Asn Ile Met Arg Lys Ile
 675 680 685
 Arg Val Met Pro Asp Val Ile Lys Val Thr Arg Asn Arg Asn
 690 695 700

<210> 392

<211> 229

<212> PRT

<213> Escherichia coli

<400> 392

Met Asn Pro Thr Arg Tyr Ala Arg Ile Cys Glu Met Leu Ala Arg Arg
 1 5 10 15
 Gln Pro Asp Leu Thr Val Cys Met Glu Gln Val His Lys Pro His Asn
 20 25 30
 Val Ser Ala Ile Ile Arg Thr Ala Asp Ala Val Gly Val His Glu Val
 35 40 45
 His Ala Val Trp Pro Gly Ser Arg Met Arg Thr Met Ala Ser Ala Ala
 50 55 60
 Ala Gly Ser Asn Ser Trp Val Gln Val Lys Thr His Arg Thr Ile Gly
 65 70 75 80
 Asp Ala Val Ala His Leu Lys Gly Gln Gly Met Gln Ile Leu Ala Thr
 85 90 95
 His Leu Ser Asp Asn Ala Val Asp Phe Arg Glu Ile Asp Tyr Thr Arg
 100 105 110
 Pro Thr Cys Ile Leu Met Gly Gln Glu Lys Thr Gly Ile Thr Gln Glu
 115 120 125
 Ala Leu Ala Leu Ala Asp Gln Asp Ile Ile Ile Pro Met Ile Gly Met
 130 135 140
 Val Gln Ser Leu Asn Val Ser Val Ala Ser Ala Leu Ile Leu Tyr Glu
 145 150 155 160
 Ala Gln Arg Gln Arg Gln Asn Ala Gly Met Tyr Leu Arg Glu Asn Ser

```

          165          170          175
Met Leu Pro Glu Ala Glu Gln Gln Arg Leu Leu Phe Glu Gly Gly Tyr
          180          185          190
Pro Val Leu Ala Lys Val Ala Lys Arg Lys Gly Leu Pro Tyr Pro His
          195          200          205
Val Asn Gln Gln Gly Glu Ile Glu Ala Asp Ala Asp Trp Trp Ala Thr
          210          215          220
Met Gln Ala Ala Gly
225

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<210> 393
<211> 693
<212> PRT
<213> Escherichia coli

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<400> 393
Met Lys Gly Arg Leu Leu Asp Ala Val Pro Leu Ser Ser Leu Thr Gly
 1          5          10          15
Val Gly Ala Ala Leu Ser Asn Lys Leu Ala Lys Ile Asn Leu His Thr
          20          25          30
Val Gln Asp Leu Leu Leu His Leu Pro Leu Arg Tyr Glu Asp Arg Thr
          35          40          45
His Leu Tyr Pro Ile Gly Glu Leu Leu Pro Gly Val Tyr Ala Thr Val
 50          55          60
Glu Gly Glu Val Leu Asn Cys Asn Ile Ser Phe Gly Gly Arg Arg Met
65          70          75          80
Met Thr Cys Gln Ile Ser Asp Gly Ser Gly Ile Leu Thr Met Arg Phe
          85          90          95
Phe Asn Phe Ser Ala Ala Met Lys Asn Ser Leu Ala Ala Gly Arg Arg
          100          105          110
Val Leu Ala Tyr Gly Glu Ala Lys Arg Gly Lys Tyr Gly Ala Glu Met
115          120          125
Ile His Pro Glu Tyr Arg Val Gln Gly Asp Leu Ser Thr Pro Glu Leu
130          135          140
Gln Glu Thr Leu Thr Pro Val Tyr Pro Thr Thr Glu Gly Val Lys Gln
145          150          155          160
Ala Thr Leu Arg Lys Leu Thr Asp Gln Ala Leu Asp Leu Leu Asp Thr
          165          170          175
Cys Ala Ile Glu Glu Leu Leu Pro Pro Glu Leu Ser Gln Gly Met Met
180          185          190
Thr Leu Pro Glu Ala Leu Arg Thr Leu His Arg Pro Pro Pro Thr Leu
195          200          205
Gln Leu Ser Asp Leu Glu Thr Gly Gln His Pro Ala Gln Arg Arg Leu
210          215          220
Ile Leu Glu Glu Leu Leu Ala His Asn Leu Ser Met Leu Ala Leu Arg
225          230          235          240
Ala Gly Ala Gln Arg Phe His Ala Gln Pro Leu Ser Ala Asn Asp Thr
          245          250          255
Leu Lys Asn Lys Leu Leu Ala Ala Leu Pro Phe Lys Pro Thr Gly Ala
260          265          270
Gln Ala Arg Val Val Ala Glu Ile Glu Arg Asp Met Ala Leu Asp Val
275          280          285
Pro Met Met Arg Leu Val Gln Gly Asp Val Gly Ser Gly Lys Thr Leu
290          295          300
Val Ala Ala Leu Ala Ala Leu Arg Ala Ile Ala His Gly Lys Gln Val
305          310          315          320
Ala Leu Met Ala Pro Thr Glu Leu Leu Ala Glu Gln His Ala Asn Asn
          325          330          335
Phe Arg Asn Trp Phe Ala Pro Leu Gly Ile Glu Val Gly Trp Leu Ala
340          345          350

```

Gly Lys Gln Lys Gly Lys Ala Arg Leu Ala Gln Gln Glu Ala Ile Ala
 355 360 365
 Ser Gly Gln Val Gln Met Ile Val Gly Thr His Ala Ile Phe Gln Glu
 370 375 380
 Gln Val Gln Phe Asn Gly Leu Ala Leu Val Ile Ile Asp Glu Gln His
 385 390 395 400
 Arg Phe Gly Val His Gln Arg Leu Ala Leu Trp Glu Lys Gly Gln Gln
 405 410 415
 Gln Gly Phe His Pro His Gln Leu Ile Met Thr Ala Thr Pro Ile Pro
 420 425 430
 Arg Thr Leu Ala Met Thr Ala Tyr Ala Asp Leu Asp Thr Ser Val Ile
 435 440 445
 Asp Glu Leu Pro Pro Gly Arg Thr Pro Val Thr Thr Val Ala Ile Pro
 450 455 460
 Asp Thr Arg Arg Thr Asp Ile Ile Asp Arg Val His His Ala Cys Ile
 465 470 475 480
 Thr Glu Gly Arg Gln Ala Tyr Trp Val Cys Thr Leu Ile Glu Glu Ser
 485 490 495
 Glu Leu Leu Glu Ala Gln Ala Ala Glu Ala Thr Trp Glu Glu Leu Lys
 500 505 510
 Leu Ala Leu Pro Glu Leu Asn Val Gly Leu Val His Gly Arg Met Lys
 515 520 525
 Pro Ala Glu Lys Gln Ala Val Met Ala Ser Phe Lys Gln Gly Glu Leu
 530 535 540
 His Leu Leu Val Ala Thr Thr Val Ile Glu Val Gly Val Asp Val Pro
 545 550 555 560
 Asn Ala Ser Leu Met Ile Ile Glu Asn Pro Glu Arg Leu Gly Leu Ala
 565 570 575
 Gln Leu His Gln Leu Arg Gly Arg Val Gly Arg Gly Ala Val Ala Ser
 580 585 590
 His Cys Val Leu Leu Tyr Lys Thr Pro Leu Ser Lys Thr Ala Gln Ile
 595 600 605
 Arg Leu Gln Val Leu Arg Asp Ser Asn Asp Gly Phe Val Ile Ala Gln
 610 615 620
 Lys Asp Leu Glu Ile Arg Gly Pro Gly Glu Leu Leu Gly Thr Arg Gln
 625 630 635 640
 Thr Gly Asn Ala Glu Phe Lys Val Ala Asp Leu Leu Arg Asp Gln Ala
 645 650 655
 Met Ile Pro Glu Val Gln Arg Leu Ala Arg His Ile His Glu Arg Tyr
 660 665 670
 Pro Gln Gln Ala Lys Ala Leu Ile Glu Arg Trp Met Pro Glu Thr Glu
 675 680 685
 Arg Tyr Ser Asn Ala
 690

<210> 394

<211> 428

<212> PRT

<213> Escherichia coli

<400> 394

Met Lys Thr Ser Leu Phe Lys Ser Leu Tyr Phe Gln Val Leu Thr Ala
 1 5 10 15
 Ile Ala Ile Gly Ile Leu Leu Gly His Phe Tyr Pro Glu Ile Gly Glu
 20 25 30
 Gln Met Lys Pro Leu Gly Asp Gly Phe Val Lys Leu Ile Lys Met Ile
 35 40 45
 Ile Ala Pro Val Ile Phe Cys Thr Val Val Thr Gly Ile Ala Gly Met
 50 55 60
 Glu Ser Met Lys Ala Val Gly Arg Thr Gly Ala Val Ala Leu Leu Tyr

65					70					75				80	
Phe	Glu	Ile	Val	Ser	Thr	Ile	Ala	Leu	Ile	Ile	Gly	Leu	Ile	Ile	Val
				85					90					95	
Asn	Val	Val	Gln	Pro	Gly	Ala	Gly	Met	Asn	Val	Asp	Pro	Ala	Thr	Leu
			100					105					110		
Asp	Ala	Lys	Ala	Val	Ala	Val	Tyr	Ala	Asp	Gln	Ala	Lys	Asp	Gln	Gly
		115					120				125				
Ile	Val	Ala	Phe	Ile	Met	Asp	Val	Ile	Pro	Ala	Ser	Val	Ile	Gly	Ala
	130				135						140				
Phe	Ala	Ser	Gly	Asn	Ile	Leu	Gln	Val	Leu	Leu	Phe	Ala	Val	Leu	Phe
145				150					155					160	
Gly	Phe	Ala	Leu	His	Arg	Leu	Gly	Ser	Lys	Gly	Gln	Leu	Ile	Phe	Asn
			165					170					175		
Val	Ile	Glu	Ser	Phe	Ser	Gln	Val	Ile	Phe	Gly	Ile	Ile	Asn	Met	Ile
		180					185					190			
Met	Arg	Leu	Ala	Pro	Ile	Gly	Ala	Phe	Gly	Ala	Met	Ala	Phe	Thr	Ile
	195					200					205				
Gly	Lys	Tyr	Gly	Val	Gly	Thr	Leu	Val	Gln	Leu	Gly	Gln	Leu	Ile	Ile
	210					215					220				
Cys	Phe	Tyr	Ile	Thr	Cys	Ile	Leu	Phe	Val	Val	Leu	Val	Leu	Gly	Ser
225				230				235						240	
Ile	Ala	Lys	Ala	Thr	Gly	Phe	Ser	Ile	Phe	Lys	Phe	Ile	Arg	Tyr	Ile
			245					250					255		
Arg	Glu	Glu	Leu	Leu	Ile	Val	Leu	Gly	Thr	Ser	Ser	Ser	Glu	Ser	Ala
		260					265						270		
Leu	Pro	Arg	Met	Leu	Asp	Lys	Met	Glu	Lys	Leu	Gly	Cys	Arg	Lys	Ser
	275					280						285			
Val	Val	Gly	Leu	Val	Ile	Pro	Thr	Gly	Tyr	Ser	Phe	Asn	Leu	Asp	Gly
	290				295						300				
Thr	Ser	Ile	Tyr	Leu	Thr	Met	Ala	Ala	Val	Phe	Ile	Ala	Gln	Ala	Thr
305				310					315					320	
Asn	Ser	Gln	Met	Asp	Ile	Val	His	Gln	Ile	Thr	Leu	Leu	Ile	Val	Leu
			325					330					335		
Leu	Leu	Ser	Ser	Lys	Gly	Ala	Ala	Gly	Val	Thr	Gly	Ser	Gly	Phe	Ile
		340						345				350			
Val	Leu	Ala	Ala	Thr	Leu	Ser	Ala	Val	Gly	His	Leu	Pro	Val	Ala	Gly
	355					360					365				
Leu	Ala	Leu	Ile	Leu	Gly	Ile	Asp	Arg	Phe	Met	Ser	Glu	Ala	Arg	Ala
	370				375					380					
Leu	Thr	Asn	Leu	Val	Gly	Asn	Gly	Val	Ala	Thr	Ile	Val	Val	Ala	Lys
385				390				395						400	
Trp	Val	Lys	Glu	Leu	Asp	His	Lys	Lys	Leu	Asp	Asp	Val	Leu	Asn	Asn
			405					410					415		
Arg	Ala	Pro	Asp	Gly	Lys	Thr	His	Glu	Leu	Ser	Ser				
		420						425							

<210> 395

<211> 396

<212> PRT

<213> Escherichia coli

<400> 395

Met	Thr	Thr	Arg	Gln	His	Ser	Ser	Phe	Ala	Ile	Val	Phe	Ile	Leu	Gly
1				5				10						15	
Leu	Leu	Ala	Met	Leu	Met	Pro	Leu	Ser	Ile	Asp	Met	Tyr	Leu	Pro	Ala
		20						25					30		
Leu	Pro	Val	Ile	Ser	Ala	Gln	Phe	Gly	Val	Pro	Ala	Gly	Ser	Thr	Gln
		35				40						45			
Met	Thr	Leu	Ser	Thr	Tyr	Ile	Leu	Gly	Phe	Ala	Leu	Gly	Gln	Leu	Ile
	50					55					60				

Tyr Gly Pro Met Ala Asp Ser Phe Gly Arg Lys Pro Val Val Leu Gly
 65 70 75 80
 Gly Thr Leu Val Phe Ala Ala Ala Val Ala Cys Ala Leu Ala Asn
 85 90 95
 Thr Ile Asp Gln Leu Ile Val Met Arg Phe Phe His Gly Leu Ala Ala
 100 105 110
 Ala Ala Ala Ser Val Val Ile Asn Ala Leu Met Arg Asp Ile Tyr Pro
 115 120 125
 Lys Glu Glu Phe Ser Arg Met Met Ser Phe Val Met Leu Val Thr Thr
 130 135 140
 Ile Ala Pro Leu Met Ala Pro Ile Val Gly Gly Trp Val Leu Val Trp
 145 150 155 160
 Leu Ser Trp His Tyr Ile Phe Trp Ile Leu Ala Leu Ala Ala Ile Leu
 165 170 175
 Ala Ser Ala Met Ile Phe Phe Leu Ile Lys Glu Thr Leu Pro Pro Glu
 180 185 190
 Arg Arg Gln Pro Phe His Ile Arg Thr Thr Ile Gly Asn Phe Ala Ala
 195 200 205
 Leu Phe Arg His Lys Arg Val Leu Ser Tyr Met Leu Ala Ser Gly Phe
 210 215 220
 Ser Phe Ala Gly Met Phe Ser Phe Leu Ser Ala Gly Pro Phe Val Tyr
 225 230 235 240
 Ile Glu Ile Asn His Val Ala Pro Glu Asn Phe Gly Tyr Tyr Phe Ala
 245 250 255
 Leu Asn Ile Val Phe Leu Phe Val Met Thr Ile Phe Asn Ser Arg Phe
 260 265 270
 Val Arg Arg Ile Gly Ala Leu Asn Met Phe Arg Ser Gly Leu Trp Ile
 275 280 285
 Gln Phe Ile Met Ala Ala Trp Met Val Ile Ser Ala Leu Leu Gly Leu
 290 295 300
 Gly Phe Trp Ser Leu Val Val Gly Val Ala Ala Phe Val Gly Cys Val
 305 310 315 320
 Ser Met Val Ser Ser Asn Ala Met Ala Val Ile Leu Asp Glu Phe Pro
 325 330 335
 His Met Ala Gly Thr Ala Ser Ser Leu Ala Gly Thr Phe Arg Phe Gly
 340 345 350
 Ile Gly Ala Ile Val Gly Ala Leu Leu Ser Leu Ala Thr Phe Asn Ser
 355 360 365
 Ala Trp Pro Met Ile Trp Ser Ile Ala Phe Cys Ala Thr Ser Ser Ile
 370 375 380
 Leu Phe Cys Leu Tyr Ala Ser Arg Pro Lys Lys Arg
 385 390 395

<210> 396

<211> 231

<212> PRT

<213> Escherichia coli

<400> 396

Met Arg Leu Asp Lys Phe Ile Ala Gln Gln Leu Gly Val Ser Arg Ala
 1 5 10 15
 Ile Ala Gly Arg Glu Ile Arg Gly Asn Arg Val Thr Val Asp Gly Glu
 20 25 30
 Ile Val Arg Asn Ala Ala Phe Lys Leu Leu Pro Glu His Asp Val Ala
 35 40 45
 Tyr Asp Gly Asn Pro Leu Ala Gln Gln His Gly Pro Arg Tyr Phe Met
 50 55 60
 Leu Asn Lys Pro Gln Gly Tyr Val Cys Ser Thr Asp Asp Pro Asp His
 65 70 75 80
 Pro Thr Val Leu Tyr Phe Leu Asp Glu Pro Val Ala Trp Lys Leu His

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<210> 397
<211> 442
<212> PRT
<213> Escherichia coli
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Glu Val Asn Phe Asp Thr Gln Gln Met Ile Asp Phe Ile Asn Arg Phe
 275 280 285
 Asn Thr Asn Lys Trp Leu Ile Asp Lys Asn Asn Asn Phe Phe Ile Gln
 290 295 300
 Leu Ile Asp Gln Ala Leu Arg Ser Thr Asp Asp Met Ile Lys Ala Asn
 305 310 315 320
 Val Trp His Leu Tyr Lys Glu Trp Ile Arg Ser Asp Asp Val Ser Pro
 325 330 335
 Ile Phe Ile Glu Thr Glu Asp Asn Leu Arg Thr Phe Asn Thr Asn Glu
 340 345 350
 Leu Thr Arg Asn Asp Asn Ile Phe Ile Leu Phe Ser Ser Val Asp Asp
 355 360 365
 Gly Pro Val Met Val Val Ser Ser Gln Arg Leu His Asp Met Leu Asn
 370 375 380
 Pro Thr Lys Asp Thr Asn Trp Asn Ser Thr Tyr Ile Tyr Lys Ser Arg
 385 390 395 400
 His Glu Met Leu Pro Val Asn Leu Thr Gln Glu Thr Leu Phe Ser Ser
 405 410 415
 Lys Ser His Gly Lys Tyr Ala Leu Phe Pro Ile Phe Thr Ala Ser Trp
 420 425 430
 Arg Ala His Arg Ile Met Asn Lys Gly Val
 435 440

<210> 398

<211> 238

<212> PRT

<213> Escherichia coli

<400> 398

Met Gly Arg Lys Trp Ala Asn Ile Val Ala Lys Lys Thr Ala Lys Asp
 1 5 10 15
 Gly Ala Thr Ser Lys Ile Tyr Ala Lys Phe Gly Val Glu Ile Tyr Ala
 20 25 30
 Ala Ala Lys Gln Gly Glu Pro Asp Pro Glu Leu Asn Thr Ser Leu Lys
 35 40 45
 Phe Val Ile Glu Arg Ala Lys Gln Ala Gln Val Pro Lys His Val Ile
 50 55 60
 Asp Lys Ala Ile Asp Lys Ala Lys Gly Gly Gly Asp Glu Thr Phe Val
 65 70 75 80
 Gln Gly Arg Tyr Glu Gly Phe Gly Pro Asn Gly Ser Met Ile Ile Ala
 85 90 95
 Glu Thr Leu Thr Ser Asn Val Asn Arg Thr Ile Ala Asn Val Arg Thr
 100 105 110
 Ile Phe Asn Lys Lys Gly Gly Asn Ile Gly Ala Ala Gly Ser Val Ser
 115 120 125
 Tyr Met Phe Asp Asn Thr Gly Val Ile Val Phe Lys Gly Thr Asp Pro
 130 135 140
 Asp His Ile Phe Glu Ile Leu Leu Glu Ala Glu Val Asp Val Arg Asp
 145 150 155 160
 Val Thr Glu Glu Glu Gly Asn Ile Val Ile Tyr Thr Glu Pro Thr Asp
 165 170 175
 Leu His Lys Gly Ile Ala Ala Leu Lys Ala Ala Gly Ile Thr Glu Phe
 180 185 190
 Ser Thr Thr Glu Leu Glu Met Ile Ala Gln Ser Glu Val Glu Leu Ser
 195 200 205
 Pro Glu Asp Leu Glu Ile Phe Glu Gly Leu Val Asp Ala Leu Glu Asp
 210 215 220
 Asp Asp Asp Val Gln Lys Val Tyr His Asn Val Ala Asn Leu
 225 230 235

<210> 399
 <211> 261
 <212> PRT
 <213> Escherichia coli

<400> 399

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Met Val Leu Met Ser Glu Thr Lys Asn Glu Leu Glu Asp Leu Leu Glu
 1           5           10           15
Lys Ala Ala Thr Glu Pro Ala His Arg Pro Ala Phe Phe Arg Thr Leu
           20           25           30
Leu Glu Ser Thr Val Trp Val Pro Gly Thr Ala Ala Gln Gly Glu Ala
           35           40           45
Val Val Glu Asp Ser Ala Leu Asp Leu Gln His Trp Glu Lys Glu Asp
           50           55           60
Gly Thr Ser Val Ile Pro Phe Phe Thr Ser Leu Glu Ala Leu Gln Gln
65           70           75           80
Ala Val Glu Asp Glu Gln Ala Phe Val Val Met Pro Val Arg Thr Leu
           85           90           95
Phe Glu Met Thr Leu Gly Glu Thr Leu Phe Leu Asn Ala Lys Leu Pro
           100          105          110
Thr Gly Lys Glu Phe Met Pro Arg Glu Ile Ser Leu Leu Ile Gly Glu
           115          120          125
Glu Gly Asn Pro Leu Ser Ser Gln Glu Ile Leu Glu Gly Gly Glu Ser
130          135          140
Leu Ile Leu Ser Glu Val Ala Glu Pro Pro Ala Gln Met Ile Asp Ser
145          150          155          160
Leu Thr Thr Leu Phe Lys Thr Ile Lys Pro Val Lys Arg Ala Phe Ile
           165          170          175
Cys Ser Ile Lys Glu Asn Glu Glu Ala Gln Pro Asn Leu Leu Ile Gly
           180          185          190
Ile Glu Ala Asp Gly Asp Ile Glu Glu Ile Ile Gln Ala Thr Gly Ser
           195          200          205
Val Ala Thr Asp Thr Leu Pro Gly Asp Glu Pro Ile Asp Ile Cys Gln
210          215          220
Val Lys Lys Gly Glu Lys Gly Ile Ser His Phe Ile Thr Glu His Ile
225          230          235          240
Ala Pro Phe Tyr Glu Arg Arg Trp Gly Gly Phe Leu Arg Asp Phe Lys
           245          250          255
Gln Asn Arg Ile Ile
           260

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<210> 400
 <211> 421
 <212> PRT
 <213> Escherichia coli

<400> 400

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Met Leu Thr Lys Lys Lys Trp Ala Leu Phe Ser Leu Leu Thr Leu Cys
 1           5           10           15
Gly Gly Thr Ile Tyr Lys Leu Pro Ser Leu Lys Asp Ala Phe Tyr Ile
           20           25           30
Pro Met Gln Glu Tyr Phe His Leu Thr Asn Gly Gln Ile Gly Asn Ala
           35           40           45
Met Ser Val Asn Ser Phe Val Thr Thr Val Gly Phe Phe Leu Ser Ile
           50           55           60
Tyr Phe Ala Asp Lys Leu Pro Arg Arg Tyr Thr Met Ser Phe Ser Leu
65           70           75           80
Ile Ala Thr Gly Leu Leu Gly Val Tyr Leu Thr Thr Met Pro Gly Tyr
           85           90           95

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Trp Gly Ile Leu Phe Val Trp Ala Leu Phe Gly Val Thr Cys Asp Met
 100 105 110
 Met Asn Trp Trp Val Leu Leu Lys Ser Val Ser Arg Leu Gly Asn Ser
 115 120 125
 Glu Gln Gln Gly Arg Leu Phe Gly Phe Phe Glu Thr Gly Arg Gly Ile
 130 135 140
 Val Asp Thr Val Val Ala Phe Ser Ala Leu Ala Val Phe Thr Trp Phe
 145 150 155 160
 Gly Ser Gly Leu Leu Gly Phe Lys Ala Gly Ile Trp Phe Tyr Ser Leu
 165 170 175
 Ile Val Ile Ala Val Gly Ile Ile Ile Phe Phe Val Leu Asn Asp Lys
 180 185 190
 Glu Glu Ala Pro Ser Val Glu Val Lys Lys Glu Asp Gly Ala Ser Lys
 195 200 205
 Asn Thr Ser Met Thr Ser Val Leu Lys Asp Lys Thr Ile Trp Leu Ile
 210 215 220
 Ala Phe Asn Val Phe Phe Val Tyr Ala Val Tyr Cys Gly Leu Thr Phe
 225 230 235 240
 Phe Ile Pro Phe Leu Lys Asn Ile Tyr Leu Leu Pro Val Ala Leu Val
 245 250 255
 Gly Ala Tyr Gly Ile Ile Asn Gln Tyr Cys Leu Lys Met Ile Gly Gly
 260 265 270
 Pro Ile Gly Gly Met Ile Ser Asp Lys Ile Leu Lys Ser Pro Ser Lys
 275 280 285
 Tyr Leu Cys Tyr Thr Phe Ile Ile Ser Thr Ala Ala Leu Val Leu Leu
 290 295 300
 Ile Met Leu Pro His Glu Ser Met Pro Val Tyr Leu Gly Met Ala Cys
 305 310 315 320
 Thr Leu Gly Phe Gly Ala Ile Val Phe Thr Gln Arg Ala Val Phe Phe
 325 330 335
 Ala Pro Ile Gly Glu Ala Lys Ile Ala Glu Asn Lys Thr Gly Ala Ala
 340 345 350
 Met Ala Leu Gly Ser Phe Ile Gly Tyr Ala Pro Ala Met Phe Cys Phe
 355 360 365
 Ser Leu Tyr Gly Tyr Ile Leu Asp Leu Asn Pro Gly Ile Ile Gly Tyr
 370 375 380
 Lys Ile Val Phe Gly Ile Met Ala Cys Phe Ala Phe Ser Gly Ala Val
 385 390 395 400
 Val Ser Val Met Leu Val Lys Arg Ile Ser Gln Arg Lys Lys Glu Met
 405 410 415
 Leu Ala Ala Glu Ala
 420

<210> 401

<211> 770

<212> PRT

<213> Escherichia coli

<400> 401

Met Pro Arg Leu Leu Thr Lys Arg Gly Cys Trp Ile Thr Leu Ala Ala
 1 5 10 15
 Ala Pro Phe Leu Leu Phe Leu Ala Ala Trp Gly Ala Asp Lys Leu Trp
 20 25 30
 Pro Leu Pro Leu His Glu Val Asn Pro Ala Arg Val Val Val Ala Gln
 35 40 45
 Asp Gly Thr Pro Leu Trp Arg Phe Ala Asp Ala Asp Gly Ile Trp Arg
 50 55 60
 Tyr Pro Val Thr Ile Glu Asp Val Ser Pro Arg Tyr Leu Glu Ala Leu
 65 70 75 80
 Ile Asn Tyr Glu Asp Arg Trp Phe Trp Lys His Pro Gly Val Asn Pro

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Pro Asn Ser Val Thr Arg Gly Val Ile Cys Trp Pro Gly Gly Gln Ser
 580 585 590
 Leu Pro Glu Gly Asp Gly Asn Cys Arg Arg Arg Leu Ala Thr Trp Leu
 595 600 605
 Leu Asp Gly Ser Gln Pro Pro Thr Leu Leu Leu Pro Glu Gln Glu Gly
 610 615 620
 Ile Asn Gly Ile Arg Phe Pro Ile Trp Leu Asp Glu Asn Gly Lys Arg
 625 630 635 640
 Val Ala Ala Asp Cys Pro Gln Ala Arg Gln Glu Met Ile Asn Val Trp
 645 650 655
 Pro Leu Pro Leu Glu Pro Trp Leu Pro Ala Ser Glu Arg Arg Ala Val
 660 665 670
 Arg Leu Pro Pro Ala Ser Thr Ser Cys Pro Pro Tyr Gly His Asp Ala
 675 680 685
 Gln Leu Pro Leu Gln Leu Thr Gly Val Arg Asp Gly Ala Ile Ile Lys
 690 695 700
 Arg Leu Pro Gly Ala Ala Glu Ala Thr Leu Pro Leu Gln Ser Ser Gly
 705 710 715 720
 Gly Ala Gly Glu Arg Trp Trp Phe Leu Asn Gly Glu Pro Leu Thr Glu
 725 730 735
 Arg Gly Arg Asn Val Thr Leu His Leu Thr Asp Lys Gly Asp Tyr Gln
 740 745 750
 Leu Leu Val Met Asp Asp Val Gly Gln Ile Ala Thr Val Lys Phe Val
 755 760 765
 Met Gln
 770

<210> 402

<211> 1653

<212> PRT

<213> Escherichia coli

<400> 402

Met Lys Lys Leu Arg Val Ala Ala Cys Met Leu Met Leu Ala Leu Ala
 1 5 10 15
 Gly Cys Asp Asn Asn Asp Asn Ala Pro Thr Ala Val Lys Lys Asp Ala
 20 25 30
 Pro Ser Glu Val Thr Lys Ala Ala Ser Ser Glu Asn Ala Ser Ser Ala
 35 40 45
 Lys Leu Ser Val Pro Glu Arg Gln Lys Leu Ala Gln Gln Ser Ala Gly
 50 55 60
 Lys Val Leu Thr Leu Leu Asp Leu Ser Glu Val Gln Leu Asp Gly Ala
 65 70 75 80
 Ala Thr Leu Val Leu Thr Phe Ser Ile Pro Leu Asp Pro Asp Gln Asp
 85 90 95
 Phe Ser Arg Val Ile His Val Val Asp Lys Lys Ser Gly Lys Val Asp
 100 105 110
 Gly Ala Trp Glu Leu Ser Asp Asn Leu Lys Glu Leu Arg Leu Arg His
 115 120 125
 Leu Glu Pro Lys Arg Asp Leu Ile Val Thr Ile Gly Lys Glu Val Lys
 130 135 140
 Ala Leu Asn Asn Ala Thr Phe Ser Lys Asp Tyr Glu Lys Thr Ile Thr
 145 150 155 160
 Thr Arg Asp Ile Gln Pro Ser Val Gly Phe Ala Ser Arg Gly Ser Leu
 165 170 175
 Leu Pro Gly Lys Val Val Glu Gly Leu Pro Val Met Ala Leu Asn Val
 180 185 190
 Asn Asn Val Asp Val Asn Phe Phe Arg Val Lys Pro Glu Ser Leu Pro
 195 200 205
 Ala Phe Ile Ser Gln Trp Glu Tyr Arg Asn Ser Leu Ala Asn Trp Gln

210	215	220
Ser Asp Lys Leu Leu	Gln Met Ala Asp Leu Val Tyr Thr Gly Arg Phe	
225	230	235
Asp Leu Asn Pro Ala	Arg Asn Thr Arg Glu Lys Leu Leu Leu Pro Leu	
	245	250
Gly Asp Ile Lys Pro	Leu Gln Gln Ala Gly Val Tyr Leu Ala Val Met	
	260	265
Asn Gln Ala Gly Arg	Tyr Asp Tyr Ser Asn Pro Ala Thr Leu Phe Thr	
	275	280
Leu Ser Asp Ile Gly	Val Ser Ala His Arg Tyr His Asn Arg Leu Asp	
	290	295
Ile Phe Thr Gln Ser	Leu Glu Asn Gly Ala Ala Gln Gln Gly Ile Glu	
305	310	315
Val Ser Leu Leu Asn	Glu Lys Gly Gln Thr Leu Thr Gln Ala Thr Ser	
	325	330
Asp Ala Gln Gly His	Val Gln Leu Glu Asn Asp Lys Asn Ala Ala Leu	
	340	345
Leu Leu Ala Arg Lys	Asp Gly Gln Thr Thr Leu Leu Asp Leu Lys Leu	
	355	360
Pro Ala Leu Asp Leu	Ala Glu Phe Asn Ile Ala Gly Ala Pro Gly Tyr	
	370	375
Ser Lys Gln Phe Phe	Met Phe Gly Pro Arg Asp Leu Tyr Arg Pro Gly	
385	390	395
Glu Thr Val Ile Leu	Asn Gly Leu Leu Arg Asp Ala Asp Gly Lys Ala	
	405	410
Leu Pro Asn Gln Pro	Ile Lys Leu Asp Val Ile Lys Pro Asp Gly Gln	
	420	425
Val Leu Arg Ser Val	Val Ser Gln Pro Glu Asn Gly Leu Tyr His Phe	
	435	440
Thr Trp Pro Leu Asp	Ser Asn Ala Ala Thr Gly Met Trp His Ile Arg	
	450	455
Ala Asn Thr Gly Asp	Asn Gln Tyr Arg Met Trp Asp Phe His Val Glu	
465	470	475
Asp Phe Met Pro Glu	Arg Met Ala Leu Asn Leu Thr Gly Glu Lys Thr	
	485	490
Pro Leu Thr Pro Lys	Asp Glu Val Lys Phe Ser Val Val Gly Tyr Tyr	
	500	505
Leu Tyr Gly Ala Pro	Ala Asn Gly Asn Thr Leu Gln Gly Gln Leu Phe	
	515	520
Leu Arg Pro Leu Arg	Glu Ala Val Ser Ala Leu Pro Gly Phe Glu Phe	
	530	535
Gly Asp Ile Ala Ala	Glu Asn Leu Ser Arg Thr Leu Asp Glu Val Gln	
545	550	555
Leu Thr Leu Asp Asp	Lys Gly Arg Gly Glu Val Ser Thr Glu Ser Gln	
	565	570
Trp Lys Glu Thr His	Ser Pro Leu Gln Val Ile Phe Gln Gly Ser Leu	
	580	585
Leu Glu Ser Gly Gly	Arg Pro Val Thr Arg Arg Ala Glu Gln Ala Ile	
	595	600
Trp Pro Ala Asp Ala	Leu Pro Gly Ile Arg Pro Gln Phe Ala Ser Lys	
	610	615
Ser Val Tyr Asp Tyr	Arg Thr Asp Ser Thr Val Lys Gln Pro Ile Val	
625	630	635
Asp Glu Gly Ser Asn	Ala Ala Phe Asp Ile Val Tyr Ser Asp Ala Gln	
	645	650
Gly Val Lys Lys Ala	Val Ser Gly Leu Gln Val Arg Leu Ile Arg Glu	
	660	665
Arg Arg Asp Tyr Trp	Asn Trp Ser Glu Asp Glu Gly Trp Gln Ser	
	675	680
Gln Phe Asp Gln Lys	Asp Leu Ile Glu Asn Glu Gln Thr Leu Asp Leu	
	690	695
		700

Lys Ala Asp Glu Thr Gly Lys Val Ser Phe Pro Val Glu Trp Gly Ala
 705 710 715 720
 Tyr Arg Leu Glu Val Lys Ala Pro Asn Glu Ala Val Ser Ser Val Arg
 725 730 735
 Phe Trp Ala Gly Tyr Ser Trp Gln Asp Asn Ser Asp Gly Ser Gly Ala
 740 745 750
 Val Arg Pro Asp Arg Val Thr Leu Lys Leu Asp Lys Ala Ser Tyr Arg
 755 760 765
 Pro Gly Asp Thr Ile Lys Leu His Ile Ala Ala Pro Thr Ala Gly Lys
 770 775 780
 Gly Tyr Ala Met Val Glu Ser Ser Glu Gly Pro Leu Trp Trp Gln Glu
 785 790 795 800
 Ile Asp Val Arg Ala Gln Gly Leu Asp Leu Thr Ile Pro Val Asp Lys
 805 810 815
 Thr Trp Asn Arg His Asp Leu Tyr Leu Ser Thr Leu Val Val Arg Pro
 820 825 830
 Gly Asp Lys Ser Arg Ser Ala Thr Pro Lys Arg Ala Val Gly Val Leu
 835 840 845
 His Leu Pro Leu Gly Asp Glu Asn Arg Arg Leu Asp Leu Ala Leu Glu
 850 855 860
 Thr Pro Ala Lys Met Arg Pro Asn Gln Pro Leu Thr Val Lys Ile Lys
 865 870 875 880
 Ala Ser Thr Lys Asn Gly Glu Lys Pro Lys Gln Val Asn Val Leu Val
 885 890 895
 Ser Ala Val Asp Ser Gly Val Leu Asn Ile Thr Asp Tyr Val Thr Pro
 900 905 910
 Asp Pro Trp Gln Ala Phe Phe Gly Gln Lys Arg Tyr Gly Ala Asp Ile
 915 920 925
 Tyr Asp Ile Tyr Gly Gln Val Ile Glu Gly Gln Gly Arg Leu Ala Ala
 930 935 940
 Leu Arg Phe Gly Gly Asp Gly Asp Glu Leu Lys Arg Gly Gly Lys Pro
 945 950 955 960
 Pro Val Asn His Val Asn Ile Val Val Gln Gln Ala Leu Pro Val Thr
 965 970 975
 Leu Asn Glu Gln Gly Glu Gly Ser Val Thr Leu Pro Ile Gly Asp Phe
 980 985 990
 Asn Gly Glu Leu Arg Val Met Ala Gln Ala Trp Thr Ala Asp Asp Phe
 995 1000 1005
 Gly Ser Asn Glu Ser Lys Val Ile Val Ala Ala Pro Val Ile Ala Glu
 1010 1015 1020
 Leu Asn Met Pro Arg Phe Met Ala Ser Gly Asp Thr Ser Arg Leu Thr
 1025 1030 1035 1040
 Leu Asp Ile Thr Asn Leu Thr Asp Lys Pro Gln Lys Leu Asn Val Ala
 1045 1050 1055
 Leu Thr Ala Ser Gly Leu Leu Glu Leu Val Ser Asp Ser Pro Ala Ala
 1060 1065 1070
 Val Glu Leu Ala Pro Gly Val Arg Thr Thr Leu Phe Ile Pro Val Arg
 1075 1080 1085
 Ala Leu Pro Gly Tyr Gly Asp Gly Glu Ile Gln Ala Thr Ile Ser Gly
 1090 1095 1100
 Leu Ala Leu Pro Gly Glu Thr Val Ala Asp Gln His Lys Gln Trp Lys
 1105 1110 1115 1120
 Ile Gly Val Arg Pro Ala Phe Pro Ala Gln Thr Val Asn Tyr Gly Thr
 1125 1130 1135
 Ala Leu Gln Pro Gly Glu Thr Trp Ala Ile Pro Ala Asp Gly Leu Gln
 1140 1145 1150
 Asn Phe Ser Pro Val Thr Leu Glu Gly Gln Leu Leu Leu Ser Gly Lys
 1155 1160 1165
 Pro Pro Leu Asn Ile Ala Arg Tyr Ile Lys Glu Leu Lys Ala Tyr Pro
 1170 1175 1180
 Tyr Gly Cys Leu Glu Gln Thr Ala Ser Gly Leu Phe Pro Ser Leu Tyr

1185	1190	1195	1200
Thr Asn Ala Ala Gln Leu Gln Ala Leu Gly Ile Lys Gly Asp Ser Asp			
	1205	1210	1215
Glu Lys Arg Arg Ala Ser Val Asp Ile Gly Ile Ser Arg Leu Leu Gln			
	1220	1225	1230
Met Gln Arg Asp Asn Gly Gly Phe Ala Leu Trp Asp Lys Asn Gly Asp			
	1235	1240	1245
Glu Glu Tyr Trp Leu Thr Ala Tyr Val Met Asp Phe Leu Val Arg Ala			
	1250	1255	1260
Gly Glu Gln Gly Tyr Ser Val Pro Thr Asp Ala Ile Asn Arg Gly Asn			
1265	1270	1275	1280
Glu Arg Leu Leu Arg Tyr Leu Gln Asp Pro Gly Met Met Ser Ile Pro			
	1285	1290	1295
Tyr Ala Asp Asn Leu Lys Ala Ser Lys Phe Ala Val Gln Ser Tyr Ala			
	1300	1305	1310
Ala Leu Val Leu Ala Arg Gln Gln Lys Ala Pro Leu Gly Ala Leu Arg			
	1315	1320	1325
Glu Ile Trp Glu His Arg Ala Asp Ala Ala Ser Gly Leu Pro Leu Leu			
	1330	1335	1340
Gln Leu Gly Val Ala Leu Lys Thr Met Gly Asp Ala Thr Arg Gly Glu			
1345	1350	1355	1360
Glu Ala Ile Ala Leu Ala Leu Lys Thr Pro Arg Asn Ser Asp Glu Arg			
	1365	1370	1375
Ile Trp Leu Gly Asp Tyr Gly Ser Ser Leu Arg Asp Asn Ala Leu Met			
	1380	1385	1390
Leu Ser Leu Leu Glu Glu Asn Lys Leu Leu Pro Asp Glu Gln Tyr Thr			
	1395	1400	1405
Leu Leu Asn Thr Leu Ser Gln Gln Ala Phe Gly Glu Arg Trp Leu Ser			
	1410	1415	1420
Thr Gln Glu Ser Asn Ala Leu Phe Leu Ala Ala Arg Thr Ile Gln Asp			
1425	1430	1435	1440
Leu Pro Gly Lys Trp Gln Ala Gln Thr Ser Phe Ser Ala Glu Gln Leu			
	1445	1450	1455
Thr Gly Glu Lys Ala Gln Asn Ser Asn Leu Asn Ser Asp Gln Leu Val			
	1460	1465	1470
Thr Leu Gln Val Ser Asn Ser Gly Asp Gln Pro Leu Trp Leu Arg Met			
	1475	1480	1485
Asp Ala Ser Gly Tyr Pro Gln Ser Ala Pro Leu Pro Ala Asn Asn Val			
	1490	1495	1500
Leu Gln Ile Glu Arg His Ile Leu Gly Thr Asp Gly Lys Ser Lys Ser			
1505	1510	1515	1520
Leu Asp Ser Leu Arg Ser Gly Asp Leu Val Leu Val Trp Leu Gln Val			
	1525	1530	1535
Lys Ala Ser Asn Ser Val Pro Asp Ala Leu Val Val Asp Leu Leu Pro			
	1540	1545	1550
Ala Gly Leu Glu Leu Glu Asn Gln Asn Leu Ala Asn Gly Ser Ala Ser			
	1555	1560	1565
Leu Glu Gln Ser Gly Gly Glu Val Gln Asn Leu Leu Asn Gln Met Gln			
	1570	1575	1580
Gln Ala Ser Ile Lys His Ile Glu Phe Arg Asp Asp Arg Phe Val Ala			
1585	1590	1595	1600
Ala Val Ala Val Asp Glu Tyr Gln Pro Val Thr Leu Val Tyr Leu Ala			
	1605	1610	1615
Arg Ala Val Thr Pro Gly Thr Tyr Gln Val Pro Gln Pro Met Val Glu			
	1620	1625	1630
Ser Met Tyr Val Pro Gln Trp Arg Ala Thr Gly Ala Ala Glu Asp Leu			
	1635	1640	1645
Leu Ile Val Arg Pro			
1650			

<210> 403
 <211> 264
 <212> PRT
 <213> Escherichia coli

<400> 403
 Met Asp Leu Leu Tyr Arg Val Lys Thr Leu Trp Ala Ala Leu Arg Gly
 1 5 10 15
 Asn His Tyr Thr Trp Pro Ala Ile Asp Ile Thr Leu Pro Gly Asn Arg
 20 25 30
 His Phe His Leu Ile Gly Ser Ile His Met Gly Ser His Asp Met Ala
 35 40 45
 Pro Leu Pro Thr Arg Leu Leu Lys Lys Leu Lys Asn Ala Asp Ala Leu
 50 55 60
 Ile Val Glu Ala Asp Val Ser Thr Ser Asp Thr Pro Phe Ala Asn Leu
 65 70 75 80
 Pro Ala Cys Glu Ala Leu Glu Glu Arg Ile Ser Glu Glu Gln Leu Gln
 85 90 95
 Asn Leu Gln His Ile Ser Gln Glu Met Gly Ile Ser Pro Ser Leu Phe
 100 105 110
 Ser Thr Gln Pro Leu Trp Gln Ile Ala Met Val Leu Gln Ala Thr Gln
 115 120 125
 Ala Gln Lys Leu Gly Leu Arg Ala Glu Tyr Gly Ile Asp Tyr Gln Leu
 130 135 140
 Leu Gln Ala Ala Lys Gln Gln His Lys Pro Val Ile Glu Leu Glu Gly
 145 150 155 160
 Ala Glu Asn Gln Ile Ala Met Leu Leu Gln Leu Pro Asp Lys Gly Leu
 165 170 175
 Ala Leu Leu Asp Asp Thr Leu Thr His Trp His Thr Asn Ala Arg Leu
 180 185 190
 Leu Gln Gln Met Met Ser Trp Trp Leu Asn Ala Pro Pro Gln Asn Asn
 195 200 205
 Asp Ile Thr Leu Pro Asn Thr Phe Ser Gln Ser Leu Tyr Asp Val Leu
 210 215 220
 Met His Gln Arg Asn Leu Ala Trp Arg Asp Lys Leu Arg Ala Met Pro
 225 230 235 240
 Pro Gly Arg Tyr Val Val Ala Val Gly Ala Leu His Leu Tyr Gly Glu
 245 250 255
 Gly Asn Leu Pro Gln Met Leu Arg
 260

<210> 404
 <211> 322
 <212> PRT
 <213> Escherichia coli

<400> 404
 Met Asp Asn Phe Leu Ala Leu Thr Leu Thr Gly Lys Lys Pro Val Ile
 1 5 10 15
 Thr Glu Arg Glu Ile Asn Gly Val Arg Trp Arg Trp Leu Gly Asp Gly
 20 25 30
 Val Leu Glu Leu Thr Pro Leu Thr Pro Pro Gln Gly Ala Leu Val Ile
 35 40 45
 Ser Ala Gly Ile His Gly Asn Glu Thr Ala Pro Val Glu Met Leu Asp
 50 55 60
 Ala Leu Leu Gly Ala Ile Ser His Gly Glu Ile Pro Leu Arg Trp Arg
 65 70 75 80
 Leu Leu Val Ile Leu Gly Asn Pro Pro Ala Leu Lys Gln Gly Lys Arg
 85 90 95
 Tyr Cys His Ser Asp Met Asn Arg Met Phe Gly Gly Arg Trp Gln Leu

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      100      105      110
Phe Ala Glu Ser Gly Glu Thr Cys Arg Ala Arg Glu Leu Glu Gln Cys
      115      120      125
Leu Glu Asp Phe Tyr Asp Gln Gly Lys Glu Ser Val Arg Trp His Leu
      130      135      140
Asp Leu His Thr Ala Ile Arg Gly Ser Leu His Pro Gln Phe Gly Val
      145      150      155      160
Leu Pro Gln Arg Asp Ile Pro Trp Asp Glu Lys Phe Leu Thr Trp Leu
      165      170      175
Gly Ala Ala Gly Leu Glu Ala Leu Val Phe His Gln Glu Pro Gly Gly
      180      185      190
Thr Phe Thr His Phe Ser Ala Arg His Phe Gly Ala Leu Ala Cys Thr
      195      200      205
Leu Glu Leu Gly Lys Ala Leu Pro Phe Gly Gln Asn Asp Leu Arg Gln
      210      215      220
Phe Ala Val Thr Ala Ser Ala Ile Ala Ala Leu Leu Ser Gly Glu Ser
      225      230      235      240
Val Gly Ile Val Arg Thr Pro Pro Leu Arg Tyr Arg Val Val Ser Gln
      245      250      255
Ile Thr Arg His Ser Pro Ser Phe Glu Met His Met Ala Ser Asp Thr
      260      265      270
Leu Asn Phe Met Pro Phe Glu Lys Gly Thr Leu Leu Ala Gln Asp Gly
      275      280      285
Glu Glu Arg Phe Thr Val Thr His Asp Val Glu Tyr Val Leu Phe Pro
      290      295      300
Asn Pro Leu Val Ala Leu Gly Leu Arg Ala Gly Leu Met Leu Glu Lys
      305      310      315      320
Ile Ser

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<210> 405

<211> 447

<212> PRT

<213> Escherichia coli

<400> 405

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Met Asn Ala Trp Glu Val Asn Phe Asp Gly Leu Val Gly Leu Thr His
  1          5          10          15
His Tyr Ala Gly Leu Ser Phe Gly Asn Glu Ala Ser Thr Arg His Arg
      20      25      30
Phe Gln Val Ser Asn Pro Arg Leu Ala Ala Lys Gln Gly Leu Leu Lys
      35      40      45
Met Lys Ala Leu Ala Asp Ala Gly Phe Pro Gln Ala Val Ile Pro Pro
      50      55      60
His Glu Arg Pro Phe Ile Pro Val Leu Arg Gln Leu Gly Phe Ser Gly
      65      70      75      80
Ser Asp Glu Gln Val Leu Glu Lys Val Ala Arg Gln Ala Pro His Trp
      85      90      95
Leu Ser Ser Val Ser Ser Ala Ser Pro Met Trp Val Ala Asn Ala Ala
      100      105      110
Thr Ile Ala Pro Ser Ala Asp Thr Leu Asp Gly Lys Val His Leu Thr
      115      120      125
Val Ala Asn Leu Asn Asn Lys Phe His Arg Ser Leu Glu Ala Pro Val
      130      135      140
Thr Glu Ser Leu Leu Lys Ala Ile Phe Asn Asp Glu Glu Lys Phe Ser
      145      150      155      160
Val His Ser Ala Leu Pro Gln Val Ala Leu Leu Gly Asp Glu Gly Ala
      165      170      175
Ala Asn His Asn Arg Leu Gly Gly His Tyr Gly Glu Pro Gly Met Gln
      180      185      190

```

Leu Phe Val Tyr Gly Arg Glu Glu Gly Asn Asp Thr Arg Pro Ser Arg
 195 200 205
 Tyr Pro Ala Arg Gln Thr Arg Glu Ala Ser Glu Ala Val Ala Arg Leu
 210 215 220
 Asn Gln Val Asn Pro Gln Gln Val Ile Phe Ala Gln Gln Asn Pro Asp
 225 230 235 240
 Val Ile Asp Gln Gly Val Phe His Asn Asp Val Ile Ala Val Ser Asn
 245 250 255
 Arg Gln Val Leu Phe Cys His Gln Gln Ala Phe Ala Arg Gln Ser Gln
 260 265 270
 Leu Leu Ala Asn Leu Arg Ala Arg Val Asn Gly Phe Met Ala Ile Glu
 275 280 285
 Val Pro Ala Thr Gln Val Ser Val Ser Asp Thr Val Ser Thr Tyr Leu
 290 295 300
 Phe Asn Ser Gln Leu Leu Ser Arg Asp Asp Gly Ser Met Met Leu Val
 305 310 315 320
 Leu Pro Gln Glu Cys Arg Glu His Ala Gly Val Trp Gly Tyr Leu Asn
 325 330 335
 Glu Leu Leu Ala Ala Asp Asn Pro Ile Ser Glu Leu Lys Val Phe Asp
 340 345 350
 Leu Arg Glu Ser Met Ala Asn Gly Gly Gly Pro Ala Cys Leu Arg Leu
 355 360 365
 Arg Val Val Leu Thr Glu Glu Glu Arg Arg Ala Val Asn Pro Ala Val
 370 375 380
 Met Met Asn Asp Thr Leu Phe Asn Ala Leu Asn Asp Trp Val Asp Arg
 385 390 395 400
 Tyr Tyr Arg Asp Arg Leu Thr Ala Ala Asp Leu Ala Asp Pro Gln Leu
 405 410 415
 Leu Arg Glu Gly Arg Glu Ala Leu Asp Val Leu Ser Gln Leu Leu Asn
 420 425 430
 Leu Gly Ser Val Tyr Pro Phe Gln Arg Glu Gly Gly Gly Asn Gly
 435 440 445

<210> 406

<211> 492

<212> PRT

<213> Escherichia coli

<400> 406

Met Thr Leu Trp Ile Asn Gly Asp Trp Ile Thr Gly Gln Gly Ala Ser
 1 5 10 15
 Arg Val Lys Arg Asn Pro Val Ser Gly Glu Val Leu Trp Gln Gly Asn
 20 25 30
 Asp Ala Asp Ala Ala Gln Val Glu Gln Ala Cys Arg Ala Ala Arg Ala
 35 40 45
 Ala Phe Pro Arg Trp Ala Arg Leu Ser Phe Ala Glu Arg His Ala Val
 50 55 60
 Val Glu Arg Phe Ala Ala Leu Leu Glu Ser Asn Lys Ala Glu Leu Thr
 65 70 75 80
 Ala Ile Ile Ala Arg Glu Thr Gly Lys Pro Arg Trp Glu Ala Ala Thr
 85 90 95
 Glu Val Thr Ala Met Ile Asn Lys Ile Ala Ile Ser Ile Lys Ala Tyr
 100 105 110
 His Val Arg Thr Gly Glu Gln Arg Ser Glu Met Pro Asp Gly Ala Ala
 115 120 125
 Ser Leu Arg His Arg Pro His Gly Val Leu Ala Val Phe Gly Pro Tyr
 130 135 140
 Asn Phe Pro Gly His Leu Pro Asn Gly His Ile Val Pro Ala Leu Leu
 145 150 155 160
 Ala Gly Asn Thr Ile Ile Phe Lys Pro Ser Glu Leu Thr Pro Trp Ser

```

      165      170      175
Gly Glu Ala Val Met Arg Leu Trp Gln Gln Ala Gly Leu Pro Pro Gly
      180      185      190
Val Leu Asn Leu Val Gln Gly Gly Arg Glu Thr Gly Gln Ala Leu Ser
      195      200      205
Ala Leu Glu Asp Leu Asp Gly Leu Leu Phe Thr Gly Ser Ala Asn Thr
      210      215      220
Gly Tyr Gln Leu His Arg Gln Leu Ser Gly Gln Pro Glu Lys Ile Leu
      225      230      235
Ala Leu Glu Met Gly Gly Asn Asn Pro Leu Ile Ile Asp Glu Val Ala
      245      250      255
Asp Ile Asp Ala Ala Val His Leu Thr Ile Gln Ser Ala Phe Val Thr
      260      265      270
Ala Gly Gln Arg Cys Thr Cys Ala Arg Arg Leu Leu Leu Lys Ser Gly
      275      280      285
Ala Gln Gly Asp Ala Phe Leu Ala Arg Leu Val Ala Val Ser Gln Arg
      290      295      300
Leu Thr Pro Gly Asn Trp Asp Asp Glu Pro Gln Pro Phe Ile Gly Gly
      305      310      315
Leu Ile Ser Glu Gln Ala Ala Gln Gln Val Val Thr Ala Trp Gln Gln
      325      330      335
Leu Glu Ala Met Gly Gly Arg Pro Leu Leu Ala Pro Arg Leu Leu Gln
      340      345      350
Ala Gly Thr Ser Leu Leu Thr Pro Gly Ile Ile Glu Met Thr Gly Val
      355      360      365
Ala Gly Val Pro Asp Glu Glu Val Phe Gly Pro Leu Leu Arg Val Trp
      370      375      380
Arg Tyr Asp Thr Phe Asp Glu Ala Ile Arg Met Ala Asn Asn Thr Arg
      385      390      395
Phe Gly Leu Ser Cys Gly Leu Val Ser Pro Glu Arg Glu Lys Phe Asp
      405      410      415
Gln Leu Leu Leu Glu Ala Arg Ala Gly Ile Val Asn Trp Asn Lys Pro
      420      425      430
Leu Thr Gly Ala Ala Ser Thr Ala Pro Phe Gly Gly Ile Gly Ala Ser
      435      440      445
Gly Asn His Arg Pro Ser Ala Trp Tyr Ala Ala Asp Tyr Cys Ala Trp
      450      455      460
Pro Met Ala Ser Leu Glu Ser Asp Ser Leu Thr Leu Pro Ala Thr Leu
      465      470      475
Asn Pro Gly Leu Asp Phe Ser Asp Glu Val Val Arg
      485      490

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<210> 407

<211> 344

<212> PRT

<213> Escherichia coli

<400> 407

```

Met Met Val Ile Arg Pro Val Glu Arg Ser Asp Val Ser Ala Leu Met
 1          5          10          15
Gln Leu Ala Ser Lys Thr Gly Gly Gly Leu Thr Ser Leu Pro Ala Asn
      20      25      30
Glu Ala Thr Leu Ser Ala Arg Ile Glu Arg Ala Ile Lys Thr Trp Gln
      35      40      45
Gly Glu Leu Pro Lys Ser Glu Gln Gly Tyr Val Phe Val Leu Glu Asp
      50      55      60
Ser Glu Thr Gly Thr Val Ala Gly Ile Cys Ala Ile Glu Val Ala Val
      65      70      75      80
Gly Leu Asn Asp Pro Trp Tyr Asn Tyr Arg Val Gly Thr Leu Val His
      85      90      95

```

Ala Ser Lys Glu Leu Asn Val Tyr Asn Ala Leu Pro Thr Leu Phe Leu
 100 105 110
 Ser Asn Asp His Thr Gly Ser Ser Glu Leu Cys Thr Leu Phe Leu Asp
 115 120 125
 Pro Asp Trp Arg Lys Glu Gly Asn Gly Tyr Leu Leu Ser Lys Ser Arg
 130 135 140
 Phe Met Phe Met Ala Ala Phe Arg Asp Lys Phe Asn Asp Lys Val Val
 145 150 155 160
 Ala Glu Met Arg Gly Val Ile Asp Glu His Gly Tyr Ser Pro Phe Trp
 165 170 175
 Gln Ser Leu Gly Lys Arg Phe Phe Ser Met Asp Phe Ser Arg Ala Asp
 180 185 190
 Phe Leu Cys Gly Thr Gly Gln Lys Ala Phe Ile Ala Glu Leu Met Pro
 195 200 205
 Lys His Pro Ile Tyr Thr His Phe Leu Ser Gln Glu Ala Gln Asp Val
 210 215 220
 Ile Gly Gln Val His Pro Gln Thr Ala Pro Ala Arg Ala Val Leu Glu
 225 230 235 240
 Lys Glu Gly Phe Arg Tyr Arg Asn Tyr Ile Asp Ile Phe Asp Gly Gly
 245 250 255
 Pro Thr Leu Glu Cys Asp Ile Asp Arg Val Arg Ala Ile Arg Lys Ser
 260 265 270
 Arg Leu Val Glu Val Ala Glu Gly Gln Pro Ala Gln Gly Asp Phe Pro
 275 280 285
 Ala Cys Leu Val Ala Asn Glu Asn Tyr His His Phe Arg Val Val Leu
 290 295 300
 Val Arg Thr Asp Pro Ala Thr Glu Arg Leu Ile Leu Thr Ala Ala Gln
 305 310 315 320
 Leu Asp Ala Leu Lys Cys His Ala Gly Asp Arg Val Arg Leu Val Arg
 325 330 335
 Leu Cys Ala Glu Glu Lys Thr Ala
 340

<210> 408

<211> 406

<212> PRT

<213> Escherichia coli

<400> 408

Met Ser Gln Pro Ile Thr Arg Glu Asn Phe Asp Glu Trp Met Ile Pro
 1 5 10 15
 Val Tyr Ala Pro Ala Pro Phe Ile Pro Val Arg Gly Glu Gly Ser Arg
 20 25 30
 Leu Trp Asp Gln Gln Gly Lys Glu Tyr Ile Asp Phe Ala Gly Gly Ile
 35 40 45
 Ala Val Asn Ala Leu Gly His Ala His Pro Glu Leu Arg Glu Ala Leu
 50 55 60
 Asn Glu Gln Ala Ser Lys Phe Trp His Thr Gly Asn Gly Tyr Thr Asn
 65 70 75 80
 Glu Pro Val Leu Arg Leu Ala Lys Lys Leu Ile Asp Ala Thr Phe Ala
 85 90 95
 Asp Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala
 100 105 110
 Leu Lys Leu Ala Arg Lys Phe Ala His Asp Arg Tyr Gly Ser His Lys
 115 120 125
 Ser Gly Ile Val Ala Phe Lys Asn Ala Phe His Gly Arg Thr Leu Phe
 130 135 140
 Thr Val Ser Ala Gly Gly Gln Pro Ala Tyr Ser Gln Asp Phe Ala Pro
 145 150 155 160
 Leu Pro Ala Asp Ile Arg His Ala Ala Tyr Asn Asp Ile Asn Ser Ala

```

165      170      175
Ser Ala Leu Ile Asp Asp Ser Thr Cys Ala Val Ile Val Glu Pro Ile
180      185      190
Gln Gly Glu Gly Gly Val Val Pro Ala Ser Asn Ala Phe Leu Gln Gly
195      200      205
Leu Arg Glu Leu Cys Asn Arg His Asn Ala Leu Leu Ile Phe Asp Glu
210      215      220
Val Gln Thr Gly Val Gly Arg Thr Gly Glu Leu Tyr Ala Tyr Met His
225      230      235
Tyr Gly Val Thr Pro Asp Leu Leu Thr Thr Ala Lys Ala Leu Gly Gly
245      250      255
Gly Phe Pro Val Gly Ala Leu Leu Ala Thr Glu Glu Cys Ala Arg Val
260      265      270
Met Thr Val Gly Thr His Gly Thr Thr Tyr Gly Gly Asn Pro Leu Ala
275      280      285
Ser Ala Val Ala Gly Lys Val Leu Glu Leu Ile Asn Thr Pro Glu Met
290      295      300
Leu Asn Gly Val Lys Gln Arg His Asp Trp Phe Val Glu Arg Leu Asn
305      310      315
Thr Ile Asn His Arg Tyr Gly Leu Phe Ser Glu Val Arg Gly Leu Gly
325      330      335
Leu Leu Ile Gly Cys Val Leu Asn Ala Asp Tyr Ala Gly Gln Ala Lys
340      345      350
Gln Ile Ser Gln Glu Ala Ala Lys Ala Gly Val Met Val Leu Ile Ala
355      360      365
Gly Gly Asn Val Val Arg Phe Ala Pro Ala Leu Asn Val Ser Glu Glu
370      375      380
Glu Val Thr Thr Gly Leu Asp Arg Phe Ala Ala Cys Glu His Phe
385      390      395
Val Ser Arg Gly Ser Ser
405

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<210> 409

<211> 1048

<212> PRT

<213> Escherichia coli

<400> 409

```

Met Lys Ile Leu Ser Leu Arg Leu Lys Asn Leu Asn Ser Leu Lys Gly
1      5      10      15
Glu Trp Lys Ile Asp Phe Thr Arg Glu Pro Phe Ala Ser Asn Gly Leu
20      25      30
Phe Ala Ile Thr Gly Pro Thr Gly Ala Gly Lys Thr Thr Leu Leu Asp
35      40      45
Ala Ile Cys Leu Ala Leu Tyr His Glu Thr Pro Arg Leu Ser Asn Val
50      55      60
Ser Gln Ser Gln Asn Asp Leu Met Thr Arg Asp Thr Ala Glu Cys Leu
65      70      75
Ala Glu Val Glu Phe Glu Val Lys Gly Glu Ala Tyr Arg Ala Phe Trp
85      90      95
Ser Gln Asn Arg Ala Arg Asn Gln Pro Asp Gly Asn Leu Gln Val Pro
100      105      110
Arg Val Glu Leu Ala Arg Cys Ala Asp Gly Lys Ile Leu Ala Asp Lys
115      120      125
Val Lys Asp Lys Leu Glu Leu Thr Ala Thr Leu Thr Gly Leu Asp Tyr
130      135      140
Gly Arg Phe Thr Arg Ser Met Leu Leu Ser Gln Gly Gln Phe Ala Ala
145      150      155
Phe Leu Asn Ala Lys Pro Lys Glu Arg Ala Glu Leu Leu Glu Glu Leu
165      170      175

```

Thr Gly Thr Glu Ile Tyr Gly Gln Ile Ser Ala Met Val Phe Glu Gln
 180 185 190
 His Lys Ser Ala Arg Thr Glu Leu Glu Lys Leu Gln Ala Gln Ala Ser
 195 200 205
 Gly Val Thr Leu Leu Thr Pro Glu Gln Val Gln Ser Leu Thr Ala Ser
 210 215 220
 Leu Gln Val Leu Thr Asp Glu Glu Lys Gln Leu Ile Thr Ala Gln Gln
 225 230 235 240
 Gln Glu Gln Gln Ser Leu Asn Trp Leu Thr Arg Gln Asp Glu Leu Gln
 245 250 255
 Gln Glu Ala Ser Arg Arg Gln Gln Ala Leu Gln Gln Ala Leu Ala Glu
 260 265 270
 Glu Glu Lys Ala Gln Pro Gln Leu Ala Ala Leu Ser Leu Ala Gln Pro
 275 280 285
 Ala Arg Asn Leu Arg Pro His Trp Glu Arg Ile Ala Glu His Ser Ala
 290 295 300
 Ala Leu Ala His Ile Arg Gln Gln Ile Glu Glu Val Asn Thr Arg Leu
 305 310 315 320
 Gln Ser Thr Met Ala Leu Arg Ala Ser Ile Arg His His Ala Ala Lys
 325 330 335
 Gln Ser Ala Glu Leu Gln Gln Gln Gln Gln Ser Leu Asn Thr Trp Leu
 340 345 350
 Gln Glu His Asp Arg Phe Arg Gln Trp Asn Asn Glu Pro Ala Gly Trp
 355 360 365
 Arg Ala Gln Phe Ser Gln Gln Thr Ser Asp Arg Glu His Leu Arg Gln
 370 375 380
 Trp Gln Gln Gln Leu Thr His Ala Glu Gln Lys Leu Asn Ala Leu Ala
 385 390 395 400
 Ala Ile Thr Leu Thr Leu Thr Ala Asp Glu Val Ala Thr Ala Leu Ala
 405 410 415
 Gln His Ala Glu Gln Arg Pro Leu Arg Gln His Leu Val Ala Leu His
 420 425 430
 Gly Gln Ile Val Pro Gln Gln Lys Arg Leu Ala Gln Leu Gln Val Ala
 435 440 445
 Ile Gln Asn Val Thr Gln Glu Gln Thr Gln Arg Asn Ala Ala Leu Asn
 450 455 460
 Glu Met Arg Gln Arg Tyr Lys Glu Lys Thr Gln Gln Leu Ala Asp Val
 465 470 475 480
 Lys Thr Ile Cys Glu Gln Glu Ala Arg Ile Lys Thr Leu Glu Ala Gln
 485 490 495
 Arg Ala Gln Leu Gln Ala Gly Gln Pro Cys Pro Leu Cys Gly Ser Thr
 500 505 510
 Ser His Pro Ala Val Glu Ala Tyr Gln Ala Leu Glu Pro Gly Val Asn
 515 520 525
 Gln Ser Arg Leu Leu Ala Leu Glu Asn Glu Val Lys Lys Leu Gly Glu
 530 535 540
 Glu Gly Ala Thr Leu Arg Gly Gln Leu Asp Ala Ile Thr Lys Gln Leu
 545 550 555 560
 Gln Arg Asp Glu Asn Glu Ala Gln Ser Leu Arg Gln Asp Glu Gln Ala
 565 570 575
 Leu Thr Gln Gln Trp Gln Ala Val Thr Ala Ser Leu Asn Ile Thr Leu
 580 585 590
 Gln Pro Leu Asp Asp Ile Gln Pro Trp Leu Asp Ala Gln Asp Glu His
 595 600 605
 Glu Arg Gln Leu Arg Leu Leu Ser Gln Arg His Glu Leu Gln Gly Gln
 610 615 620
 Ile Ala Ala His Asn Gln Gln Ile Ile Gln Tyr Gln Gln Gln Ile Glu
 625 630 635 640
 Gln Arg Gln Gln Leu Leu Thr Thr Leu Thr Gly Tyr Ala Leu Thr
 645 650 655
 Leu Pro Gln Glu Asp Glu Glu Glu Ser Trp Leu Ala Thr Arg Gln Gln

660										665					670				
Glu	Ala	Gln	Ser	Trp	Gln	Gln	Arg	Gln	Asn	Glu	Leu	Thr	Ala	Leu	Gln				
		675						680					685						
Asn	Arg	Ile	Gln	Gln	Leu	Thr	Pro	Ile	Leu	Glu	Thr	Leu	Pro	Gln	Ser				
		690				695						700							
Asp	Glu	Leu	Pro	His	Cys	Glu	Glu	Thr	Val	Val	Leu	Glu	Asn	Trp	Arg				
705					710					715					720				
Gln	Val	His	Glu	Gln	Cys	Leu	Ala	Leu	His	Ser	Gln	Gln	Gln	Thr	Leu				
				725					730					735					
Gln	Gln	Gln	Asp	Val	Leu	Ala	Ala	Gln	Ser	Leu	Gln	Lys	Ala	Gln	Ala				
			740					745					750						
Gln	Phe	Asp	Thr	Ala	Leu	Gln	Ala	Ser	Val	Phe	Asp	Asp	Gln	Gln	Ala				
		755				760					765								
Phe	Leu	Ala	Ala	Leu	Met	Asp	Glu	Gln	Thr	Leu	Thr	Gln	Leu	Glu	Gln				
		770				775					780								
Leu	Lys	Gln	Asn	Leu	Glu	Asn	Gln	Arg	Arg	Gln	Ala	Gln	Thr	Leu	Val				
785					790					795					800				
Thr	Gln	Thr	Ala	Glu	Thr	Leu	Ala	Gln	His	Gln	Gln	His	Arg	Pro	Asp				
			805					810						815					
Asp	Gly	Leu	Ala	Leu	Thr	Val	Thr	Val	Glu	Gln	Ile	Gln	Gln	Glu	Leu				
			820					825					830						
Ala	Gln	Thr	His	Gln	Lys	Leu	Arg	Glu	Asn	Thr	Thr	Ser	Gln	Gly	Glu				
		835					840					845							
Ile	Arg	Gln	Gln	Leu	Lys	Gln	Asp	Ala	Asp	Asn	Arg	Gln	Gln	Gln	Gln				
	850					855				860									
Thr	Leu	Met	Gln	Gln	Ile	Ala	Gln	Met	Thr	Gln	Val	Glu	Asp	Trp					
865					870					875				880					
Gly	Tyr	Leu	Asn	Ser	Leu	Ile	Gly	Ser	Lys	Glu	Gly	Asp	Lys	Phe	Arg				
			885					890					895						
Lys	Phe	Ala	Gln	Gly	Leu	Thr	Leu	Asp	Asn	Leu	Val	His	Leu	Ala	Asn				
		900						905					910						
Gln	Gln	Leu	Thr	Arg	Leu	His	Gly	Arg	Tyr	Leu	Leu	Gln	Arg	Lys	Ala				
		915					920					925							
Ser	Glu	Ala	Leu	Glu	Val	Glu	Val	Val	Asp	Thr	Trp	Gln	Ala	Asp	Ala				
		930				935					940								
Val	Arg	Asp	Thr	Arg	Thr	Leu	Ser	Gly	Gly	Glu	Ser	Phe	Leu	Val	Ser				
945					950					955					960				
Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ser	Asp	Leu	Val	Ser	His	Lys	Thr	Arg				
			965					970					975						
Ile	Asp	Ser	Leu	Phe	Leu	Asp	Glu	Gly	Phe	Gly	Thr	Leu	Asp	Ser	Glu				
		980					985					990							
Thr	Leu	Asp	Thr	Ala	Leu	Asp	Ala	Leu	Asp	Ala	Leu	Asn	Ala	Ser	Gly				
		995					1000					1005							
Lys	Thr	Ile	Gly	Val	Ile	Ser	His	Val	Glu	Ala	Met	Lys	Glu	Arg	Ile				
		1010				1015					1020								
Pro	Val	Gln	Ile	Lys	Val	Lys	Lys	Ile	Asn	Gly	Leu	Gly	Tyr	Ser	Lys				
1025				1030						1035					1040				
Leu	Glu	Ser	Thr	Phe	Ala	Val	Lys												
				1045															

<210> 410

<211> 400

<212> PRT

<213> Escherichia coli

<400> 410

Met	Arg	Ile	Leu	His	Thr	Ser	Asp	Trp	His	Leu	Gly	Gln	Asn	Phe	Tyr
1			5						10					15	
Ser	Lys	Ser	Arg	Glu	Ala	Glu	His	Gln	Ala	Phe	Leu	Asp	Trp	Leu	Leu
			20					25					30		

Glu Thr Ala Gln Thr His Gln Val Asp Ala Ile Ile Val Ala Gly Asp
 35 40 45
 Val Phe Asp Thr Gly Ser Pro Pro Ser Tyr Ala Arg Thr Leu Tyr Asn
 50 55 60
 Arg Phe Val Val Asn Leu Gln Gln Thr Gly Cys His Leu Val Val Leu
 65 70 75 80
 Ala Gly Asn His Asp Ser Val Ala Thr Leu Asn Glu Ser Arg Asp Ile
 85 90 95
 Met Ala Phe Leu Asn Thr Thr Val Val Ala Ser Ala Gly His Ala Pro
 100 105 110
 Gln Ile Leu Pro Arg Arg Asp Gly Thr Pro Gly Ala Val Leu Cys Pro
 115 120 125
 Ile Pro Phe Leu Arg Pro Arg Asp Ile Ile Thr Ser Gln Ala Gly Leu
 130 135 140
 Asn Gly Ile Glu Lys Gln Gln His Leu Leu Ala Ala Ile Thr Asp Tyr
 145 150 155 160
 Tyr Gln Gln His Tyr Ala Asp Ala Cys Lys Leu Arg Gly Asp Gln Pro
 165 170 175
 Leu Pro Ile Ile Ala Thr Gly His Leu Thr Thr Val Gly Ala Ser Lys
 180 185 190
 Ser Asp Ala Val Arg Asp Ile Tyr Ile Gly Thr Leu Asp Ala Phe Pro
 195 200 205
 Ala Gln Asn Phe Pro Pro Ala Asp Tyr Ile Ala Leu Gly His Ile His
 210 215 220
 Arg Ala Gln Ile Ile Gly Gly Met Glu His Val Arg Tyr Cys Gly Ser
 225 230 235 240
 Pro Ile Pro Leu Ser Phe Asp Glu Cys Gly Lys Ser Lys Tyr Val His
 245 250 255
 Leu Val Thr Phe Ser Asn Gly Lys Leu Glu Ser Val Glu Asn Leu Asn
 260 265 270
 Val Pro Val Thr Gln Pro Met Ala Val Leu Lys Gly Asp Leu Ala Ser
 275 280 285
 Ile Thr Ala Gln Leu Glu Gln Trp Arg Asp Val Ser Gln Glu Pro Pro
 290 295 300
 Val Trp Leu Asp Ile Glu Ile Thr Thr Asp Glu Tyr Leu His Asp Ile
 305 310 315 320
 Gln Arg Lys Ile Gln Ala Leu Thr Glu Ser Leu Pro Val Glu Val Leu
 325 330 335
 Leu Val Arg Arg Ser Arg Glu Gln Arg Glu Arg Val Leu Ala Ser Gln
 340 345 350
 Gln Arg Glu Thr Leu Ser Glu Leu Ser Val Glu Glu Val Phe Asn Arg
 355 360 365
 Arg Leu Ala Leu Glu Glu Leu Asp Glu Ser Gln Gln Gln Arg Leu Gln
 370 375 380
 His Leu Phe Thr Thr Thr Leu His Thr Leu Ala Gly Glu His Glu Ala
 385 390 395 400

<210> 411

<211> 254

<212> PRT

<213> Escherichia coli

<400> 411

Met Asn Asp Leu Phe Ser Leu Ala Gly Lys Asn Ile Leu Ile Thr Gly
 1 5 10 15
 Ser Ala Gln Gly Ile Gly Phe Leu Leu Ala Thr Gly Leu Gly Lys Tyr
 20 25 30
 Gly Ala Gln Ile Ile Ile Asn Asp Ile Thr Ala Glu Arg Ala Glu Leu
 35 40 45
 Ala Val Glu Lys Leu His Gln Glu Gly Ile Gln Ala Val Ala Ala Pro

50		55		60
Phe Asn Val Thr His	Lys His Glu Ile Asp Ala Val Glu His Ile			
65	70	75	80	
Glu Lys Asp Ile Gly	Pro Ile Asp Val Leu Val Asn Asn Ala Gly Ile			
	85	90	95	
Gln Arg Arg His Pro	Phe Thr Glu Phe Pro Glu Gln Glu Trp Asn Asp			
	100	105	110	
Val Ile Ala Val Asn	Gln Thr Ala Val Phe Leu Val Ser Gln Ala Val			
	115	120	125	
Thr Arg His Met Val	Glu Arg Lys Ala Gly Lys Val Ile Asn Ile Cys			
	130	135	140	
Ser Met Gln Ser Glu	Leu Gly Arg Asp Thr Ile Thr Pro Tyr Ala Ala			
145	150	155	160	
Ser Lys Gly Ala Val	Lys Met Leu Thr Arg Gly Met Cys Val Glu Leu			
	165	170	175	
Ala Arg His Asn Ile	Gln Val Asn Gly Ile Ala Pro Gly Tyr Phe Lys			
	180	185	190	
Thr Glu Met Thr Lys	Ala Leu Val Glu Asp Glu Ala Phe Thr Ala Trp			
	195	200	205	
Leu Cys Lys Arg Thr	Pro Ala Ala Arg Trp Gly Asp Pro Gln Glu Leu			
	210	215	220	
Ile Gly Ala Ala Val	Phe Leu Ser Ser Lys Ala Ser Asp Phe Val Asn			
225	230	235	240	
Gly His Leu Leu Phe	Val Asp Gly Gly Met Leu Val Ala Val			
	245	250		

<210> 412

<211> 343

<212> PRT

<213> Escherichia coli

<400> 412

Met Gln Val Lys Thr	Gln Ser Cys Val Val Ala Gly Lys Lys Thr Val
1	5 10 15
Ala Val Thr Glu Gln	Thr Ile Asp Trp Asn Asn Asn Gly Thr Leu Val
	20 25 30
Gln Ile Thr Arg Gly	Gly Ile Cys Gly Ser Asp Leu His Tyr Tyr Gln
	35 40 45
Glu Gly Lys Val Gly	Asn Phe Met Ile Lys Ala Pro Met Val Leu Gly
	50 55 60
His Glu Val Ile Gly	Lys Val Ile His Ser Asp Ser Ser Glu Leu His
65	70 75 80
Glu Gly Gln Thr Val	Ala Ile Asn Pro Ser Lys Pro Cys Gly His Cys
	85 90 95
Lys Tyr Cys Ile Glu	His Asn Glu Asn Gln Cys Thr Asp Met Arg Phe
	100 105 110
Phe Gly Ser Ala Met	Tyr Phe Pro His Val Asp Gly Gly Phe Thr Arg
	115 120 125
Tyr Lys Met Val Glu	Thr Ser Gln Cys Val Pro Tyr Pro Ala Lys Ala
	130 135 140
Asp Glu Lys Val Met	Ala Phe Ala Glu Pro Leu Ala Val Ala Ile His
145	150 155 160
Ala Ala His Gln Ala	Gly Glu Leu Gln Gly Lys Arg Val Phe Ile Ser
	165 170 175
Gly Val Gly Pro Ile	Gly Cys Leu Ile Val Ser Ala Val Lys Thr Leu
	180 185 190
Gly Ala Ala Glu Ile	Val Cys Ala Asp Val Ser Pro Arg Ser Leu Ser
	195 200 205
Leu Gly Lys Glu Met	Gly Ala Asp Val Leu Val Asn Pro Gln Asn Asp
	210 215 220

Asp Met Asp His Trp Lys Ala Glu Lys Gly Tyr Phe Asp Val Ser Phe
 225 230 235 240
 Glu Val Ser Gly His Pro Ser Ser Val Asn Thr Cys Leu Glu Val Thr
 245 250 255
 Arg Ala Arg Gly Val Met Val Gln Val Gly Met Gly Gly Ala Met Ala
 260 265 270
 Glu Phe Pro Met Met Thr Leu Ile Gly Lys Glu Ile Ser Leu Arg Gly
 275 280 285
 Ser Phe Arg Phe Thr Ser Glu Phe Asn Thr Ala Val Ser Trp Leu Ala
 290 295 300
 Asn Gly Val Ile Asn Pro Leu Pro Leu Leu Ser Ala Glu Tyr Pro Phe
 305 310 315 320
 Thr Asp Leu Glu Glu Ala Leu Arg Phe Ala Gly Asp Lys Thr Gln Ala
 325 330 335
 Ala Lys Val Gln Leu Val Phe
 340

<210> 413

<211> 548

<212> PRT

<213> Escherichia coli

<400> 413

Met Asp Ser Gln Arg Asn Leu Leu Val Ile Ala Leu Leu Phe Val Ser
 1 5 10 15
 Phe Met Ile Trp Gln Ala Trp Glu Gln Asp Lys Asn Pro Gln Pro Gln
 20 25 30
 Ala Gln Gln Thr Thr Gln Thr Thr Thr Thr Ala Ala Gly Ser Ala Ala
 35 40 45
 Asp Gln Gly Val Pro Ala Ser Gly Gln Gly Lys Leu Ile Ser Val Lys
 50 55 60
 Thr Asp Val Leu Asp Leu Thr Ile Asn Thr Arg Gly Gly Asp Val Glu
 65 70 75 80
 Gln Ala Leu Leu Pro Ala Tyr Pro Lys Glu Leu Asn Ser Thr Gln Pro
 85 90 95
 Phe Gln Leu Leu Glu Thr Ser Pro Gln Phe Ile Tyr Gln Ala Gln Ser
 100 105 110
 Gly Leu Thr Gly Arg Asp Gly Pro Asp Asn Pro Ala Asn Gly Pro Arg
 115 120 125
 Pro Leu Tyr Asn Val Glu Lys Asp Ala Tyr Val Leu Ala Glu Gly Gln
 130 135 140
 Asn Glu Leu Gln Val Pro Met Thr Tyr Thr Asp Ala Ala Gly Asn Thr
 145 150 155 160
 Phe Thr Lys Thr Phe Val Leu Lys Arg Gly Asp Tyr Ala Val Asn Val
 165 170 175
 Asn Tyr Asn Val Gln Asn Ala Gly Glu Lys Pro Leu Glu Ile Ser Ser
 180 185 190
 Phe Gly Gln Leu Lys Gln Ser Ile Thr Leu Pro Pro His Leu Asp Thr
 195 200 205
 Gly Ser Ser Asn Phe Ala Leu His Thr Phe Arg Gly Ala Ala Tyr Ser
 210 215 220
 Thr Pro Asp Glu Lys Tyr Glu Lys Tyr Lys Phe Asp Thr Ile Ala Asp
 225 230 235 240
 Asn Glu Asn Leu Asn Ile Ser Ser Lys Gly Gly Trp Val Ala Met Leu
 245 250 255
 Gln Gln Tyr Phe Ala Thr Ala Trp Ile Pro His Asn Asp Gly Thr Asn
 260 265 270
 Asn Phe Tyr Thr Ala Asn Leu Gly Asn Gly Ile Ala Ala Ile Gly Tyr
 275 280 285
 Lys Ser Gln Pro Val Leu Val Gln Pro Gly Gln Thr Gly Ala Met Asn

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      290              295              300
Ser Thr Leu Trp Val Gly Pro Glu Ile Gln Asp Lys Met Ala Ala Val
305              310              315              320
Ala Pro His Leu Asp Leu Thr Val Asp Tyr Gly Trp Leu Trp Phe Ile
      325              330              335
Ser Gln Pro Leu Phe Lys Leu Leu Lys Trp Ile His Ser Phe Val Gly
      340              345              350
Asn Trp Gly Phe Ser Ile Ile Ile Ile Thr Phe Ile Val Arg Gly Ile
      355              360              365
Met Tyr Pro Leu Thr Lys Ala Gln Tyr Thr Ser Met Ala Lys Met Arg
      370              375              380
Met Leu Gln Pro Lys Ile Gln Ala Met Arg Glu Arg Leu Gly Asp Asp
385              390              395              400
Lys Gln Arg Ile Ser Gln Glu Met Met Ala Leu Tyr Lys Ala Glu Lys
      405              410              415
Val Asn Pro Leu Gly Gly Cys Phe Pro Leu Leu Ile Gln Met Pro Ile
      420              425              430
Phe Leu Ala Leu Tyr Tyr Met Leu Met Gly Ser Val Glu Leu Arg Gln
      435              440              445
Ala Pro Phe Ala Leu Trp Ile His Asp Leu Ser Ala Gln Asp Pro Tyr
      450              455              460
Tyr Ile Leu Pro Ile Leu Met Gly Val Thr Met Phe Phe Ile Gln Lys
465              470              475              480
Met Ser Pro Thr Thr Val Thr Asp Pro Met Gln Gln Lys Ile Met Thr
      485              490              495
Phe Met Pro Val Ile Phe Thr Val Phe Phe Leu Trp Phe Pro Ser Gly
      500              505              510
Leu Val Leu Tyr Tyr Ile Val Ser Asn Leu Val Thr Ile Ile Gln Gln
      515              520              525
Gln Leu Ile Tyr Arg Gly Leu Glu Lys Arg Gly Leu His Ser Arg Glu
      530              535              540
Lys Lys Lys Ser
545

```

<210> 414

<211> 542

<212> PRT

<213> Escherichia coli

<400> 414

```

Met Lys Thr Arg Asp Ser Gln Ser Ser Asp Val Ile Ile Ile Gly Gly
1      5      10      15
Gly Ala Thr Gly Ala Gly Ile Ala Arg Asp Cys Ala Leu Arg Gly Leu
      20      25      30
Arg Val Ile Leu Val Glu Arg His Asp Ile Ala Thr Gly Ala Thr Gly
      35      40      45
Arg Asn His Gly Leu Leu His Ser Gly Ala Arg Tyr Ala Val Thr Asp
      50      55      60
Ala Glu Ser Ala Arg Glu Cys Ile Ser Glu Asn Gln Ile Leu Lys Arg
65      70      75      80
Ile Ala Arg His Cys Val Glu Pro Thr Asn Gly Leu Phe Ile Thr Leu
      85      90      95
Pro Glu Asp Asp Leu Ser Phe Gln Ala Thr Phe Ile Arg Ala Cys Glu
      100      105      110
Glu Ala Gly Ile Ser Ala Glu Ala Ile Asp Pro Gln Gln Ala Arg Ile
      115      120      125
Ile Glu Pro Ala Val Asn Pro Ala Leu Ile Gly Ala Val Lys Val Pro
      130      135      140
Asp Gly Thr Val Asp Pro Phe Arg Leu Thr Ala Ala Asn Met Leu Asp
145      150      155      160

```

Ala Lys Glu His Gly Ala Val Ile Leu Thr Ala His Glu Val Thr Gly
 165 170 175
 Leu Ile Arg Glu Gly Ala Thr Val Cys Gly Val Arg Val Arg Asn His
 180 185 190
 Leu Thr Gly Glu Thr Gln Ala Leu His Ala Pro Val Val Val Asn Ala
 195 200 205
 Ala Gly Ile Trp Gly Gln His Ile Ala Glu Tyr Ala Asp Leu Arg Ile
 210 215 220
 Arg Met Phe Pro Ala Lys Gly Ser Leu Leu Ile Met Asp His Arg Ile
 225 230 235 240
 Asn Gln His Val Ile Asn Arg Cys Arg Lys Pro Ser Asp Ala Asp Ile
 245 250 255
 Leu Val Pro Gly Asp Thr Ile Ser Leu Ile Gly Thr Thr Ser Leu Arg
 260 265 270
 Ile Asp Tyr Asn Glu Ile Asp Asp Asn Arg Val Thr Ala Glu Glu Val
 275 280 285
 Asp Ile Leu Leu Arg Glu Gly Glu Lys Leu Ala Pro Val Met Ala Lys
 290 295 300
 Thr Arg Ile Leu Arg Ala Tyr Ser Gly Val Arg Pro Leu Val Ala Ser
 305 310 315 320
 Asp Asp Asp Pro Ser Gly Arg Asn Val Ser Arg Gly Ile Val Leu Leu
 325 330 335
 Asp His Ala Glu Arg Asp Gly Leu Asp Gly Phe Ile Thr Ile Thr Gly
 340 345 350
 Gly Lys Leu Met Thr Tyr Arg Leu Met Ala Glu Trp Ala Thr Asp Ala
 355 360 365
 Val Cys Arg Lys Leu Gly Asn Thr Arg Pro Cys Thr Thr Ala Asp Leu
 370 375 380
 Ala Leu Pro Gly Ser Gln Glu Pro Ala Glu Val Thr Leu Arg Lys Val
 385 390 395 400
 Ile Ser Leu Pro Ala Pro Leu Arg Gly Ser Ala Val Tyr Arg His Gly
 405 410 415
 Asp Arg Thr Pro Ala Trp Leu Ser Glu Gly Arg Leu His Arg Ser Leu
 420 425 430
 Val Cys Glu Cys Glu Ala Val Thr Ala Gly Glu Val Gln Tyr Ala Val
 435 440 445
 Glu Asn Leu Asn Val Asn Ser Leu Leu Asp Leu Arg Arg Arg Thr Arg
 450 455 460
 Val Gly Met Gly Thr Cys Gln Gly Glu Leu Cys Ala Cys Arg Ala Ala
 465 470 475 480
 Gly Leu Leu Gln Arg Phe Asn Val Thr Thr Ser Ala Gln Ser Ile Glu
 485 490 495
 Gln Leu Ser Thr Phe Leu Asn Glu Arg Trp Lys Gly Val Gln Pro Ile
 500 505 510
 Ala Trp Gly Asp Ala Leu Arg Glu Ser Glu Phe Thr Arg Trp Val Tyr
 515 520 525
 Gln Gly Leu Cys Gly Leu Glu Lys Glu Gln Lys Asp Ala Leu
 530 535 540

<210> 415

<211> 419

<212> PRT

<213> Escherichia coli

<400> 415

Met Arg Phe Asp Thr Val Ile Met Gly Gly Gly Leu Ala Gly Leu Leu
 1 5 10 15
 Cys Gly Leu Gln Leu Gln Lys His Gly Leu Arg Cys Ala Ile Val Thr
 20 25 30
 Arg Gly Gln Ser Ala Leu His Phe Ser Ser Gly Ser Leu Asp Leu Leu

35 40 45
 Ser His Leu Pro Asp Gly Gln Pro Val Thr Asp Ile His Ser Gly Leu
 50 55 60
 Glu Ser Leu Arg Gln Gln Ala Pro Ala His Pro Tyr Ser Leu Leu Glu
 65 70 75 80
 Pro Gln Arg Val Leu Asp Leu Ala Cys Gln Ala Gln Ala Leu Ile Ala
 85 90 95
 Glu Ser Gly Ala Gln Leu Gln Gly Ser Val Glu Leu Ala His Gln Arg
 100 105 110
 Val Thr Pro Leu Gly Thr Leu Arg Ser Thr Trp Leu Ser Ser Pro Glu
 115 120 125
 Val Pro Val Trp Pro Leu Pro Ala Lys Lys Ile Cys Val Val Gly Ile
 130 135 140
 Ser Gly Leu Met Asp Phe Gln Ala His Leu Ala Ala Ala Ser Leu Arg
 145 150 155 160
 Glu Leu Gly Leu Ala Val Glu Thr Ala Glu Ile Glu Leu Pro Glu Leu
 165 170 175
 Asp Val Leu Arg Asn Asn Ala Thr Glu Phe Arg Ala Val Asn Ile Ala
 180 185 190
 Arg Phe Leu Asp Asn Glu Glu Asn Trp Pro Leu Leu Leu Asp Ala Leu
 195 200 205
 Ile Pro Val Ala Asn Thr Cys Glu Met Ile Leu Met Pro Ala Cys Phe
 210 215 220
 Gly Leu Ala Asp Asp Lys Leu Trp Arg Trp Leu Asn Glu Lys Leu Pro
 225 230 235 240
 Cys Ser Leu Met Leu Leu Pro Thr Leu Pro Pro Ser Val Leu Gly Ile
 245 250 255
 Arg Leu Gln Asn Gln Leu Gln Arg Gln Phe Val Arg Gln Gly Gly Val
 260 265 270
 Trp Met Pro Gly Asp Glu Val Lys Lys Val Thr Cys Lys Asn Gly Val
 275 280 285
 Val Asn Glu Ile Trp Thr Arg Asn His Ala Asp Ile Pro Leu Arg Pro
 290 295 300
 Arg Phe Ala Val Leu Ala Ser Gly Ser Phe Phe Ser Gly Gly Leu Val
 305 310 315 320
 Ala Glu Arg Asn Gly Ile Arg Glu Pro Ile Leu Gly Leu Asp Val Leu
 325 330 335
 Gln Thr Ala Thr Arg Gly Glu Trp Tyr Lys Gly Asp Phe Phe Ala Pro
 340 345 350
 Gln Pro Trp Gln Gln Phe Gly Val Thr Thr Asp Glu Thr Leu Arg Pro
 355 360 365
 Ser Gln Ala Gly Gln Thr Ile Glu Asn Leu Phe Ala Ile Gly Ser Val
 370 375 380
 Leu Gly Gly Phe Asp Pro Ile Ala Gln Gly Cys Gly Gly Gly Val Cys
 385 390 395 400
 Ala Val Ser Ala Leu His Ala Ala Gln Gln Ile Ala Gln Arg Ala Gly
 405 410 415
 Gly Gln Gln

<210> 416

<211> 396

<212> PRT

<213> Escherichia coli

<400> 416

Met Asn Asp Thr Ser Phe Glu Asn Cys Ile Lys Cys Thr Val Cys Thr
 1 5 10 15
 Thr Ala Cys Pro Val Ser Arg Val Asn Pro Gly Tyr Pro Gly Pro Lys
 20 25 30

Gln Ala Gly Pro Asp Gly Glu Arg Leu Arg Leu Lys Asp Gly Ala Leu
 35 40 45
 Tyr Asp Glu Ala Leu Lys Tyr Cys Ile Asn Cys Lys Arg Cys Glu Val
 50 55 60
 Ala Cys Pro Ser Asp Val Lys Ile Gly Asp Ile Ile Gln Arg Ala Arg
 65 70 75 80
 Ala Lys Tyr Asp Thr Thr Arg Pro Ser Leu Arg Asn Phe Val Leu Ser
 85 90 95
 His Thr Asp Leu Met Gly Ser Val Ser Thr Pro Phe Ala Pro Ile Val
 100 105 110
 Asn Thr Ala Thr Ser Leu Lys Pro Val Arg Gln Leu Leu Asp Ala Ala
 115 120 125
 Leu Lys Ile Asp His Arg Arg Thr Leu Pro Lys Tyr Ser Phe Gly Thr
 130 135 140
 Phe Arg Arg Trp Tyr Arg Ser Val Ala Ala Gln Gln Ala Gln Tyr Lys
 145 150 155 160
 Asp Gln Val Ala Phe Phe His Gly Cys Phe Val Asn Tyr Asn His Pro
 165 170 175
 Gln Leu Gly Lys Asp Leu Ile Lys Val Leu Asn Ala Met Gly Thr Gly
 180 185 190
 Val Gln Leu Leu Ser Lys Glu Lys Cys Cys Gly Val Pro Leu Ile Ala
 195 200 205
 Asn Gly Phe Thr Asp Lys Ala Arg Lys Gln Ala Ile Thr Asn Val Glu
 210 215 220
 Ser Ile Arg Glu Ala Val Gly Val Lys Gly Ile Pro Val Ile Ala Thr
 225 230 235 240
 Ser Ser Thr Cys Thr Phe Ala Leu Arg Asp Glu Tyr Pro Glu Val Leu
 245 250 255
 Asn Val Asp Asn Lys Gly Leu Arg Asp His Ile Glu Leu Ala Thr Arg
 260 265 270
 Trp Leu Trp Arg Lys Leu Asp Glu Gly Lys Thr Leu Pro Leu Lys Pro
 275 280 285
 Leu Pro Leu Lys Val Val Tyr His Thr Pro Cys His Met Glu Lys Met
 290 295 300
 Gly Trp Thr Leu Tyr Thr Leu Glu Leu Leu Arg Asn Ile Pro Gly Leu
 305 310 315 320
 Glu Leu Thr Val Leu Asp Ser Gln Cys Cys Gly Ile Ala Gly Thr Tyr
 325 330 335
 Gly Phe Lys Lys Glu Asn Tyr Pro Thr Ser Gln Ala Ile Gly Ala Pro
 340 345 350
 Leu Phe Arg Gln Ile Glu Glu Ser Gly Ala Asp Leu Val Val Thr Asp
 355 360 365
 Cys Glu Thr Cys Lys Trp Gln Ile Glu Met Ser Thr Ser Leu Arg Cys
 370 375 380
 Glu His Pro Ile Thr Leu Leu Ala Gln Ala Leu Ala
 385 390 395

<210> 417

<211> 302

<212> PRT

<213> Escherichia coli

<400> 417

Met Gln Leu Arg Lys Pro Ala Thr Ala Ile Leu Ala Leu Ala Leu Ser
 1 5 10 15
 Ala Gly Leu Ala Gln Ala Asp Asp Ala Ala Pro Ala Ala Gly Ser Thr
 20 25 30
 Leu Asp Lys Ile Ala Lys Asn Gly Val Ile Val Val Gly His Arg Glu
 35 40 45
 Ser Ser Val Pro Phe Ser Tyr Tyr Asp Asn Gln Gln Lys Val Val Gly

50				55				60							
Tyr 65	Ser	Gln	Asp	Tyr 70	Ser	Asn	Ala	Ile	Val	Glu 75	Ala	Val	Lys	Lys	Lys 80
Leu	Asn	Lys	Pro	Asp 85	Leu	Gln	Val	Lys	Leu 90	Ile	Pro	Ile	Thr	Ser	Gln
Asn	Arg	Ile	Pro 100	Leu	Leu	Gln	Asn	Gly 105	Thr	Phe	Asp	Phe	Glu 110	Cys	Gly
Ser	Thr	Thr 115	Asn	Asn	Val	Glu	Arg	Gln 120	Lys	Gln	Ala	Ala 125	Phe	Ser	Asp
Thr	Ile	Phe 130	Val	Val	Gly	Thr	Arg	Leu 135	Leu	Thr	Lys 140	Lys	Gly	Gly	Asp
Ile 145	Lys	Asp	Phe	Ala	Asn 150	Leu	Lys	Asp	Lys	Ala 155	Val	Val	Val	Thr	Ser
Gly	Thr	Thr	Ser	Glu 165	Val	Leu	Leu	Asn	Lys 170	Leu	Asn	Glu	Glu	Gln 175	Lys
Met	Asn	Met	Arg 180	Ile	Ile	Ser	Ala	Lys 185	Asp	His	Gly	Asp	Ser 190	Phe	Arg
Thr	Leu	Glu	Ser 195	Gly	Arg	Ala	Val	Ala 200	Phe	Met	Met	Asp 205	Asp	Ala	Leu
Leu	Ala	Gly	Glu 210	Arg	Ala	Lys 215	Ala	Lys	Lys	Pro	Asp 220	Asn	Trp	Glu	Ile
Val 225	Gly	Lys	Pro	Gln	Ser 230	Gln	Glu	Ala	Tyr	Gly 235	Cys	Met	Leu	Arg	Lys 240
Asp	Asp	Pro	Gln 245	Phe	Lys	Lys	Leu	Met	Asp 250	Asp	Thr	Ile	Ala 255	Gln	Val
Gln	Thr	Ser	Gly 260	Glu	Ala	Glu	Lys	Trp 265	Phe	Asp	Lys	Trp	Phe 270	Lys	Asn
Pro	Ile	Pro 275	Pro	Lys	Asn	Leu	Asn	Met 280	Asn	Phe	Glu	Leu 285	Ser	Asp	Glu
Met	Lys	Ala 290	Leu	Phe	Lys	Glu 295	Pro	Asn	Asp	Lys	Ala 300	Leu	Asn		

<210> 418

<211> 328

<212> PRT

<213> Escherichia coli

<400> 418

Met 1	Asn	Asn	Ser	Ala 5	Phe	Thr	Phe	Gln	Thr 10	Leu	His	Pro	Asp	Thr 15	Ile
Met	Asp	Ala	Leu 20	Phe	Glu	His	Gly	Ile 25	Arg	Val	Asp	Ser	Gly 30	Leu	Thr
Pro	Leu 35	Asn	Ser	Tyr	Glu	Asn	Arg 40	Val	Tyr	Gln	Phe	Gln 45	Asp	Glu	Asp
Arg 50	Arg	Arg	Phe	Val	Val 55	Lys	Phe	Tyr	Arg	Pro	Glu 60	Arg	Trp	Thr	Ala
Asp 65	Gln	Ile	Leu	Glu 70	Glu	His	Gln	Phe	Ala 75	Leu	Gln	Leu	Val	Asn 80	Asp
Glu	Val	Pro	Val 85	Ala	Ala	Pro	Val	Ala 90	Phe	Asn	Gly	Gln	Thr 95	Leu	Leu
Asn	His	Gln 100	Gly	Phe	Tyr	Phe	Ala 105	Val	Phe	Pro	Ser	Val 110	Gly	Gly	Arg
Gln	Phe 115	Glu	Ala	Asp	Asn	Ile	Asp 120	Gln	Met	Glu	Ala 125	Val	Gly	Arg	Tyr
Leu 130	Gly	Arg	Met	His	Gln	Thr 135	Gly	Arg	Lys	Gln 140	Leu	Phe	Ile	His	Arg
Pro 145	Thr	Ile	Gly	Leu 150	Asn	Glu	Tyr	Leu 155	Ile	Glu	Pro	Arg	Lys	Leu 160	Phe
Glu	Asp	Ala	Thr 165	Leu	Ile	Pro	Ser	Gly 170	Leu	Lys	Ala 175	Ala	Phe	Leu	Lys

Ala Thr Asp Glu Leu Ile Ala Ala Val Thr Ala His Trp Arg Glu Asp
 180 185 190
 Phe Thr Val Leu Arg Leu His Gly Asp Cys His Ala Gly Asn Ile Leu
 195 200 205
 Trp Arg Asp Gly Pro Met Phe Val Asp Leu Asp Asp Ala Arg Asn Gly
 210 215 220
 Pro Ala Val Gln Asp Leu Trp Met Leu Leu Asn Gly Asp Lys Ala Glu
 225 230 235 240
 Gln Arg Met Gln Leu Glu Thr Ile Ile Glu Ala Tyr Glu Glu Phe Ser
 245 250 255
 Glu Phe Asp Thr Ala Glu Ile Gly Leu Ile Glu Pro Leu Arg Ala Met
 260 265 270
 Arg Leu Val Tyr Tyr Leu Ala Trp Leu Met Arg Arg Trp Ala Asp Pro
 275 280 285
 Ala Phe Pro Lys Asn Phe Pro Trp Leu Thr Gly Glu Asp Tyr Trp Leu
 290 295 300
 Arg Gln Thr Ala Thr Phe Ile Glu Gln Ala Lys Val Leu Gln Glu Pro
 305 310 315 320
 Pro Leu Gln Leu Thr Pro Met Tyr
 325

<210> 419

<211> 208

<212> PRT

<213> Escherichia coli

<400> 419

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
 1 5 10 15
 Ala Ser Ala Ala Gln Tyr Glu Asp Gly Lys Gln Tyr Thr Thr Leu Glu
 20 25 30
 Lys Pro Val Ala Gly Ala Pro Gln Val Leu Glu Phe Phe Ser Phe Phe
 35 40 45
 Cys Pro His Cys Tyr Gln Phe Glu Glu Val Leu His Ile Ser Asp Asn
 50 55 60
 Val Lys Lys Lys Leu Pro Glu Gly Val Lys Met Thr Lys Tyr His Val
 65 70 75 80
 Asn Phe Met Gly Gly Asp Leu Gly Lys Asp Leu Thr Gln Ala Trp Ala
 85 90 95
 Val Ala Met Ala Leu Gly Val Glu Asp Lys Val Thr Val Pro Leu Phe
 100 105 110
 Glu Gly Val Gln Lys Thr Gln Thr Ile Arg Ser Ala Ser Asp Ile Arg
 115 120 125
 Asp Val Phe Ile Asn Ala Gly Ile Lys Gly Glu Glu Tyr Asp Ala Ala
 130 135 140
 Trp Asn Ser Phe Val Val Lys Ser Leu Val Ala Gln Gln Glu Lys Ala
 145 150 155 160
 Ala Ala Asp Val Gln Leu Arg Gly Val Pro Ala Met Phe Val Asn Gly
 165 170 175
 Lys Tyr Gln Leu Asn Pro Gln Gly Met Asp Thr Ser Asn Met Asp Val
 180 185 190
 Phe Val Gln Gln Tyr Ala Asp Thr Val Lys Tyr Leu Ser Glu Lys Lys
 195 200 205

<210> 420

<211> 112

<212> PRT

<213> Escherichia coli

<400> 420

```

Met Thr Met Asn Ser Phe Glu Arg Arg Asn Lys Ile Ile Gln Leu Val
 1          5          10          15
Asn Glu Gln Gly Thr Val Leu Val Gln Asp Leu Ala Gly Val Phe Ala
          20          25          30
Ala Ser Glu Ala Thr Ile Arg Ala Asp Leu Arg Phe Leu Glu Gln Lys
          35          40          45
Gly Val Val Thr Arg Phe His Gly Gly Ala Ala Lys Ile Met Ser Gly
 50          55          60
Asn Ser Glu Thr Glu Thr Gln Glu Val Gly Phe Lys Glu Arg Phe Gln
 65          70          75          80
Leu Ala Ser Ala Pro Lys Asn Arg Ile Ala Gln Ala Ala Val Lys Met
          85          90          95
Ile His Glu Gly Met Thr Asp Pro Thr His Val Ile Trp Thr Gln Ala
          100          105          110

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<210> 421

<211> 346

<212> PRT

<213> Escherichia coli

<400> 421

```

Met Lys Ser Val Val Asn Asp Thr Asp Gly Ile Val Arg Val Ala Glu
 1          5          10          15
Ser Val Ile Pro Glu Ile Lys His Gln Asp Glu Val Arg Val Lys Ile
          20          25          30
Ala Ser Ser Gly Leu Cys Gly Ser Asp Leu Pro Arg Ile Phe Lys Asn
          35          40          45
Gly Ala His Tyr Tyr Pro Ile Thr Leu Gly His Glu Phe Ser Gly Tyr
 50          55          60
Ile Asp Ala Val Gly Ser Gly Val Asp Asp Leu His Pro Gly Asp Ala
 65          70          75          80
Val Ala Cys Val Pro Leu Leu Pro Cys Phe Thr Cys Pro Glu Cys Leu
          85          90          95
Lys Gly Phe Tyr Ser Gln Cys Ala Lys Tyr Asp Phe Ile Gly Ser Arg
          100          105          110
Arg Asp Gly Gly Phe Ala Glu Tyr Ile Val Val Lys Arg Lys Asn Val
          115          120          125
Phe Ala Leu Pro Thr Asp Met Pro Ile Glu Asp Gly Ala Phe Ile Glu
          130          135          140
Pro Ile Thr Val Gly Leu His Ala Phe His Leu Ala Gln Gly Cys Glu
          145          150          155          160
Asn Lys Asn Val Ile Ile Ile Gly Ala Gly Thr Ile Gly Leu Leu Ala
          165          170          175
Ile Gln Cys Ala Val Ala Leu Gly Ala Lys Ser Val Thr Ala Ile Asp
          180          185          190
Ile Ser Ser Glu Lys Leu Ala Leu Ala Lys Ser Phe Gly Ala Met Gln
          195          200          205
Thr Phe Asn Ser Ser Glu Met Ser Ala Pro Gln Met Gln Ser Val Leu
          210          215          220
Arg Glu Leu Arg Phe Asn Gln Leu Ile Leu Glu Thr Ala Gly Val Pro
          225          230          235          240
Gln Thr Val Glu Leu Ala Val Glu Ile Ala Gly Pro His Ala Gln Leu
          245          250          255
Ala Leu Val Gly Thr Leu His Gln Asp Leu His Leu Thr Ser Ala Thr
          260          265          270
Phe Gly Lys Ile Leu Arg Lys Glu Leu Thr Val Ile Gly Ser Trp Met
          275          280          285
Asn Tyr Ser Ser Pro Trp Pro Gly Gln Glu Trp Glu Thr Ala Ser Arg
          290          295          300

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Leu Leu Thr Glu Arg Lys Leu Ser Leu Glu Pro Leu Ile Ala His Arg
 305 310 315 320
 Gly Ser Phe Glu Ser Phe Ala Gln Ala Val Arg Asp Ile Ala Arg Asn
 325 330 335
 Ala Met Pro Gly Lys Val Leu Leu Ile Pro
 340 345

<210> 422

<211> 451

<212> PRT

<213> Escherichia coli

<400> 422

Met Phe Ser Glu Val Met Arg Tyr Ile Leu Asp Leu Gly Pro Thr Val
 1 5 10 15
 Met Leu Pro Ile Val Ile Ile Ile Phe Ser Lys Ile Leu Gly Met Lys
 20 25 30
 Ala Gly Asp Cys Phe Lys Ala Gly Leu His Ile Gly Ile Gly Phe Val
 35 40 45
 Gly Ile Gly Leu Val Ile Gly Leu Met Leu Asp Ser Ile Gly Pro Ala
 50 55 60
 Ala Lys Ala Met Ala Glu Asn Phe Asp Leu Asn Leu His Val Val Asp
 65 70 75 80
 Val Gly Trp Pro Gly Ser Ser Pro Met Thr Trp Ala Ser Gln Ile Ala
 85 90 95
 Leu Val Ala Ile Pro Ile Ala Ile Leu Val Asn Val Ala Met Leu Leu
 100 105 110
 Thr Arg Met Thr Arg Val Val Asn Val Asp Ile Trp Asn Ile Trp His
 115 120 125
 Met Thr Phe Thr Gly Ala Leu Leu His Leu Ala Thr Gly Ser Trp Met
 130 135 140
 Ile Gly Met Ala Gly Val Val Ile His Ala Ala Phe Val Tyr Lys Leu
 145 150 155 160
 Gly Asp Trp Phe Ala Arg Asp Thr Arg Asn Phe Phe Glu Leu Glu Gly
 165 170 175
 Ile Ala Ile Pro His Gly Thr Ser Ala Tyr Met Gly Pro Ile Ala Val
 180 185 190
 Leu Val Asp Ala Ile Ile Glu Lys Ile Pro Gly Val Asn Arg Ile Lys
 195 200 205
 Phe Ser Ala Asp Asp Ile Gln Arg Lys Phe Gly Pro Phe Gly Glu Pro
 210 215 220
 Val Thr Val Gly Phe Val Met Gly Leu Ile Ile Gly Ile Leu Ala Gly
 225 230 235 240
 Tyr Asp Val Lys Gly Val Leu Gln Leu Ala Val Lys Thr Ala Ala Val
 245 250 255
 Met Leu Leu Met Pro Arg Val Ile Lys Pro Ile Met Asp Gly Leu Thr
 260 265 270
 Pro Ile Ala Lys Gln Ala Arg Ser Arg Leu Gln Ala Lys Phe Gly Gly
 275 280 285
 Gln Glu Phe Leu Ile Gly Leu Asp Pro Ala Leu Leu Gly His Thr
 290 295 300
 Ala Val Val Ser Ala Ser Leu Ile Phe Ile Pro Leu Thr Ile Leu Ile
 305 310 315 320
 Ala Val Cys Val Pro Gly Asn Gln Val Leu Pro Phe Gly Asp Leu Ala
 325 330 335
 Thr Ile Gly Phe Phe Val Ala Met Ala Val Ala Val His Arg Gly Asn
 340 345 350
 Leu Phe Arg Thr Leu Ile Ser Gly Val Ile Ile Met Ser Ile Thr Leu
 355 360 365
 Trp Ile Ala Thr Gln Thr Ile Gly Leu His Thr Gln Leu Ala Ala Asn

370		375		380
Ala Gly Ala Leu Lys	Ala Gly Gly Met Val	Ala Ser Met Asp Gln Gly		
385	390	395		400
Gly Ser Pro Ile Thr	Trp Leu Leu Ile Gln Val	Phe Ser Pro Gln Asn		
	405	410		415
Ile Pro Gly Phe Ile	Ile Ile Gly Ala Ile Tyr	Leu Thr Gly Ile Phe		
	420	425		430
Met Thr Trp Arg Arg	Ala Arg Gly Phe Ile Lys	Gln Glu Lys Val Val		
	435	440		445
Leu Ala Glu				
450				

<210> 423

<211> 94

<212> PRT

<213> Escherichia coli

<400> 423

Met Lys Arg Lys Ile	Ile Val Ala Cys Gly Gly	Ala Val Ala Thr Ser
1	5	10
Thr Met Ala Ala Glu	Glu Ile Lys Glu Leu Cys	Gln Asn His Asn Ile
	20	25
Pro Val Glu Leu Ile	Gln Cys Arg Val Asn Glu	Ile Glu Thr Tyr Met
	35	40
Asp Gly Val His Leu	Ile Cys Thr Thr Ala Lys	Val Asp Arg Ser Phe
	50	55
Gly Asp Ile Pro Leu	Val His Gly Met Pro Phe	Ile Ser Gly Ile Gly
	65	70
Ile Glu Ala Leu Gln	Asn Lys Ile Leu Thr	Ile Leu Gln Gly
	85	90

<210> 424

<211> 150

<212> PRT

<213> Escherichia coli

<400> 424

Met Thr Asn Leu Phe	Val Arg Ser Gly Ile Ser	Phe Val Asp Arg Ser
1	5	10
Glu Val Leu Thr His	Ile Gly Asn Glu Met Leu	Ala Lys Gly Val Val
	20	25
His Asp Thr Trp Pro	Gln Ala Leu Ile Ala Arg	Glu Ala Glu Phe Pro
	35	40
Thr Gly Ile Met Leu	Glu Gln His Ala Ile Ala	Ile Pro His Cys Glu
	50	55
Ala Ile His Ala Lys	Ser Ser Ala Ile Tyr Leu	Leu Arg Pro Thr Asn
	65	70
Lys Val His Phe Gln	Gln Ala Asp Asp Asp Asn	Asp Val Ala Val Ser
	85	90
Leu Val Ile Ala Leu	Ile Val Glu Asn Pro Gln	Gln Gln Leu Lys Leu
	100	105
Leu Arg Cys Leu Phe	Gly Lys Leu Gln Gln Pro	Asp Ile Val Glu Thr
	115	120
Leu Ile Thr Leu Pro	Glu Thr Gln Leu Lys Glu	Tyr Phe Thr Lys Tyr
	130	135
Val Leu Asp Ser Asp	Glu	
145	150	

<210> 425
 <211> 420
 <212> PRT
 <213> Escherichia coli

<400> 425

```

Met Lys Thr Leu Ile Ala Arg His Lys Ala Gly Glu His Ile Gly Ile
 1          5          10          15
Cys Ser Val Cys Ser Ala His Pro Leu Val Ile Glu Ala Ala Leu Ala
 20          25          30
Phe Asp Arg Asn Ser Thr Arg Lys Val Leu Ile Glu Ala Thr Ser Asn
 35          40          45
Gln Val Asn Gln Phe Gly Gly Tyr Thr Gly Met Thr Pro Ala Asp Phe
 50          55          60
Arg Glu Phe Val Phe Thr Ile Ala Asp Lys Val Gly Phe Ala Arg Glu
 65          70          75          80
Arg Ile Ile Leu Gly Gly Asp His Leu Gly Pro Asn Cys Trp Gln Gln
 85          90          95
Glu Asn Ala Asp Ala Ala Met Glu Lys Ser Val Glu Leu Val Lys Glu
100          105          110
Tyr Val Arg Ala Gly Phe Ser Lys Ile His Leu Asp Ala Ser Met Ser
115          120          125
Cys Ala Gly Asp Pro Ile Pro Leu Ala Pro Glu Thr Val Ala Glu Arg
130          135          140
Ala Ala Val Leu Cys Phe Ala Ala Glu Ser Val Ala Thr Asp Cys Gln
145          150          155          160
Arg Glu Gln Leu Ser Tyr Val Ile Gly Thr Glu Val Pro Val Pro Gly
165          170          175
Gly Glu Ala Ser Ala Ile Gln Ser Val His Ile Thr His Val Glu Asp
180          185          190
Ala Ala Asn Thr Leu Arg Thr His Gln Lys Ala Phe Ile Ala Arg Gly
195          200          205
Leu Thr Glu Ala Leu Thr Arg Val Ile Ala Ile Val Val Gln Pro Gly
210          215          220
Val Glu Phe Asp His Ser Asn Ile Ile His Tyr Gln Pro Gln Glu Ala
225          230          235          240
Gln Pro Leu Ala Gln Trp Ile Glu Asn Thr Arg Met Val Tyr Glu Ala
245          250          255
His Ser Thr Asp Tyr Gln Thr Arg Thr Ala Tyr Trp Glu Leu Val Arg
260          265          270
Asp His Phe Ala Ile Leu Lys Val Gly Pro Ala Leu Thr Phe Ala Leu
275          280          285
Arg Glu Ala Ile Phe Ala Leu Ala Gln Ile Glu Gln Glu Leu Ile Ala
290          295          300
Pro Glu Asn Arg Ser Gly Cys Leu Ala Val Ile Glu Glu Val Met Leu
305          310          315          320
Asp Glu Pro Gln Tyr Trp Lys Lys Tyr Tyr Arg Thr Gly Phe Asn Asp
325          330          335
Ser Leu Leu Asp Ile Arg Tyr Ser Leu Ser Asp Arg Ile Arg Tyr Tyr
340          345          350
Trp Pro His Ser Arg Ile Lys Asn Ser Val Glu Thr Met Met Val Asn
355          360          365
Leu Glu Gly Val Asp Ile Pro Leu Gly Met Ile Ser Gln Tyr Leu Pro
370          375          380
Lys Gln Phe Glu Arg Ile Gln Ser Gly Glu Leu Ser Ala Ile Pro His
385          390          395          400
Gln Leu Ile Met Asp Lys Ile Tyr Asp Val Leu Arg Ala Tyr Arg Tyr
405          410          415
Gly Cys Ala Glu
420

```

<210> 426
 <211> 286
 <212> PRT
 <213> Escherichia coli

<400> 426

```

Met Lys Met Tyr Val Val Ser Thr Lys Gln Met Leu Asn Asn Ala Gln
 1          5          10          15
Arg Gly Gly Tyr Ala Val Pro Ala Phe Asn Ile His Asn Leu Glu Thr
      20          25          30
Met Gln Val Val Val Glu Thr Ala Ala Asn Leu His Ala Pro Val Ile
      35          40          45
Ile Ala Gly Thr Pro Gly Thr Phe Thr His Ala Gly Thr Glu Asn Leu
      50          55          60
Leu Ala Leu Val Ser Ala Met Ala Lys Gln Tyr His His Pro Leu Ala
      65          70          75          80
Ile His Leu Asp His His Thr Lys Phe Asp Asp Ile Ala Gln Lys Val
      85          90          95
Arg Ser Gly Val Arg Ser Val Met Ile Asp Ala Ser His Leu Pro Phe
      100          105          110
Ala Gln Asn Ile Ser Arg Val Lys Glu Val Val Asp Phe Cys His Arg
      115          120          125
Phe Asp Val Ser Val Glu Ala Glu Leu Gly Gln Leu Gly Gly Gln Glu
      130          135          140
Asp Asp Val Gln Val Asn Glu Ala Asp Ala Leu Tyr Thr Asn Pro Ala
      145          150          155          160
Gln Ala Arg Glu Phe Ala Glu Ala Thr Gly Ile Asp Ser Leu Ala Val
      165          170          175
Ala Ile Gly Thr Ala His Gly Met Tyr Ala Ser Ala Pro Ala Leu Asp
      180          185          190
Phe Ser Arg Leu Glu Asn Ile Arg Gln Trp Val Asn Leu Pro Leu Val
      195          200          205
Leu His Gly Ala Ser Gly Leu Ser Thr Lys Asp Ile Gln Gln Thr Ile
      210          215          220
Lys Leu Gly Ile Cys Lys Ile Asn Val Ala Thr Glu Leu Lys Asn Ala
      225          230          235          240
Phe Ser Gln Ala Leu Lys Asn Tyr Leu Thr Glu His Pro Glu Ala Thr
      245          250          255
Asp Pro Arg Asp Tyr Leu Gln Ser Ala Lys Ser Ala Met Arg Asp Val
      260          265          270
Val Ser Lys Val Ile Ala Asp Cys Gly Cys Glu Gly Arg Ala
      275          280          285

```

<210> 427
 <211> 157
 <212> PRT
 <213> Escherichia coli

<400> 427

```

Met Ser Gln Asn Asp Ile Ile Ile Arg Thr His Tyr Lys Ser Pro His
 1          5          10          15
Arg Leu His Ile Asp Ser Asp Ile Pro Thr Pro Ser Ser Glu Pro Ile
      20          25          30
Asn Gln Phe Ala Arg Gln Leu Ile Thr Leu Leu Asp Thr Ser Asp Leu
      35          40          45
Ser Ser Met Leu Ser Tyr Cys Val Thr Gln Glu Phe Thr Ala Asn Cys
      50          55          60
Arg Lys Ile Ser Gln Asn Cys Tyr Ser Thr Ala Leu Phe Thr Ile Asn
      65          70          75          80

```

Phe Ala Thr Ser Pro Ile His Thr Glu Asn Ile Leu Ile Thr Leu His
 85 90 95
 Tyr Lys Lys Glu Ile Ile Ser Leu Leu Leu Glu Thr Thr Pro Ile Lys
 100 105 110
 Ala Asn His Leu Arg Ser Ile Leu Asp Tyr Ile Glu Gln Glu Gln Leu
 115 120 125
 Thr Ala Glu Asp Arg Asn His Cys Met Lys Leu Ser Lys Lys Ile His
 130 135 140
 Arg Glu Lys Asn Tyr Thr Pro Asn Ser Lys Ser Gln Trp
 145 150 155

<210> 428

<211> 471

<212> PRT

<213> Escherichia coli

<400> 428

Met Gln Ser Pro Ser Asp Ala Ile Phe Cys Arg His Leu Ser Leu Gln
 1 5 10 15
 Tyr Ala Leu Asp Ser Leu Arg Asn Gly Lys Gly Lys Val Asn Leu Ile
 20 25 30
 Lys His Tyr Ser Ser Val Glu Ser Ile Gln Gln His Val Pro Leu Val
 35 40 45
 Arg Asp Ala Glu Phe Arg Ala Leu Leu Arg His Pro Pro Ala Gly Ser
 50 55 60
 Arg Val Ile Ala Ser Lys Asp Phe Gly Phe Ala Leu Asp Ile Phe Phe
 65 70 75 80
 Cys Arg Met Met Ala Asn Asn Val Ser His Met Ser Ala Ile Leu Tyr
 85 90 95
 Ile Asp Asn His Thr Leu Ser Val Arg Leu Arg Ile Lys Gln Ser Val
 100 105 110
 Tyr Gly Gln Leu Asn Tyr Val Val Ser Val Tyr Asp Pro Asn Asp Thr
 115 120 125
 Asn Val Ala Val Arg Asp Thr His Arg Thr Ala Arg Gly Phe Leu Ser
 130 135 140
 Leu Asp Lys Phe Ile Ser Ser Gly Pro Asp Ala Gln Thr Trp Ala Asp
 145 150 155 160
 Arg Tyr Val Arg Asn Cys Ala Ile Ala Ile Leu Pro Leu Leu Pro Val
 165 170 175
 Gly Val Pro Gly Ala Ile Phe Ala Gly Ile Ala Ser Arg Met Pro Phe
 180 185 190
 Ala Pro Ile His Pro Ser Ala Met Leu Leu Ile Met Ala Thr Gly Gln
 195 200 205
 Ser Gln Gln Leu Ile Thr Leu Phe Lys Gln Leu Pro Ile Leu Pro Glu
 210 215 220
 Lys Glu Ile Ile Glu Ile Ile Thr Ala Gln Asn Ser Val Gly Thr Pro
 225 230 235 240
 Ala Leu Phe Leu Ala Met Met Asn Gly His Thr Asp Asn Val Lys Ile
 245 250 255
 Phe Met Gln Glu Ile Gln Ser Leu Val Asp Asn His Ile Ile His Glu
 260 265 270
 Asp Asn Leu Val Lys Leu Leu Gln Thr Lys Ser Ala Asn Glu Thr Pro
 275 280 285
 Gly Leu Tyr Ile Ser Met Leu Tyr Gly Phe Asp Glu Ile Ile Asp Ile
 290 295 300
 Phe Leu Asn Ala Leu Thr Thr Pro Ile Ala Gln Glu Leu Leu Asn Lys
 305 310 315 320
 Lys Leu Val Met Ser Ile Leu Ala Met Lys Ile His Asp Gly Glu Pro
 325 330 335
 Gly Leu Tyr Ala Ala Met Glu Asn Asn His Pro Leu Cys Val Thr Arg

```

      340      345      350
Phe Leu Ser Lys Ile Asn Gly Ile Ala Phe Lys Tyr Lys Leu Ser Lys
      355      360      365
Ala Asn Ile Met Asp Leu Leu Lys Gly Ala Thr Ala Gln Gly Thr Pro
      370      375      380
Ala Leu Tyr Ile Ala Met Ser Lys Gly Asn Glu Asp Val Val Leu Ser
385      390      395      400
Tyr Ile Ser Thr Leu Gly Ala Phe Ala Lys Lys His Ser Phe Ser Gln
      405      410      415
His Gln Leu Phe Thr Leu Leu Ala Ala Lys Asn His Asp Asn Met Ser
      420      425      430
Ala Val His Ile Ala Ile His His Lys His Tyr Lys Thr Val Glu Thr
      435      440      445
Tyr Tyr Ala Ala Ile Asn Ala Ile Ser Gln Ser Leu Ser Phe Ser Ala
      450      455      460
Asp Glu Ile Lys Thr Tyr Leu
465      470

```

<210> 429
 <211> 128
 <212> PRT
 <213> Escherichia coli

```

<400> 429
Met Pro Ser Gly Leu Phe Met Asp Leu Leu Pro Phe Leu Leu Asp Ala
1      5      10      15
Asn Leu Ser Ala Thr Asn Pro Pro Ala Ile Pro His Trp Trp Lys Arg
      20      25      30
Gln Pro Leu Ile Pro Asn Leu Leu Ser Gln Glu Leu Lys Asn Tyr Leu
      35      40      45
Lys Leu Asn Val Lys Glu Lys Asn Ile Gln Ile Ala Asp Gln Val Ile
      50      55      60
Ile Asp Glu Thr Ala Gly Glu Val Val Ile Gly Ala Asn Thr Arg Ile
65      70      75      80
Cys His Gly Ala Val Ile Gln Gly Pro Val Val Ile Gly Ala Asn Cys
      85      90      95
Leu Ile Gly Asn Trp Ile Cys Pro Tyr Ile Ser Arg His Leu Leu Ser
      100      105      110
Leu Asn Pro Leu Gln Ala Arg Cys Arg Arg Tyr Ser Arg Gly Glu Arg
      115      120      125

```

<210> 430
 <211> 398
 <212> PRT
 <213> Escherichia coli

```

<400> 430
Met Lys Thr Trp Ile Phe Ile Cys Met Ser Ile Ala Met Leu Leu Trp
1      5      10      15
Phe Leu Ser Thr Leu Arg Arg Lys Pro Ser Gln Lys Lys Gly Cys Ile
      20      25      30
Asp Ala Ile Ile Pro Ala Tyr Asn Glu Gly Pro Cys Leu Ala Gln Ser
      35      40      45
Leu Asp Asn Leu Leu Arg Asn Pro Tyr Phe Cys Arg Val Ile Cys Val
      50      55      60
Asn Asp Gly Ser Thr Asp Asn Thr Glu Ala Val Met Ala Glu Val Lys
65      70      75      80
Arg Lys Trp Gly Asp Arg Phe Val Ala Val Thr Gln Lys Asn Thr Gly
      85      90      95

```


Lys Gly Gly Ala Leu Met Asn Gly Leu Asn Tyr Ala Thr Cys Asp Gln
 100 105 110
 Val Phe Leu Ser Asp Ala Asp Thr Tyr Val Pro Pro Asp Gln Asp Gly
 115 120 125
 Met Gly Tyr Met Leu Ala Glu Ile Glu Arg Gly Ala Asp Ala Val Gly
 130 135 140
 Gly Ile Pro Ser Thr Ala Leu Lys Gly Ala Gly Leu Leu Pro His Ile
 145 150 155 160
 Arg Ala Thr Val Lys Leu Pro Met Ile Val Met Lys Arg Thr Leu Gln
 165 170 175
 Gln Leu Leu Gly Ala Pro Phe Ile Ile Ser Gly Ala Cys Gly Met
 180 185 190
 Phe Arg Thr Asp Val Leu Arg Lys Phe Gly Phe Ser Asp Arg Thr Lys
 195 200 205
 Val Glu Asp Leu Asp Leu Thr Trp Thr Leu Val Ala Asn Gly Tyr Arg
 210 215 220
 Ile Arg Gln Ala Asn Arg Cys Ile Val Tyr Pro Gln Glu Cys Asn Ser
 225 230 235 240
 Pro Arg Glu Glu Trp Arg Arg Trp Arg Arg Trp Ile Val Gly Tyr Ala
 245 250 255
 Val Cys Met Arg Leu His Lys Arg Leu Leu Phe Ser Arg Phe Gly Ile
 260 265 270
 Phe Ser Ile Phe Pro Met Leu Leu Val Val Leu Tyr Gly Val Gly Ile
 275 280 285
 Tyr Leu Thr Thr Trp Phe Asn Glu Phe Ile Thr Thr Gly Pro His Gly
 290 295 300
 Val Val Leu Ala Met Phe Pro Leu Ile Trp Val Gly Val Val Cys Val
 305 310 315 320
 Ile Gly Ala Phe Ser Ala Trp Phe His Arg Cys Trp Leu Leu Val Pro
 325 330 335
 Leu Ala Pro Leu Ser Val Val Tyr Val Leu Leu Ala Tyr Ala Ile Trp
 340 345 350
 Ile Ile Tyr Gly Leu Ile Ala Phe Phe Thr Gly Arg Glu Pro Gln Arg
 355 360 365
 Asp Lys Pro Thr Arg Tyr Ser Ala Leu Val Glu Ala Ser Thr Ala Tyr
 370 375 380
 Ser Gln Pro Ser Val Thr Gly Thr Glu Lys Leu Ser Glu Ala
 385 390 395

<210> 431

<211> 552

<212> PRT

<213> Escherichia coli

<400> 431

Met Ile Leu Glu Arg Val Glu Ile Val Gly Phe Arg Gly Ile Asn Arg
 1 5 10 15
 Leu Ser Leu Met Leu Glu Gln Asn Asn Val Leu Ile Gly Glu Asn Ala
 20 25 30
 Trp Gly Lys Ser Ser Leu Leu Asp Ala Leu Thr Leu Leu Ser Pro
 35 40 45
 Glu Ser Asp Leu Tyr His Phe Glu Arg Asp Asp Phe Trp Phe Pro Pro
 50 55 60
 Gly Asp Ile Asn Gly Arg Glu His His Leu His Ile Ile Leu Thr Phe
 65 70 75 80
 Arg Glu Ser Leu Pro Gly Arg His Arg Val Arg Arg Tyr Arg Pro Leu
 85 90 95
 Glu Ala Cys Trp Thr Pro Cys Thr Asp Gly Tyr His Arg Ile Phe Tyr
 100 105 110
 Arg Leu Glu Gly Glu Ser Ala Glu Asp Gly Ser Val Met Thr Leu Arg

115	120	125
Ser Phe Leu Asp Lys Asp Gly His Pro Ile Asp Val Glu Asp Ile Asn		
130	135	140
Asp Gln Ala Arg His Leu Val Arg Leu Met Pro Val Leu Arg Leu Arg		
145	150	155
Asp Ala Arg Phe Met Arg Arg Ile Arg Asn Gly Thr Val Pro Asn Val		
165	170	175
Pro Asn Val Glu Val Thr Ala Arg Gln Leu Asp Phe Leu Ala Arg Glu		
180	185	190
Leu Ser Ser His Pro Gln Asn Leu Ser Asp Gly Gln Ile Arg Gln Gly		
195	200	205
Leu Ser Ala Met Val Gln Leu Leu Glu His Tyr Phe Ser Glu Gln Gly		
210	215	220
Ala Gly Gln Ala Arg Tyr Arg Leu Met Arg Arg Arg Ala Ser Asn Glu		
225	230	235
Gln Arg Ser Trp Arg Tyr Leu Asp Ile Ile Asn Arg Met Ile Asp Arg		
245	250	255
Pro Gly Gly Arg Ser Tyr Arg Val Ile Leu Leu Gly Leu Phe Ala Thr		
260	265	270
Leu Leu Gln Ala Lys Gly Thr Leu Arg Leu Asp Lys Asp Ala Arg Pro		
275	280	285
Leu Leu Leu Ile Glu Asp Pro Glu Thr Arg Leu His Pro Ile Met Leu		
290	295	300
Ser Val Ala Trp His Leu Leu Asn Leu Leu Pro Leu Gln Arg Ile Ala		
305	310	315
Thr Thr Asn Ser Gly Glu Leu Leu Ser Leu Thr Pro Val Glu His Val		
325	330	335
Cys Arg Leu Val Arg Glu Ser Ser Arg Val Ala Ala Trp Arg Leu Gly		
340	345	350
Pro Ser Gly Leu Ser Thr Glu Asp Ser Arg Arg Ile Ser Phe His Ile		
355	360	365
Arg Phe Asn Arg Pro Ser Ser Leu Phe Ala Arg Cys Trp Leu Leu Val		
370	375	380
Glu Gly Glu Thr Glu Thr Trp Val Ile Asn Glu Leu Ala Arg Gln Cys		
385	390	395
Gly His His Phe Asp Ala Glu Gly Ile Lys Val Ile Glu Phe Ala Gln		
405	410	415
Ser Gly Leu Lys Pro Leu Val Lys Phe Ala Arg Arg Met Gly Ile Glu		
420	425	430
Trp His Val Leu Val Asp Gly Asp Glu Ala Gly Lys Lys Tyr Ala Ala		
435	440	445
Thr Val Arg Ser Leu Leu Asn Asn Asp Arg Glu Ala Glu Arg Glu His		
450	455	460
Leu Thr Ala Leu Pro Ala Leu Asp Met Glu His Phe Met Tyr Arg Gln		
465	470	475
Gly Phe Ser Asp Val Phe His Arg Met Ala Gln Ile Pro Glu Asn Val		
485	490	495
Pro Met Asn Leu Arg Lys Ile Ile Ser Lys Ala Ile His Arg Ser Ser		
500	505	510
Lys Pro Asp Leu Ala Ile Glu Val Ala Met Glu Ala Gly Arg Arg Gly		
515	520	525
Val Asp Ser Val Pro Thr Leu Leu Lys Lys Met Phe Ser Arg Val Leu		
530	535	540
Trp Leu Ala Arg Gly Arg Ala Asp		
545	550	

<210> 432

<211> 352

<212> PRT

<213> Escherichia coli

<400> 432

```

Met Leu Pro Ser Ile Ser Ile Asn Asn Thr Ser Ala Ala Tyr Pro Glu
 1           5           10           15
Ser Ile Asn Glu Asn Asn Asn Asp Glu Val Asn Gly Leu Val Gln Glu
 20           25           30
Phe Lys Asn Leu Phe Asn Gly Lys Glu Gly Ile Ser Thr Cys Ile Lys
 35           40           45
His Leu Leu Glu Leu Ile Lys Asn Ala Ile Arg Val Asn Asp Asp Pro
 50           55           60
Tyr Arg Phe Asn Ile Asn Asn Ser Ser Val Thr Tyr Ile Asp Ile Asp
 65           70           75           80
Ser Asn Asp Thr Asp His Ile Thr Ile Gly Ile Asp Asn Gln Glu Pro
 85           90           95
Ile Glu Leu Pro Ala Asn Tyr Lys Asp Lys Glu Leu Val Arg Thr Ile
 100          105          110
Ile Asn Asp Asn Ile Val Glu Lys Thr His Asp Ile Asn Asn Lys Glu
 115          120          125
Met Ile Phe Ser Ala Leu Lys Glu Ile Tyr Asp Gly Asp Pro Gly Phe
 130          135          140
Ile Phe Asp Lys Ile Ser His Lys Leu Arg His Thr Val Thr Glu Phe
 145          150          155          160
Asp Glu Ser Gly Lys Ser Glu Pro Thr Asp Leu Phe Thr Trp Tyr Gly
 165          170          175
Lys Asp Lys Lys Gly Asp Ser Leu Ala Ile Val Ile Lys Asn Lys Asn
 180          185          190
Gly Asn Asp Tyr Leu Ser Leu Gly Tyr Tyr Asp Gln Asp Asp Tyr His
 195          200          205
Ile Gln Arg Gly Ile Arg Ile Asn Gly Asp Ser Leu Thr Gln Tyr Cys
 210          215          220
Ser Glu Asn Ala Arg Ser Ala Ser Ala Trp Phe Glu Ser Ser Lys Ala
 225          230          235          240
Ile Met Ala Glu Ser Phe Ala Thr Gly Ser Asp His Gln Val Val Asn
 245          250          255
Glu Leu Asn Gly Glu Arg Leu Arg Glu Pro Asn Asp Val Phe Lys Arg
 260          265          270
Tyr Gly Arg Ala Ile Arg Tyr Asp Phe Gln Val Asp Asp Ala Lys Tyr
 275          280          285
Lys Cys Asp His Leu Lys Glu Ile Val Ser Thr Leu Val Gly Asn Lys
 290          295          300
Ile Asn Val Gly His Ser Gln Lys Ile Tyr Lys His Phe Lys Asp Leu
 305          310          315          320
Glu Gly Lys Ile Glu Glu Arg Leu Gln Asn Arg Gln Ala Glu Tyr Gln
 325          330          335
Asn Glu Ile Asn Gln Pro Ser Ala Pro Gly Val Asn Phe Asp Asp Ile
 340          345          350

```

<210> 433

<211> 375

<212> PRT

<213> Escherichia coli

<400> 433

```

Met Met Arg His Leu Arg Asn Ile Phe Asn Leu Gly Ile Lys Glu Leu
 1           5           10           15
Arg Ser Leu Leu Gly Asp Lys Ala Met Leu Thr Leu Ile Val Phe Ser
 20           25           30
Phe Thr Val Ser Val Tyr Ser Ser Ala Thr Val Thr Pro Gly Ser Leu
 35           40           45
Asn Leu Ala Pro Ile Ala Ile Ala Asp Met Asp Gln Ser Gln Leu Ser

```

50	55	60
Asn Arg Ile Val Asn Ser Phe Tyr Arg Pro Trp Phe Leu Pro Pro Glu		
65	70	75
Met Ile Thr Ala Asp Glu Met Asp Ala Gly Leu Asp Ala Gly Arg Tyr		80
	85	90
Thr Phe Ala Ile Asn Ile Pro Pro Asn Phe Gln Arg Asp Val Leu Ala		95
	100	105
Gly Arg Gln Pro Asp Ile Gln Val Asn Val Asp Ala Thr Arg Met Ser		110
	115	120
Gln Ala Phe Thr Gly Asn Gly Tyr Ile Gln Asn Ile Ile Asn Gly Glu		125
	130	135
Val Asn Ser Phe Val Ala Arg Tyr Arg Asp Asn Ser Glu Pro Leu Val		140
145	150	155
Ser Leu Glu Thr Arg Met Arg Phe Asn Pro Asn Leu Asp Pro Ala Trp		160
	165	170
Phe Gly Gly Val Met Ala Ile Ile Asn Asn Ile Thr Met Leu Ala Ile		175
	180	185
Val Leu Thr Gly Ser Ala Leu Ile Arg Glu Arg Glu His Gly Thr Val		190
	195	200
Glu His Leu Leu Val Met Pro Ile Thr Pro Phe Glu Ile Met Met Ala		205
	210	215
Lys Ile Trp Ser Met Gly Leu Val Val Leu Val Val Ser Gly Leu Ser		220
225	230	235
Leu Val Leu Met Val Lys Gly Val Leu Gly Val Pro Ile Glu Gly Ser		240
	245	250
Ile Pro Leu Phe Met Leu Gly Val Ala Leu Ser Leu Phe Ala Thr Thr		255
	260	265
Ser Ile Gly Ile Phe Met Gly Thr Ile Ala Arg Ser Met Pro Gln Leu		270
	275	280
Gly Leu Leu Val Ile Leu Val Leu Leu Pro Leu Gln Met Leu Ser Gly		285
	290	295
Gly Ser Thr Pro Arg Glu Ser Met Pro Gln Met Val Gln Asp Ile Met		300
305	310	315
Leu Thr Met Pro Thr Thr His Phe Val Ser Leu Ala Gln Ala Ile Leu		320
	325	330
Tyr Arg Gly Ala Gly Phe Glu Ile Val Trp Pro Gln Phe Leu Thr Leu		335
	340	345
Met Ala Ile Gly Gly Ala Phe Phe Thr Ile Ala Leu Leu Arg Phe Arg		350
	355	360
Lys Thr Ile Gly Thr Met Ala		365
370	375	

<210> 434

<211> 894

<212> PRT

<213> Escherichia coli

<400> 434

Met Ser Gln His Tyr Gly Lys Thr Val Ala Leu Asn Asn Ile Thr Leu	
1	5
Asp Ile Pro Ala Arg Cys Met Val Gly Leu Ile Gly Pro Asp Gly Val	10
	20
Gly Lys Ser Ser Leu Leu Ser Leu Ile Ser Gly Ala Arg Val Ile Glu	25
	30
Gln Gly Asn Val Met Val Leu Gly Gly Asp Met Arg Asp Pro Lys His	35
	40
Arg Arg Asp Val Cys Pro Arg Ile Ala Trp Met Pro Gln Gly Leu Gly	45
50	55
Arg Arg Asp Val Cys Pro Arg Ile Ala Trp Met Pro Gln Gly Leu Gly	60
65	70
Lys Asn Leu Tyr His Thr Leu Ser Val Tyr Glu Asn Val Asp Phe Phe	75
	80
	85
	90
	95

Ala Arg Leu Phe Gly His Asp Lys Ala Glu Arg Glu Val Arg Ile Asn
 100 105 110
 Glu Leu Leu Thr Ser Thr Gly Leu Ala Pro Phe Arg Asp Arg Pro Ala
 115 120 125
 Gly Lys Leu Ser Gly Gly Met Lys Gln Lys Leu Gly Leu Cys Cys Ala
 130 135 140
 Leu Ile His Asp Pro Glu Leu Leu Ile Leu Asp Glu Pro Thr Thr Gly
 145 150 155 160
 Val Asp Pro Leu Ser Arg Ser Gln Phe Trp Asp Leu Ile Asp Ser Ile
 165 170 175
 Arg Gln Arg Gln Ser Asn Met Ser Val Leu Val Ala Thr Ala Tyr Met
 180 185 190
 Glu Glu Ala Glu Arg Phe Asp Trp Leu Val Ala Met Asn Ala Gly Glu
 195 200 205
 Val Leu Ala Thr Gly Ser Ala Glu Glu Leu Arg Gln Gln Thr Gln Ser
 210 215 220
 Ala Thr Leu Glu Glu Ala Phe Ile Asn Leu Leu Pro Gln Ala Gln Arg
 225 230 235 240
 Gln Ala His Gln Ala Val Val Ile Pro Pro Tyr Gln Pro Glu Asn Ala
 245 250 255
 Glu Ile Ala Ile Glu Ala Arg Asp Leu Thr Met Arg Phe Gly Ser Phe
 260 265 270
 Val Ala Val Asp His Val Asn Phe Arg Ile Pro Arg Gly Glu Ile Phe
 275 280 285
 Gly Phe Leu Gly Ser Asn Gly Cys Gly Lys Ser Thr Thr Met Lys Met
 290 295 300
 Leu Thr Gly Leu Leu Pro Ala Ser Glu Gly Glu Ala Trp Leu Phe Gly
 305 310 315 320
 Gln Pro Val Asp Pro Lys Asp Ile Asp Thr Arg Arg Arg Val Gly Tyr
 325 330 335
 Met Ser Gln Ala Phe Ser Leu Tyr Asn Glu Leu Thr Val Arg Gln Asn
 340 345 350
 Leu Glu Leu His Ala Arg Leu Phe His Ile Pro Glu Ala Glu Ile Pro
 355 360 365
 Ala Arg Val Ala Glu Met Ser Glu Arg Phe Lys Leu Asn Asp Val Glu
 370 375 380
 Asp Ile Leu Pro Glu Ser Leu Pro Leu Gly Ile Arg Gln Arg Leu Ser
 385 390 395 400
 Leu Ala Val Ala Val Ile His Arg Pro Glu Met Leu Ile Leu Asp Glu
 405 410 415
 Pro Thr Ser Gly Val Asp Pro Val Ala Arg Asp Met Phe Trp Gln Leu
 420 425 430
 Met Val Asp Leu Ser Arg Gln Asp Lys Val Thr Ile Phe Ile Ser Thr
 435 440 445
 His Phe Met Asn Glu Ala Glu Arg Cys Asp Arg Ile Ser Leu Met His
 450 455 460
 Ala Gly Lys Val Leu Ala Ser Gly Thr Pro Gln Glu Leu Val Glu Lys
 465 470 475 480
 Arg Gly Ala Ala Ser Leu Glu Glu Ala Phe Ile Ala Tyr Leu Gln Glu
 485 490 495
 Ala Ala Gly Gln Ser Asn Glu Ala Glu Ala Pro Pro Val Val His Asp
 500 505 510
 Thr Thr His Ala Pro Arg Gln Gly Phe Ser Leu Arg Arg Leu Phe Ser
 515 520 525
 Tyr Ser Arg Arg Glu Ala Leu Glu Leu Arg Arg Asp Pro Val Arg Ser
 530 535 540
 Thr Leu Ala Leu Met Gly Thr Val Ile Leu Met Leu Ile Met Gly Tyr
 545 550 555 560
 Gly Ile Ser Met Asp Val Glu Asn Leu Arg Phe Ala Val Leu Asp Arg
 565 570 575
 Asp Gln Thr Val Ser Ser Gln Ala Trp Thr Leu Asn Leu Ser Gly Ser

```

      580                      585                      590
Arg Tyr Phe Ile Glu Gln Pro Pro Leu Thr Ser Tyr Asp Glu Leu Asp
      595                      600                      605
Arg Arg Met Arg Ala Gly Asp Ile Thr Val Ala Ile Glu Ile Pro Pro
      610                      615                      620
Asn Phe Gly Arg Asp Ile Ala Arg Gly Thr Pro Val Glu Leu Gly Val
      625                      630                      635
Trp Ile Asp Gly Ala Met Pro Ser Arg Ala Glu Thr Val Lys Gly Tyr
      645                      650                      655
Val Gln Ala Met His Gln Ser Trp Leu Gln Asp Val Ala Ser Arg Gln
      660                      665                      670
Ser Thr Pro Ala Ser Gln Ser Gly Leu Met Asn Ile Glu Thr Arg Tyr
      675                      680                      685
Arg Tyr Asn Pro Asp Val Lys Ser Leu Pro Ala Ile Val Pro Ala Val
      690                      695                      700
Ile Pro Leu Leu Leu Met Met Ile Pro Ser Met Leu Ser Ala Leu Ser
      705                      710                      715
Val Val Arg Glu Lys Glu Leu Gly Ser Ile Ile Asn Leu Tyr Val Thr
      725                      730                      735
Pro Thr Thr Arg Ser Glu Phe Leu Leu Gly Lys Gln Leu Pro Tyr Ile
      740                      745                      750
Ala Leu Gly Met Leu Asn Phe Phe Leu Leu Cys Gly Leu Ser Val Phe
      755                      760                      765
Val Phe Gly Val Pro His Lys Gly Ser Phe Leu Thr Leu Thr Leu Ala
      770                      775                      780
Ala Leu Leu Tyr Ile Ile Ala Thr Gly Met Gly Leu Leu Ile Ser
      785                      790                      795
Thr Phe Met Lys Ser Gln Ile Ala Ala Ile Phe Gly Thr Ala Ile Ile
      805                      810                      815
Thr Leu Ile Pro Ala Thr Gln Phe Ser Gly Met Ile Asp Pro Val Ala
      820                      825                      830
Ser Leu Glu Gly Pro Gly Arg Trp Ile Gly Glu Val Tyr Pro Thr Ser
      835                      840                      845
His Phe Leu Thr Ile Ala Arg Gly Thr Phe Ser Lys Ala Leu Asp Leu
      850                      855                      860
Thr Asp Leu Trp Gln Leu Phe Ile Pro Leu Leu Ile Ala Ile Pro Leu
      865                      870                      875
Val Met Gly Leu Ser Ile Leu Leu Leu Lys Lys Gln Glu Gly
      885                      890

```

<210> 435

<211> 355

<212> PRT

<213> Escherichia coli

<400> 435

```

Met Asp Lys Ser Lys Arg His Leu Ala Trp Trp Val Val Gly Leu Leu
  1      5      10      15
Ala Val Ala Ala Ile Val Ala Trp Trp Leu Leu Arg Pro Ala Gly Val
  20      25      30
Pro Glu Gly Phe Ala Val Ser Asn Gly Arg Ile Glu Ala Thr Glu Val
  35      40      45
Asp Ile Ala Ser Lys Ile Ala Gly Arg Ile Asp Thr Ile Leu Val Lys
  50      55      60
Glu Gly Lys Phe Val Arg Glu Gly Glu Val Leu Ala Lys Met Asp Thr
  65      70      75
Arg Val Leu Gln Glu Gln Arg Leu Glu Ala Ile Ala Gln Ile Lys Glu
  85      90      95
Ala Gln Ser Ala Val Ala Ala Ala Gln Ala Leu Leu Glu Gln Arg Gln
 100     105     110

```

Ser Glu Thr Arg Ala Ala Gln Ser Leu Val Asn Gln Arg Gln Ala Glu
 115 120 125
 Leu Asp Ser Val Ala Lys Arg His Thr Arg Ser Arg Ser Leu Ala Gln
 130 135 140
 Arg Gly Ala Ile Ser Ala Gln Gln Leu Asp Asp Asp Arg Ala Ala Ala
 145 150 155 160
 Glu Ser Ala Arg Ala Ala Leu Glu Ser Ala Lys Ala Gln Val Ser Ala
 165 170 175
 Ser Lys Ala Ala Ile Glu Ala Ala Arg Thr Asn Ile Ile Gln Ala Gln
 180 185 190
 Thr Arg Val Glu Ala Ala Gln Ala Thr Glu Arg Arg Ile Ala Ala Asp
 195 200 205
 Ile Asp Asp Ser Glu Leu Lys Ala Pro Arg Asp Gly Arg Val Gln Tyr
 210 215 220
 Arg Val Ala Glu Pro Gly Glu Val Leu Ala Ala Gly Gly Arg Val Leu
 225 230 235 240
 Asn Met Val Asp Leu Ser Asp Val Tyr Met Thr Phe Phe Leu Pro Thr
 245 250 255
 Glu Gln Ala Gly Thr Leu Lys Leu Gly Gly Glu Ala Arg Leu Ile Leu
 260 265 270
 Asp Ala Ala Pro Asp Leu Arg Ile Pro Ala Thr Ile Ser Phe Val Ala
 275 280 285
 Ser Val Ala Gln Phe Thr Pro Lys Thr Val Glu Thr Ser Asp Glu Arg
 290 295 300
 Leu Lys Leu Met Phe Arg Val Lys Ala Arg Ile Pro Pro Glu Leu Leu
 305 310 315 320
 Gln Gln His Leu Glu Tyr Val Lys Thr Gly Leu Pro Gly Val Ala Trp
 325 330 335
 Val Arg Val Asn Glu Glu Leu Pro Trp Pro Asp Asp Leu Val Val Arg
 340 345 350
 Leu Pro Gln
 355

<210> 436

<211> 235

<212> PRT

<213> Escherichia coli

<400> 436

Met Tyr Arg Tyr Leu Ser Ile Ala Ala Val Val Leu Ser Ala Ala Phe
 1 5 10 15
 Ser Gly Pro Ala Leu Ala Glu Gly Ile Asn Ser Phe Ser Gln Ala Lys
 20 25 30
 Ala Ala Ala Val Lys Val His Ala Asp Ala Pro Gly Thr Phe Tyr Cys
 35 40 45
 Gly Cys Lys Ile Asn Trp Gln Gly Lys Lys Gly Val Val Asp Leu Gln
 50 55 60
 Ser Cys Gly Tyr Gln Val Arg Lys Asn Glu Asn Arg Ala Ser Arg Val
 65 70 75 80
 Glu Trp Glu His Val Val Pro Ala Trp Gln Phe Gly His Gln Arg Gln
 85 90 95
 Cys Trp Gln Asp Gly Gly Arg Lys Asn Cys Ala Lys Asp Pro Val Tyr
 100 105 110
 Arg Lys Met Glu Ser Asp Met His Asn Leu Gln Pro Ser Val Gly Glu
 115 120 125
 Val Asn Gly Asp Arg Gly Asn Phe Met Tyr Ser Gln Trp Asn Gly Gly
 130 135 140
 Glu Gly Gln Tyr Gly Gln Cys Ala Met Lys Val Asp Phe Lys Glu Lys
 145 150 155 160
 Ala Ala Glu Pro Pro Ala Arg Ala Arg Gly Ala Ile Ala Arg Thr Tyr

				165				170					175				
Phe	Tyr	Met	Arg	Asp	Gln	Tyr	Asn	Leu	Thr	Leu	Ser	Arg	Gln	Gln	Thr		
			180					185					190				
Gln	Leu	Phe	Asn	Ala	Trp	Asn	Lys	Met	Tyr	Pro	Val	Thr	Asp	Trp	Glu		
		195					200					205					
Cys	Glu	Arg	Asp	Glu	Arg	Ile	Ala	Lys	Val	Gln	Gly	Asn	His	Asn	Pro		
	210					215					220						
Tyr	Val	Gln	Arg	Ala	Cys	Gln	Ala	Arg	Lys	Ser							
225					230					235							

<210> 437

<211> 480

<212> PRT

<213> Escherichia coli

<400> 437

Met	Ser	Arg	Arg	Leu	Arg	Arg	Thr	Lys	Ile	Val	Thr	Thr	Leu	Gly	Pro		
1				5				10					15				
Ala	Thr	Asp	Arg	Asp	Asn	Asn	Leu	Glu	Lys	Val	Ile	Ala	Ala	Gly	Ala		
		20					25					30					
Asn	Val	Val	Arg	Met	Asn	Phe	Ser	His	Gly	Ser	Pro	Glu	Asp	His	Lys		
		35				40					45						
Met	Arg	Ala	Asp	Lys	Val	Arg	Glu	Ile	Ala	Ala	Lys	Leu	Gly	Arg	His		
	50					55					60						
Val	Ala	Ile	Leu	Gly	Asp	Leu	Gln	Gly	Pro	Lys	Ile	Arg	Val	Ser	Thr		
	65				70					75					80		
Phe	Lys	Glu	Gly	Lys	Val	Phe	Leu	Asn	Ile	Gly	Asp	Lys	Phe	Leu	Leu		
			85					90						95			
Asp	Ala	Asn	Leu	Gly	Lys	Gly	Glu	Gly	Asp	Lys	Glu	Lys	Val	Gly	Ile		
		100						105					110				
Asp	Tyr	Lys	Gly	Leu	Pro	Ala	Asp	Val	Val	Pro	Gly	Asp	Ile	Leu	Leu		
		115				120						125					
Leu	Asp	Asp	Gly	Arg	Val	Gln	Leu	Lys	Val	Leu	Glu	Val	Gln	Gly	Met		
	130					135					140						
Lys	Val	Phe	Thr	Glu	Val	Thr	Val	Gly	Gly	Pro	Leu	Ser	Asn	Asn	Lys		
	145				150					155					160		
Gly	Ile	Asn	Lys	Leu	Gly	Gly	Gly	Leu	Ser	Ala	Glu	Ala	Leu	Thr	Glu		
			165					170						175			
Lys	Asp	Lys	Ala	Asp	Ile	Lys	Thr	Ala	Ala	Leu	Ile	Gly	Val	Asp	Tyr		
		180						185					190				
Leu	Ala	Val	Ser	Phe	Pro	Arg	Cys	Gly	Glu	Asp	Leu	Asn	Tyr	Ala	Arg		
		195					200					205					
Arg	Leu	Ala	Arg	Asp	Ala	Gly	Cys	Asp	Ala	Lys	Ile	Val	Ala	Lys	Val		
	210					215					220						
Glu	Arg	Ala	Glu	Ala	Val	Cys	Ser	Gln	Asp	Ala	Met	Asp	Asp	Ile	Ile		
	225				230					235					240		
Leu	Ala	Ser	Asp	Val	Val	Met	Val	Ala	Arg	Gly	Asp	Leu	Gly	Val	Glu		
			245						250						255		
Ile	Gly	Asp	Pro	Glu	Leu	Val	Gly	Ile	Gln	Lys	Ala	Leu	Ile	Arg	Arg		
		260						265					270				
Ala	Arg	Gln	Leu	Asn	Arg	Ala	Val	Ile	Thr	Ala	Thr	Gln	Met	Met	Glu		
		275					280					285					
Ser	Met	Ile	Thr	Asn	Pro	Met	Pro	Thr	Arg	Ala	Glu	Val	Met	Asp	Val		
	290					295					300						
Ala	Asn	Ala	Val	Leu	Asp	Gly	Thr	Asp	Ala	Val	Met	Leu	Ser	Ala	Glu		
	305				310					315					320		
Thr	Ala	Ala	Gly	Gln	Tyr	Pro	Ser	Glu	Thr	Val	Ala	Ala	Met	Ala	Arg		
			325					330						335			
Val	Cys	Leu	Gly	Ala	Glu	Lys	Ile	Pro	Ser	Ile	Asn	Val	Ser	Lys	His		
			340					345					350				

Arg Leu Asp Val Gln Phe Asp Asn Val Glu Glu Ala Ile Ala Met Ser
 355 360 365
 Ala Met Tyr Ala Ala Asn His Leu Lys Gly Val Thr Ala Ile Ile Thr
 370 375 380
 Met Thr Glu Ser Gly Arg Thr Ala Leu Met Thr Ser Arg Ile Ser Ser
 385 390 395 400
 Gly Leu Pro Ile Phe Ala Met Ser Arg His Glu Arg Thr Leu Asn Leu
 405 410 415
 Thr Ala Leu Tyr Arg Gly Val Thr Pro Val His Phe Asp Ser Ala Asn
 420 425 430
 Asp Gly Val Ala Ala Ala Ser Glu Ala Val Asn Leu Leu Arg Asp Lys
 435 440 445
 Gly Tyr Leu Met Ser Gly Asp Leu Val Ile Val Thr Gln Gly Asp Val
 450 455 460
 Met Ser Thr Val Gly Ser Thr Asn Thr Thr Arg Ile Leu Thr Val Glu
 465 470 475 480

<210> 438
 <211> 239
 <212> PRT
 <213> Escherichia coli

<400> 438
 Met Ile Asn Val Leu Ile Ile Asp Asp Asp Ala Met Val Ala Glu Leu
 1 5 10 15
 Asn Arg Arg Tyr Val Ala Gln Ile Pro Gly Phe Gln Cys Cys Gly Thr
 20 25 30
 Ala Ser Thr Leu Glu Lys Ala Lys Glu Ile Ile Phe Asn Ser Asp Thr
 35 40 45
 Pro Ile Asp Leu Ile Leu Leu Asp Ile Tyr Met Gln Lys Glu Asn Gly
 50 55 60
 Leu Asp Leu Leu Pro Val Leu His Asn Ala Arg Cys Lys Ser Asp Val
 65 70 75 80
 Ile Val Ile Ser Ser Ala Ala Asp Ala Ala Thr Ile Lys Asp Ser Leu
 85 90 95
 His Tyr Gly Val Val Asp Tyr Leu Ile Lys Pro Phe Gln Ala Ser Arg
 100 105 110
 Phe Glu Glu Ala Leu Thr Gly Trp Arg Gln Lys Lys Met Ala Leu Glu
 115 120 125
 Lys His Gln Tyr Tyr Asp Gln Ala Glu Leu Asp Gln Leu Ile His Gly
 130 135 140
 Ser Ser Ser Asn Glu Gln Asp Pro Arg Arg Leu Pro Lys Gly Leu Thr
 145 150 155 160
 Pro Gln Thr Leu Arg Thr Leu Cys Gln Trp Ile Asp Ala His Gln Asp
 165 170 175
 Tyr Glu Phe Ser Thr Asp Glu Leu Ala Asn Glu Val Asn Ile Ser Arg
 180 185 190
 Val Ser Cys Arg Lys Tyr Leu Ile Trp Leu Val Asn Cys His Ile Leu
 195 200 205
 Phe Thr Ser Ile His Tyr Gly Val Thr Gly Arg Pro Val Tyr Arg Tyr
 210 215 220
 Arg Ile Gln Ala Glu His Tyr Ser Leu Leu Lys Gln Tyr Cys Gln
 225 230 235

<210> 439
 <211> 543
 <212> PRT
 <213> Escherichia coli

<400> 439

```

Met Arg His Ser Leu Pro Tyr Arg Met Leu Arg Lys Arg Pro Met Lys
1          5          10          15
Leu Ser Thr Thr Val Ile Leu Met Val Ser Ala Val Leu Phe Ser Val
          20          25          30
Leu Leu Val Val His Leu Ile Tyr Phe Ser Gln Ile Ser Asp Met Thr
          35          40          45
Arg Asp Gly Leu Ala Asn Lys Ala Leu Ala Val Ala Arg Thr Leu Ala
          50          55          60
Asp Ser Pro Glu Ile Arg Gln Gly Leu Gln Lys Lys Pro Gln Glu Ser
65          70          75          80
Gly Ile Gln Ala Ile Ala Glu Ala Val Arg Lys Arg Asn Asp Leu Leu
          85          90          95
Phe Ile Val Val Thr Asp Met Gln Ser Leu Arg Tyr Ser His Pro Glu
          100          105          110
Ala Gln Arg Ile Gly Gln Pro Phe Lys Gly Asp Asp Ile Leu Lys Ala
          115          120          125
Leu Asn Gly Glu Glu Asn Val Ala Ile Asn Arg Gly Phe Leu Ala Gln
          130          135          140
Ala Leu Arg Val Phe Thr Pro Ile Tyr Asp Glu Asn His Lys Gln Ile
145          150          155          160
Gly Val Val Ala Ile Gly Leu Glu Leu Ser Arg Val Thr Gln Gln Ile
          165          170          175
Asn Asp Ser Arg Trp Ser Ile Ile Trp Ser Val Leu Phe Gly Met Leu
          180          185          190
Val Gly Leu Ile Gly Thr Cys Ile Leu Val Lys Val Leu Lys Lys Ile
          195          200          205
Leu Phe Gly Leu Glu Pro Tyr Glu Ile Ser Thr Leu Phe Glu Gln Arg
210          215          220
Gln Ala Met Leu Gln Ser Ile Lys Glu Gly Val Val Ala Val Asp Asp
225          230          235          240
Arg Gly Glu Val Thr Leu Ile Asn Asp Ala Ala Gln Glu Leu Leu Asn
          245          250          255
Tyr Arg Lys Ser Gln Asp Asp Glu Lys Leu Ser Thr Leu Ser His Ser
          260          265          270
Trp Ser Gln Val Val Asp Val Ser Glu Val Leu Arg Asp Gly Thr Pro
          275          280          285
Arg Arg Asp Glu Glu Ile Thr Ile Lys Asp Arg Leu Leu Leu Ile Asn
290          295          300
Thr Val Pro Val Arg Ser Asn Gly Val Ile Ile Gly Ala Ile Ser Thr
305          310          315          320
Phe Arg Asp Lys Thr Glu Val Arg Lys Leu Met Gln Arg Leu Asp Gly
          325          330          335
Leu Val Asn Tyr Ala Asp Ala Leu Arg Glu Arg Ser His Glu Phe Met
          340          345          350
Asn Lys Leu His Val Ile Leu Gly Leu Leu His Leu Lys Ser Tyr Lys
          355          360          365
Gln Leu Glu Asp Tyr Ile Leu Lys Thr Ala Asn Asn Tyr Gln Glu Glu
          370          375          380
Ile Gly Ser Leu Leu Gly Lys Ile Lys Ser Pro Val Ile Ala Gly Phe
385          390          395          400
Leu Ile Ser Lys Ile Asn Arg Ala Thr Asp Leu Gly His Thr Leu Ile
          405          410          415
Leu Asn Ser Glu Ser Gln Leu Pro Asp Ser Gly Ser Glu Asp Gln Val
          420          425          430
Ala Thr Leu Ile Thr Thr Leu Gly Asn Leu Ile Glu Asn Ala Leu Glu
          435          440          445
Ala Leu Gly Pro Glu Pro Gly Gly Glu Ile Ser Val Thr Leu His Tyr
          450          455          460
Arg His Gly Trp Leu His Cys Glu Val Asn Asp Asp Gly Pro Gly Ile
465          470          475          480

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Ala Pro Asp Lys Ile Asp His Ile Phe Asp Lys Gly Val Ser Thr Lys
 485 490 495
 Gly Ser Glu Arg Gly Val Gly Leu Ala Leu Val Lys Gln Gln Val Glu
 500 505 510
 Asn Leu Gly Gly Ser Ile Ala Val Glu Ser Glu Pro Gly Ile Phe Thr
 515 520 525
 Gln Phe Phe Val Gln Ile Pro Trp Asp Gly Glu Arg Ser Asn Arg
 530 535 540

<210> 440

<211> 328

<212> PRT

<213> Escherichia coli

<400> 440

Met Ser Val Pro Leu Ser Thr Trp Asn Leu Leu Arg Tyr Asn Asn Ser
 1 5 10 15
 Tyr Leu Gln Lys Val Thr Met Phe Pro Gln Cys Lys Phe Ser Arg Glu
 20 25 30
 Phe Leu His Pro Arg Tyr Trp Leu Thr Trp Phe Gly Leu Gly Val Leu
 35 40 45
 Trp Leu Trp Val Gln Leu Pro Tyr Pro Val Leu Cys Phe Leu Gly Thr
 50 55 60
 Arg Ile Gly Ala Met Ala Arg Pro Phe Leu Lys Arg Arg Glu Ser Ile
 65 70 75 80
 Ala Arg Lys Asn Leu Glu Leu Cys Phe Pro Gln His Ser Ala Glu Glu
 85 90 95
 Arg Glu Lys Met Ile Ala Glu Asn Phe Arg Ser Leu Gly Met Ala Leu
 100 105 110
 Val Glu Thr Gly Met Ala Trp Phe Trp Pro Asp Ser Arg Val Arg Lys
 115 120 125
 Trp Phe Asp Val Glu Gly Leu Asp Asn Leu Lys Arg Ala Gln Met Gln
 130 135 140
 Asn Arg Gly Val Met Val Val Gly Val His Phe Met Ser Leu Glu Leu
 145 150 155 160
 Gly Gly Arg Val Met Gly Leu Cys Gln Pro Met Met Ala Thr Tyr Arg
 165 170 175
 Pro His Asn Asn Gln Leu Met Glu Trp Val Gln Thr Arg Gly Arg Met
 180 185 190
 Arg Ser Asn Lys Ala Met Ile Gly Arg Asn Asn Leu Arg Gly Ile Val
 195 200 205
 Gly Ala Leu Lys Lys Gly Glu Ala Val Trp Phe Ala Pro Asp Gln Asp
 210 215 220
 Tyr Gly Arg Lys Gly Ser Ser Phe Ala Pro Phe Phe Ala Val Glu Asn
 225 230 235 240
 Val Ala Thr Thr Asn Gly Thr Tyr Val Leu Ser Arg Leu Ser Gly Ala
 245 250 255
 Ala Met Leu Thr Val Thr Met Val Arg Lys Ala Asp Tyr Ser Gly Tyr
 260 265 270
 Arg Leu Phe Ile Thr Pro Glu Met Glu Gly Tyr Pro Thr Asp Glu Asn
 275 280 285
 Gln Ala Ala Ala Tyr Met Asn Lys Ile Ile Glu Lys Glu Ile Met Arg
 290 295 300
 Ala Pro Glu Gln Tyr Leu Trp Ile His Arg Arg Phe Lys Thr Arg Pro
 305 310 315 320
 Val Gly Glu Ser Ser Leu Tyr Ile
 325

<210> 441

<211> 87

<212> PRT

<213> Escherichia coli

<400> 441

```

Met Ala Asn Ile Lys Ser Ala Lys Lys Arg Ala Ile Gln Ser Glu Lys
 1          5          10          15
Ala Arg Lys His Asn Ala Ser Arg Arg Ser Met Met Arg Thr Phe Ile
          20          25          30
Lys Lys Val Tyr Ala Ala Ile Glu Ala Gly Asp Lys Ala Ala Ala Gln
          35          40          45
Lys Ala Phe Asn Glu Met Gln Pro Ile Val Asp Arg Gln Ala Ala Lys
          50          55          60
Gly Leu Ile His Lys Asn Lys Ala Ala Arg His Lys Ala Asn Leu Thr
65          70          75          80
Ala Gln Ile Asn Lys Leu Ala
          85

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<210> 442

<211> 430

<212> PRT

<213> Escherichia coli

<400> 442

```

Met Arg Tyr Asn Gly Leu Asn Asn Met Phe Phe Pro Leu Cys Leu Ile
 1          5          10          15
Asn Asp Asn His Ser Val Thr Ser Pro Ser His Thr Lys Lys Thr Lys
          20          25          30
Ser Asp Asn Tyr Ser Lys His His Lys Asn Thr Leu Ile Asp Asn Lys
          35          40          45
Ala Leu Ser Leu Phe Lys Met Asp Asp His Glu Lys Val Ile Gly Leu
          50          55          60
Ile Gln Lys Met Lys Arg Ile Tyr Asp Ser Leu Pro Ser Gly Lys Ile
65          70          75          80
Thr Lys Glu Thr Asp Arg Lys Ile His Lys Tyr Phe Ile Asp Ile Ala
          85          90          95
Ser His Ala Asn Asn Lys Cys Asp Asp Arg Ile Thr Arg Arg Val Tyr
          100          105          110
Leu Asn Lys Asp Lys Glu Val Ser Ile Lys Val Val Tyr Phe Ile Asn
          115          120          125
Asn Val Thr Val His Asn Asn Thr Ile Glu Ile Pro Gln Thr Val Asn
          130          135          140
Gly Gly Tyr Asp Phe Ser His Leu Ser Leu Lys Gly Ile Val Ile Lys
145          150          155          160
Asp Glu Asp Leu Ser Asn Ser Asn Phe Ala Gly Cys Arg Leu Gln Asn
          165          170          175
Ala Ile Phe Gln Asp Cys Asn Met Tyr Lys Thr Asn Phe Asn Phe Ala
          180          185          190
Ile Met Glu Lys Ile Leu Phe Asp Asn Cys Ile Leu Asp Asp Ser Asn
          195          200          205
Phe Ala Gln Ile Lys Met Thr Asp Gly Thr Leu Asn Ser Cys Ser Ala
          210          215          220
Met His Val Gln Phe Tyr Asn Ala Thr Met Asn Arg Ala Asn Ile Lys
225          230          235          240
Asn Thr Phe Leu Asp Tyr Ser Asn Phe Tyr Met Ala Tyr Met Ala Glu
          245          250          255
Val Asn Leu Tyr Lys Val Ile Ala Pro Tyr Ile Asn Leu Phe Arg Ala
          260          265          270
Asp Leu Ser Phe Ser Lys Leu Asp Leu Ile Asn Phe Glu His Ala Asp
          275          280          285

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Leu Ser Arg Val Asn Leu Asn Lys Ala Thr Leu Gln Asn Ile Asn Leu
 290 295 300
 Ile Asp Ser Lys Leu Phe Phe Thr Arg Leu Thr Asn Thr Phe Leu Glu
 305 310 315 320
 Met Val Ile Cys Thr Asp Ser Asn Met Ala Asn Val Asn Phe Asn Asn
 325 330 335
 Ala Asn Leu Ser Asn Cys His Phe Asn Cys Ser Val Leu Thr Lys Ala
 340 345 350
 Trp Met Phe Asn Ile Arg Leu Tyr Arg Val Asn Phe Asp Glu Ala Ser
 355 360 365
 Val Gln Gly Met Gly Ile Thr Ile Leu Arg Gly Glu Glu Asn Ile Ser
 370 375 380
 Ile Asn Ser Asp Ile Leu Val Thr Leu Gln Lys Phe Phe Glu Glu Asp
 385 390 395 400
 Cys Ala Thr His Thr Gly Met Ser Gln Thr Glu Asp Asn Leu His Ala
 405 410 415
 Val Ala Met Lys Ile Thr Ala Asp Ile Met Gln Asp Ala Asp
 420 425 430

<210> 443

<211> 883

<212> PRT

<213> Escherichia coli

<400> 443

Met Asn Glu Gln Tyr Ser Ala Leu Arg Ser Asn Val Ser Met Leu Gly
 1 5 10 15
 Lys Val Leu Gly Glu Thr Ile Lys Asp Ala Leu Gly Glu His Ile Leu
 20 25 30
 Glu Arg Val Glu Thr Ile Arg Lys Leu Ser Lys Ser Ser Arg Ala Gly
 35 40 45
 Asn Asp Ala Asn Arg Gln Glu Leu Leu Thr Thr Leu Gln Asn Leu Ser
 50 55 60
 Asn Asp Glu Leu Leu Pro Val Ala Arg Ala Phe Ser Gln Phe Leu Asn
 65 70 75 80
 Leu Ala Asn Thr Ala Glu Gln Tyr His Ser Ile Ser Pro Lys Gly Glu
 85 90 95
 Ala Ala Ser Asn Pro Glu Val Ile Ala Arg Thr Leu Arg Lys Leu Lys
 100 105 110
 Asn Gln Pro Glu Leu Ser Glu Asp Thr Ile Lys Lys Ala Val Glu Ser
 115 120 125
 Leu Ser Leu Glu Leu Val Leu Thr Ala His Pro Thr Glu Ile Thr Arg
 130 135 140
 Arg Thr Leu Ile His Lys Met Val Glu Val Asn Ala Cys Leu Lys Gln
 145 150 155 160
 Leu Asp Asn Lys Asp Ile Ala Asp Tyr Glu His Asn Gln Leu Met Arg
 165 170 175
 Arg Leu Arg Gln Leu Ile Ala Gln Ser Trp His Thr Asp Glu Ile Arg
 180 185 190
 Lys Leu Arg Pro Ser Pro Val Asp Glu Ala Lys Trp Gly Phe Ala Val
 195 200 205
 Val Glu Asn Ser Leu Trp Gln Gly Val Pro Asn Tyr Leu Arg Glu Leu
 210 215 220
 Asn Glu Gln Leu Glu Glu Asn Leu Gly Tyr Lys Leu Pro Val Glu Phe
 225 230 235 240
 Val Pro Val Arg Phe Thr Ser Trp Met Gly Gly Asp Arg Asp Gly Asn
 245 250 255
 Pro Asn Val Thr Ala Asp Ile Thr Arg His Val Leu Leu Leu Ser Arg
 260 265 270
 Trp Lys Ala Thr Asp Leu Phe Leu Lys Asp Ile Gln Val Leu Val Ser

275	280	285
Glu Leu Ser Met Val	Glu Ala Thr Pro	Glu Leu Leu Ala Leu Val Gly
290	295	300
Glu Glu Gly Ala Ala	Glu Pro Tyr Arg Tyr	Leu Met Lys Asn Leu Arg
305	310	315
Ser Arg Leu Met Ala	Thr Gln Ala Trp Leu	Glu Ala Arg Leu Lys Gly
325	330	335
Glu Glu Leu Pro Lys	Pro Glu Gly Leu Leu	Thr Gln Asn Glu Glu Leu
340	345	350
Trp Glu Pro Leu Tyr	Ala Cys Tyr Gln Ser	Leu Gln Ala Cys Gly Met
355	360	365
Gly Ile Ile Ala Asn	Gly Asp Leu Leu Asp	Thr Leu Arg Arg Val Lys
370	375	380
Cys Phe Gly Val Pro	Leu Val Arg Ile Asp	Ile Arg Gln Glu Ser Thr
385	390	395
Arg His Thr Glu Ala	Leu Gly Glu Leu Thr	Arg Tyr Leu Gly Ile Gly
405	410	415
Asp Tyr Glu Ser Trp	Ser Glu Ala Asp Lys	Gln Ala Phe Leu Ile Arg
420	425	430
Glu Leu Asn Ser Lys	Arg Pro Leu Leu Pro	Arg Asn Trp Gln Pro Ser
435	440	445
Ala Glu Thr Arg Glu	Val Leu Asp Thr Cys	Gln Val Ile Ala Glu Ala
450	455	460
Pro Gln Gly Ser Ile	Ala Ala Tyr Val Ile	Ser Met Ala Lys Thr Pro
465	470	475
Ser Asp Val Leu Ala	Val His Leu Leu Leu	Lys Glu Ala Gly Ile Gly
485	490	495
Phe Ala Met Pro Val	Ala Pro Leu Phe Glu	Thr Leu Asp Asp Leu Asn
500	505	510
Asn Ala Asn Asp Val	Met Thr Gln Leu Leu	Asn Ile Asp Trp Tyr Arg
515	520	525
Gly Leu Ile Gln Gly	Lys Gln Met Val Met	Ile Gly Tyr Ser Asp Ser
530	535	540
Ala Lys Asp Ala Gly	Val Met Ala Ala Ser	Trp Ala Gln Tyr Gln Ala
545	550	555
Gln Asp Ala Leu Ile	Lys Thr Cys Glu Lys	Ala Gly Ile Glu Leu Thr
565	570	575
Leu Phe His Gly Arg	Gly Gly Ser Ile Gly	Arg Gly Gly Ala Pro Ala
580	585	590
His Ala Ala Leu Leu	Ser Gln Pro Pro Gly	Ser Leu Lys Gly Gly Leu
595	600	605
Arg Val Thr Glu Gln	Gly Glu Met Ile Arg	Phe Lys Tyr Gly Leu Pro
610	615	620
Glu Ile Thr Val Ser	Ser Leu Ser Leu Tyr	Thr Gly Ala Ile Leu Glu
625	630	635
Ala Asn Leu Leu Pro	Pro Pro Glu Pro Lys	Glu Ser Trp Arg Arg Ile
645	650	655
Met Asp Glu Leu Ser	Val Ile Ser Cys Asp	Val Tyr Arg Gly Tyr Val
660	665	670
Arg Glu Asn Lys Asp	Phe Val Pro Tyr Phe	Arg Ser Ala Thr Pro Glu
675	680	685
Gln Glu Leu Gly Lys	Leu Pro Leu Gly Ser	Arg Pro Ala Lys Arg Arg
690	695	700
Pro Thr Gly Gly Val	Glu Ser Leu Arg Ala	Ile Pro Trp Ile Phe Ala
705	710	715
Trp Thr Gln Asn Arg	Leu Met Leu Pro Ala	Trp Leu Gly Ala Gly Thr
725	730	735
Ala Leu Gln Lys Val	Val Glu Asp Gly Lys	Gln Ser Glu Leu Glu Ala
740	745	750
Met Cys Arg Asp Trp	Pro Phe Phe Ser Thr	Arg Leu Gly Met Leu Glu
755	760	765

Met Val Phe Ala Lys Ala Asp Leu Trp Leu Ala Glu Tyr Tyr Asp Gln
 770 775 780
 Arg Leu Val Asp Lys Ala Leu Trp Pro Leu Gly Lys Glu Leu Arg Asn
 785 790 795 800
 Leu Gln Glu Glu Asp Ile Lys Val Val Leu Ala Ile Ala Asn Asp Ser
 805 810 815
 His Leu Met Ala Asp Leu Pro Trp Ile Ala Glu Ser Ile Gln Leu Arg
 820 825 830
 Asn Ile Tyr Thr Asp Pro Leu Asn Val Leu Gln Ala Glu Leu Leu His
 835 840 845
 Arg Ser Arg Gln Ala Glu Lys Glu Gly Gln Glu Pro Asp Pro Arg Val
 850 855 860
 Glu Gln Ala Leu Met Val Thr Ile Ala Gly Ile Ala Ala Gly Met Arg
 865 870 875 880
 Asn Thr Gly

<210> 444

<211> 663

<212> PRT

<213> Escherichia coli

<400> 444

Met Ser Ser Arg Lys Glu Leu Ala Asn Ala Ile Arg Ala Leu Ser Met
 1 5 10 15
 Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly
 20 25 30
 Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
 35 40 45
 Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
 50 55 60
 Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
 65 70 75 80
 Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys
 85 90 95
 Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr
 100 105 110
 Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile
 115 120 125
 Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile
 130 135 140
 Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu
 145 150 155 160
 Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly
 165 170 175
 Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His
 180 185 190
 Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr
 195 200 205
 Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile
 210 215 220
 Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu
 225 230 235 240
 Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly
 245 250 255
 Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu
 260 265 270
 Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser
 275 280 285
 Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu

290	295	300
Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln		
305	310	315
Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp		
	325	330
Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro		
	340	345
Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe		
	355	360
Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro		
	370	375
Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala		
385	390	395
Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala		
	405	410
Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser		
	420	425
Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala		
	435	440
Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile		
	450	455
Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala		
465	470	475
Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln		
	485	490
Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly		
	500	505
Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Gln Glu Arg		
	515	520
Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys		
	530	535
Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu		
545	550	555
Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val		
	565	570
Lys Ala Arg Val Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln		
	580	585
Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg		
	595	600
Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly		
	610	615
Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro		
625	630	635
Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val		
	645	650
Ala Lys Ala Lys Glu Leu Leu		
	660	

<210> 445

<211> 152

<212> PRT

<213> Escherichia coli

<400> 445

Met Phe Arg Gly Ala Thr Leu Val Asn Leu Asp Ser Lys Gly Arg Leu
1 5 10 15
Ser Val Pro Thr Arg Tyr Arg Glu Gln Leu Leu Glu Asn Ala Ala Gly
20 25 30
Gln Met Val Cys Thr Ile Asp Ile Tyr His Pro Cys Leu Leu Tyr
35 40 45


```

Pro Leu Pro Glu Trp Glu Ile Ile Glu Gln Lys Leu Ser Arg Leu Ser
 50                               55                               60
Ser Met Asn Pro Val Glu Arg Arg Val Gln Arg Leu Leu Leu Gly His
65                               70                               75                               80
Ala Ser Glu Cys Gln Met Asp Gly Ala Gly Arg Leu Leu Ile Ala Pro
                               85                               90                               95
Val Leu Arg Gln His Ala Gly Leu Thr Lys Glu Val Met Leu Val Gly
                               100                              105                              110
Gln Phe Asn Lys Phe Glu Leu Trp Asp Glu Thr Thr Trp His Gln Gln
                               115                              120                              125
Val Lys Glu Asp Ile Asp Ala Glu Gln Leu Ala Thr Gly Asp Leu Ser
                               130                              135                              140
Glu Arg Leu Gln Asp Leu Ser Leu
145                               150

```

<210> 446

<211> 313

<212> PRT

<213> Escherichia coli

<400> 446

```

Met Met Glu Asn Tyr Lys His Thr Thr Val Leu Leu Asp Glu Ala Val
 1                               5                               10                               15
Asn Gly Leu Asn Ile Arg Pro Asp Gly Ile Tyr Ile Asp Gly Thr Phe
                               20                               25                               30
Gly Arg Gly Gly His Ser Arg Leu Ile Leu Ser Gln Leu Gly Glu Glu
                               35                               40                               45
Gly Arg Leu Leu Ala Ile Asp Arg Asp Pro Gln Ala Ile Ala Val Ala
                               50                               55                               60
Lys Thr Ile Asp Asp Pro Arg Phe Ser Ile Ile His Gly Pro Phe Ser
65                               70                               75                               80
Ala Leu Gly Glu Tyr Val Ala Glu Arg Asp Leu Ile Gly Lys Ile Asp
                               85                               90                               95
Gly Ile Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Leu Asp Asp Ala
                               100                              105                              110
Glu Arg Gly Phe Ser Phe Met Arg Asp Gly Pro Leu Asp Met Arg Met
                               115                              120                              125
Asp Pro Thr Arg Gly Gln Ser Ala Ala Glu Trp Leu Gln Thr Ala Glu
                               130                              135                              140
Glu Ala Asp Ile Ala Trp Val Leu Lys Thr Tyr Gly Glu Glu Arg Phe
145                               150                              155                              160
Ala Lys Arg Ile Ala Arg Ala Ile Val Glu Arg Asn Arg Glu Gln Pro
                               165                              170                              175
Met Thr Arg Thr Lys Glu Leu Ala Glu Val Val Ala Ala Ala Thr Pro
                               180                              185                              190
Val Lys Asp Lys Phe Lys His Pro Ala Thr Arg Thr Phe Gln Ala Val
                               195                              200                              205
Arg Ile Trp Val Asn Ser Glu Leu Glu Glu Ile Glu Gln Ala Leu Lys
                               210                              215                              220
Ser Ser Leu Asn Val Leu Ala Pro Gly Gly Arg Leu Ser Ile Ile Ser
225                               230                              235                              240
Phe His Ser Leu Glu Asp Arg Ile Val Lys Arg Phe Met Arg Glu Asn
                               245                              250                              255
Ser Arg Gly Pro Gln Val Pro Ala Gly Leu Pro Met Thr Glu Glu Gln
                               260                              265                              270
Leu Lys Lys Leu Gly Gly Arg Gln Leu Arg Ala Leu Gly Lys Leu Met
                               275                              280                              285
Pro Gly Glu Glu Glu Val Ala Glu Asn Pro Arg Ala Arg Ser Ser Val
                               290                              295                              300
Leu Arg Ile Ala Glu Arg Thr Asn Ala

```

305

310

<210> 447
 <211> 121
 <212> PRT
 <213> Escherichia coli

<400> 447

```

Met Ile Ser Arg Val Thr Glu Ala Leu Ser Lys Val Lys Gly Ser Met
 1           5           10           15
Gly Ser His Glu Arg His Ala Leu Pro Gly Val Ile Gly Asp Asp Leu
          20           25           30
Leu Arg Phe Gly Lys Leu Pro Leu Cys Leu Phe Ile Cys Ile Ile Leu
          35           40           45
Thr Ala Val Thr Val Val Thr Thr Ala His His Thr Arg Leu Leu Thr
          50           55           60
Ala Gln Arg Glu Gln Leu Val Leu Glu Arg Asp Ala Leu Asp Ile Glu
65           70           75           80
Trp Arg Asn Leu Ile Leu Glu Glu Asn Ala Leu Gly Asp His Ser Arg
          85           90           95
Val Glu Arg Ile Ala Thr Glu Lys Leu Gln Met Gln His Val Asp Pro
          100          105          110
Ser Gln Glu Asn Ile Val Val Gln Lys
          115          120

```

<210> 448
 <211> 588
 <212> PRT
 <213> Escherichia coli

<400> 448

```

Met Lys Ala Ala Ala Lys Thr Gln Lys Pro Lys Arg Gln Glu Glu His
 1           5           10           15
Ala Asn Phe Ile Ser Trp Arg Phe Ala Leu Leu Cys Gly Cys Ile Leu
          20           25           30
Leu Ala Leu Ala Phe Leu Leu Gly Arg Val Ala Trp Leu Gln Val Ile
          35           40           45
Ser Pro Asp Met Leu Val Lys Glu Gly Asp Met Arg Ser Leu Arg Val
          50           55           60
Gln Gln Val Ser Thr Ser Arg Gly Met Ile Thr Asp Arg Ser Gly Arg
65           70           75           80
Pro Leu Ala Val Ser Val Pro Val Lys Ala Ile Trp Ala Asp Pro Lys
          85           90           95
Glu Val His Asp Ala Gly Gly Ile Ser Val Gly Asp Arg Trp Lys Ala
          100          105          110
Leu Ala Asn Ala Leu Asn Ile Pro Leu Asp Gln Leu Ser Ala Arg Ile
          115          120          125
Asn Ala Asn Pro Lys Gly Arg Phe Ile Tyr Leu Ala Arg Gln Val Asn
          130          135          140
Pro Asp Met Ala Asp Tyr Ile Lys Lys Leu Lys Leu Pro Gly Ile His
          145          150          155          160
Leu Arg Glu Glu Ser Arg Arg Tyr Tyr Pro Ser Gly Glu Val Thr Ala
          165          170          175
His Leu Ile Gly Phe Thr Asn Val Asp Ser Gln Gly Ile Glu Gly Val
          180          185          190
Glu Lys Ser Phe Asp Lys Trp Leu Thr Gly Gln Pro Gly Glu Arg Ile
          195          200          205
Val Arg Lys Asp Arg Tyr Gly Arg Val Ile Glu Asp Ile Ser Ser Thr
          210          215          220

```

Asp Ser Gln Ala Ala His Asn Leu Ala Leu Ser Ile Asp Glu Arg Leu
 225 230 235 240
 Gln Ala Leu Val Tyr Arg Glu Leu Asn Asn Ala Val Ala Phe Asn Lys
 245 250 255
 Ala Glu Ser Gly Ser Ala Val Leu Val Asp Val Asn Thr Gly Glu Val
 260 265 270
 Leu Ala Met Ala Asn Ser Pro Ser Tyr Asn Pro Asn Asn Leu Ser Gly
 275 280 285
 Thr Pro Lys Glu Ala Met Arg Asn Arg Thr Ile Thr Asp Val Phe Glu
 290 295 300
 Pro Gly Ser Thr Val Lys Pro Met Val Val Met Thr Ala Leu Gln Arg
 305 310 315 320
 Gly Val Val Arg Glu Asn Ser Val Leu Asn Thr Ile Pro Tyr Arg Ile
 325 330 335
 Asn Gly His Glu Ile Lys Asp Val Ala Arg Tyr Ser Glu Leu Thr Leu
 340 345 350
 Thr Gly Val Leu Gln Lys Ser Ser Asn Val Gly Val Ser Lys Leu Ala
 355 360 365
 Leu Ala Met Pro Ser Ser Ala Leu Val Asp Thr Tyr Ser Arg Phe Gly
 370 375 380
 Leu Gly Lys Ala Thr Asn Leu Gly Leu Val Gly Glu Arg Ser Gly Leu
 385 390 395 400
 Tyr Pro Gln Lys Gln Arg Trp Ser Asp Ile Glu Arg Ala Thr Phe Ser
 405 410 415
 Phe Gly Tyr Gly Leu Met Val Thr Pro Leu Gln Leu Ala Arg Val Tyr
 420 425 430
 Ala Thr Ile Gly Ser Tyr Gly Ile Tyr Arg Pro Leu Ser Ile Thr Lys
 435 440 445
 Val Asp Pro Pro Val Pro Gly Glu Arg Val Phe Pro Glu Ser Ile Val
 450 455 460
 Arg Thr Val Val His Met Met Glu Ser Val Ala Leu Pro Gly Gly Gly
 465 470 475 480
 Gly Val Lys Ala Ala Ile Lys Gly Tyr Arg Ile Ala Ile Lys Thr Gly
 485 490 495
 Thr Ala Lys Lys Val Gly Pro Asp Gly Arg Tyr Ile Asn Lys Tyr Ile
 500 505 510
 Ala Tyr Thr Ala Gly Val Ala Pro Ala Ser Gln Pro Arg Phe Ala Leu
 515 520 525
 Val Val Val Ile Asn Asp Pro Gln Ala Gly Lys Tyr Tyr Gly Gly Ala
 530 535 540
 Val Ser Ala Pro Val Phe Gly Ala Ile Met Gly Gly Val Leu Arg Thr
 545 550 555 560
 Met Asn Ile Glu Pro Asp Ala Leu Thr Thr Gly Asp Lys Asn Glu Phe
 565 570 575
 Val Ile Asn Gln Gly Glu Gly Thr Gly Gly Arg Ser
 580 585

<210> 449

<211> 495

<212> PRT

<213> Escherichia coli

<400> 449

Met Ala Asp Arg Asn Leu Arg Asp Leu Leu Ala Pro Trp Val Pro Asp
 1 5 10 15
 Ala Pro Ser Arg Ala Leu Arg Glu Met Thr Leu Asp Ser Arg Val Ala
 20 25 30
 Ala Ala Gly Asp Leu Phe Val Ala Val Val Gly His Gln Ala Asp Gly
 35 40 45
 Arg Arg Tyr Ile Pro Gln Ala Ile Ala Gln Gly Val Ala Ala Ile Ile

50	55	60
Ala Glu Ala Lys Asp	Glu Ala Thr Asp Gly	Glu Ile Arg Glu Met His
65	70	75
Gly Val Pro Val Ile	Tyr Leu Ser Gln Leu	Asn Glu Arg Leu Ser Ala
85	90	95
Leu Ala Gly Arg Phe	Tyr His Glu Pro Ser	Asp Asn Leu Arg Leu Val
100	105	110
Gly Val Thr Gly Thr	Asn Gly Lys Thr Thr	Thr Thr Gln Leu Leu Ala
115	120	125
Gln Trp Ser Gln Leu	Leu Gly Glu Ile Ser	Ala Val Met Gly Thr Val
130	135	140
Gly Asn Gly Leu Leu	Gly Lys Val Ile Pro	Thr Glu Asn Thr Thr Gly
145	150	155
Ser Ala Val Asp Val	Gln His Glu Leu Ala	Gly Leu Val Asp Gln Gly
165	170	175
Ala Thr Phe Cys Ala	Met Glu Val Ser Ser	His Gly Leu Val Gln His
180	185	190
Arg Val Ala Leu Lys	Phe Ala Ser Val Phe	Thr Asn Leu Ser
195	200	205
Arg Asp His Leu Asp	Tyr His Gly Asp Met	Glu His Tyr Glu Ala Ala
210	215	220
Lys Trp Leu Leu Tyr	Ser Glu His His Cys	Gly Gln Ala Ile Ile Asn
225	230	235
Ala Asp Asp Glu Val	Gly Arg Arg Trp Leu	Ala Lys Leu Pro Asp Ala
245	250	255
Val Ala Val Ser Met	Glu Asp His Ile Asn	Pro Asn Cys His Gly Arg
260	265	270
Trp Leu Lys Ala Thr	Glu Val Asn Tyr His	Asp Ser Gly Ala Thr Ile
275	280	285
Arg Phe Ser Ser Ser	Trp Gly Asp Gly Glu	Ile Glu Ser His Leu Met
290	295	300
Gly Ala Phe Asn Val	Ser Asn Leu Leu Leu	Ala Leu Ala Thr Leu Leu
305	310	315
Ala Leu Gly Tyr Pro	Leu Ala Asp Leu Leu	Lys Thr Ala Ala Arg Leu
325	330	335
Gln Pro Val Cys Gly	Arg Met Glu Val Phe	Thr Ala Pro Gly Lys Pro
340	345	350
Thr Val Val Val Asp	Tyr Ala His Thr Pro	Asp Ala Leu Glu Lys Ala
355	360	365
Leu Gln Ala Ala Arg	Leu His Cys Ala Gly	Lys Leu Trp Cys Val Phe
370	375	380
Gly Cys Gly Gly Asp	Arg Asp Lys Gly Lys	Arg Pro Leu Met Gly Ala
385	390	395
Ile Ala Glu Glu Phe	Ala Asp Val Ala Val	Val Thr Asp Asp Asn Pro
405	410	415
Arg Thr Glu Glu Pro	Arg Ala Ile Ile Asn	Asp Ile Leu Ala Gly Met
420	425	430
Leu Asp Ala Gly His	Ala Lys Val Met Glu	Gly Arg Ala Glu Ala Val
435	440	445
Thr Cys Ala Val Met	Gln Ala Lys Glu Asn	Asp Val Val Leu Val Ala
450	455	460
Gly Lys Gly His Glu	Asp Tyr Gln Ile Val	Gly Asn Gln Arg Leu Asp
465	470	475
Tyr Ser Asp Arg Val	Thr Val Ala Arg Leu	Leu Gly Val Ile Ala
485	490	495

<210> 450

<211> 452

<212> PRT

<213> Escherichia coli

<400> 450

```

Met Ile Ser Val Thr Leu Ser Gln Leu Thr Asp Ile Leu Asn Gly Glu
 1           5           10           15
Leu Gln Gly Ala Asp Ile Thr Leu Asp Ala Val Thr Thr Asp Thr Arg
 20           25           30
Lys Leu Thr Pro Gly Cys Leu Phe Val Ala Leu Lys Gly Glu Arg Phe
 35           40           45
Asp Ala His Asp Phe Ala Asp Gln Ala Lys Ala Gly Gly Ala Gly Ala
 50           55           60
Leu Leu Val Ser Arg Pro Leu Asp Ile Asp Leu Pro Gln Leu Ile Val
 65           70           75           80
Lys Asp Thr Arg Leu Ala Phe Gly Glu Leu Ala Ala Trp Val Arg Gln
 85           90           95
Gln Val Pro Ala Arg Val Val Ala Leu Thr Gly Ser Ser Gly Lys Thr
100           105           110
Ser Val Lys Glu Met Thr Ala Ala Ile Leu Ser Gln Cys Gly Asn Thr
115           120           125
Leu Tyr Thr Ala Gly Asn Leu Asn Asn Asp Ile Gly Val Pro Met Thr
130           135           140
Leu Leu Arg Leu Thr Pro Glu Tyr Asp Tyr Ala Val Ile Glu Leu Gly
145           150           155           160
Ala Asn His Gln Gly Glu Ile Ala Trp Thr Val Ser Leu Thr Arg Pro
165           170           175
Glu Ala Ala Leu Val Asn Asn Leu Ala Ala Ala His Leu Glu Gly Phe
180           185           190
Gly Ser Leu Ala Gly Val Ala Lys Ala Lys Gly Glu Ile Phe Ser Gly
195           200           205
Leu Pro Glu Asn Gly Ile Ala Ile Met Asn Ala Asp Asn Asn Asp Trp
210           215           220
Leu Asn Trp Gln Ser Val Ile Gly Ser Arg Lys Val Trp Arg Phe Ser
225           230           235           240
Pro Asn Ala Ala Asn Ser Asp Phe Thr Ala Thr Asn Ile His Val Thr
245           250           255
Ser His Gly Thr Glu Phe Thr Leu Gln Thr Pro Thr Gly Ser Val Asp
260           265           270
Val Leu Leu Pro Leu Pro Gly Arg His Asn Ile Ala Asn Ala Leu Ala
275           280           285
Ala Ala Ala Leu Ser Met Ser Val Gly Ala Thr Leu Asp Ala Ile Lys
290           295           300
Ala Gly Leu Ala Asn Leu Lys Ala Val Pro Gly Arg Leu Phe Pro Ile
305           310           315           320
Gln Leu Ala Glu Asn Gln Leu Leu Leu Asp Asp Ser Tyr Asn Ala Asn
325           330           335
Val Gly Ser Met Thr Ala Ala Val Gln Val Leu Ala Glu Met Pro Gly
340           345           350
Tyr Arg Val Leu Val Val Gly Asp Met Ala Glu Leu Gly Ala Glu Ser
355           360           365
Glu Ala Cys His Val Gln Val Gly Glu Ala Ala Lys Ala Ala Gly Ile
370           375           380
Asp Arg Val Leu Ser Val Gly Lys Gln Ser His Ala Ile Ser Thr Ala
385           390           395           400
Ser Gly Val Gly Glu His Phe Ala Asp Lys Thr Ala Leu Ile Thr Arg
405           410           415
Leu Lys Leu Leu Ile Ala Glu Gln Gln Val Ile Thr Ile Leu Val Lys
420           425           430
Gly Ser Arg Ser Ala Ala Met Glu Glu Val Val Arg Ala Leu Gln Glu
435           440           445
Asn Gly Thr Cys
450

```

<210> 451
 <211> 360
 <212> PRT
 <213> Escherichia coli

<400> 451

```

Met Leu Val Trp Leu Ala Glu His Leu Val Lys Tyr Tyr Ser Gly Phe
 1          5          10          15
Asn Val Phe Ser Tyr Leu Thr Phe Arg Ala Ile Val Ser Leu Leu Thr
          20          25          30
Ala Leu Phe Ile Ser Leu Trp Met Gly Pro Arg Met Ile Ala His Leu
          35          40          45
Gln Lys Leu Ser Phe Gly Gln Val Val Arg Asn Asp Gly Pro Glu Ser
          50          55          60
His Phe Ser Lys Arg Gly Thr Pro Thr Met Gly Gly Ile Met Ile Leu
65          70          75          80
Thr Ala Ile Val Ile Ser Val Leu Leu Trp Ala Tyr Pro Ser Asn Pro
          85          90          95
Tyr Val Trp Cys Val Leu Val Val Leu Val Gly Tyr Gly Val Ile Gly
          100          105          110
Phe Val Asp Asp Tyr Arg Lys Val Val Arg Lys Asp Thr Lys Gly Leu
          115          120          125
Ile Ala Arg Trp Lys Tyr Phe Trp Met Ser Val Ile Ala Leu Gly Val
          130          135          140
Ala Phe Ala Leu Tyr Leu Ala Gly Lys Asp Thr Pro Ala Thr Gln Leu
145          150          155          160
Val Val Pro Phe Phe Lys Asp Val Met Pro Gln Leu Gly Leu Phe Tyr
          165          170          175
Ile Leu Leu Ala Tyr Phe Val Ile Val Gly Thr Gly Asn Ala Val Asn
          180          185          190
Leu Thr Asp Gly Leu Asp Gly Leu Ala Ile Met Pro Thr Val Phe Val
          195          200          205
Ala Gly Gly Phe Ala Leu Val Ala Trp Ala Thr Gly Asn Met Asn Phe
          210          215          220
Ala Ser Tyr Leu His Ile Pro Tyr Leu Arg His Ala Gly Glu Leu Val
225          230          235          240
Ile Val Cys Thr Ala Ile Val Gly Ala Gly Leu Gly Phe Leu Trp Phe
          245          250          255
Asn Thr Tyr Pro Ala Gln Val Phe Met Gly Asp Val Gly Ser Leu Ala
          260          265          270
Leu Gly Gly Ala Leu Gly Ile Ile Ala Val Leu Leu Arg Gln Glu Phe
          275          280          285
Leu Leu Val Ile Met Gly Gly Val Phe Val Val Glu Thr Leu Ser Val
          290          295          300
Ile Leu Gln Val Gly Ser Phe Lys Leu Arg Gly Gln Arg Ile Phe Arg
305          310          315          320
Met Ala Pro Ile His His Tyr Glu Leu Lys Gly Trp Pro Glu Pro
          325          330          335
Arg Val Ile Val Arg Phe Trp Ile Ile Ser Leu Met Leu Val Leu Ile
          340          345          350
Gly Leu Ala Thr Leu Lys Val Arg
          355          360

```

<210> 452
 <211> 438
 <212> PRT
 <213> Escherichia coli

<400> 452

```

Met Ala Asp Tyr Gln Gly Lys Asn Val Val Ile Ile Gly Leu Gly Leu
 1          5          10          15
Thr Gly Leu Ser Cys Val Asp Phe Phe Leu Ala Arg Gly Val Thr Pro
 20          25          30
Arg Val Met Asp Thr Arg Met Thr Pro Pro Gly Leu Asp Lys Leu Pro
 35          40          45
Glu Ala Val Glu Arg His Thr Gly Ser Leu Asn Asp Glu Trp Leu Met
 50          55          60
Ala Ala Asp Leu Ile Val Ala Ser Pro Gly Ile Ala Leu Ala His Pro
 65          70          75          80
Ser Leu Ser Ala Ala Ala Asp Ala Gly Ile Glu Ile Val Gly Asp Ile
 85          90          95
Glu Leu Phe Cys Arg Glu Ala Gln Ala Pro Ile Val Ala Ile Thr Gly
 100          105          110
Ser Asn Gly Lys Ser Thr Val Thr Thr Leu Val Gly Glu Met Ala Lys
 115          120          125
Ala Ala Gly Val Asn Val Gly Val Gly Gly Asn Ile Gly Leu Pro Ala
 130          135          140
Leu Met Leu Leu Asp Asp Glu Cys Glu Leu Tyr Val Leu Glu Leu Ser
 145          150          155          160
Ser Phe Gln Leu Glu Thr Thr Ser Ser Leu Gln Ala Val Ala Ala Thr
 165          170          175
Ile Leu Asn Val Thr Glu Asp His Met Asp Arg Tyr Pro Phe Gly Leu
 180          185          190
Gln Gln Tyr Arg Ala Ala Lys Leu Arg Ile Tyr Glu Asn Ala Lys Val
 195          200          205
Cys Val Val Asn Ala Asp Asp Ala Leu Thr Met Pro Ile Arg Gly Ala
 210          215          220
Asp Glu Arg Cys Val Ser Phe Gly Val Asn Met Gly Asp Tyr His Leu
 225          230          235          240
Asn His Gln Gln Gly Glu Thr Trp Leu Arg Val Lys Gly Glu Lys Val
 245          250          255
Leu Asn Val Lys Glu Met Lys Leu Ser Gly Gln His Asn Tyr Thr Asn
 260          265          270
Ala Leu Ala Ala Leu Ala Leu Ala Asp Ala Ala Gly Leu Pro Arg Ala
 275          280          285
Ser Ser Leu Lys Ala Leu Thr Thr Phe Thr Gly Leu Pro His Arg Phe
 290          295          300
Glu Val Val Leu Glu His Asn Gly Val Arg Trp Ile Asn Asp Ser Lys
 305          310          315          320
Ala Thr Asn Val Gly Ser Thr Glu Ala Ala Leu Asn Gly Leu His Val
 325          330          335
Asp Gly Thr Leu His Leu Leu Leu Gly Gly Asp Gly Lys Ser Ala Asp
 340          345          350
Phe Ser Pro Leu Ala Arg Tyr Leu Asn Gly Asp Asn Val Arg Leu Tyr
 355          360          365
Cys Phe Gly Arg Asp Gly Ala Gln Leu Ala Ala Leu Arg Pro Glu Val
 370          375          380
Ala Glu Gln Thr Glu Thr Met Glu Gln Ala Met Arg Leu Leu Ala Pro
 385          390          395          400
Arg Val Gln Pro Gly Asp Met Val Leu Leu Ser Pro Ala Cys Ala Ser
 405          410          415
Leu Asp Gln Phe Lys Asn Phe Glu Gln Arg Gly Asn Glu Phe Ala Arg
 420          425          430
Leu Ala Lys Glu Leu Gly
 435

```

<210> 453

<211> 414

<212> PRT

<213> Escherichia coli

<400> 453

```

Met Arg Leu Ser Leu Pro Arg Leu Lys Met Pro Arg Leu Pro Gly Phe
 1           5           10           15
Ser Ile Leu Val Trp Ile Ser Thr Ala Leu Lys Gly Trp Val Met Gly
          20           25           30
Ser Arg Glu Lys Asp Thr Asp Ser Leu Ile Met Tyr Asp Arg Thr Leu
          35           40           45
Leu Trp Leu Thr Phe Gly Leu Ala Ala Ile Gly Phe Ile Met Val Thr
          50           55           60
Ser Ala Ser Met Pro Ile Gly Gln Arg Leu Thr Asn Asp Pro Phe Phe
65           70           75           80
Phe Ala Lys Arg Asp Gly Val Tyr Leu Ile Leu Ala Phe Ile Leu Ala
          85           90           95
Ile Ile Thr Leu Arg Leu Pro Met Glu Phe Trp Gln Arg Tyr Ser Ala
          100          105          110
Thr Met Leu Leu Gly Ser Ile Ile Leu Leu Met Ile Val Leu Val Val
          115          120          125
Gly Ser Ser Val Lys Gly Ala Ser Arg Trp Ile Asp Leu Gly Leu Leu
          130          135          140
Arg Ile Gln Pro Ala Glu Leu Thr Lys Leu Ser Leu Phe Cys Tyr Ile
145          150          155          160
Ala Asn Tyr Leu Val Arg Lys Gly Asp Glu Val Arg Asn Asn Leu Arg
          165          170          175
Gly Phe Leu Lys Pro Met Gly Val Ile Leu Val Leu Ala Val Leu Leu
          180          185          190
Leu Ala Gln Pro Asp Leu Gly Thr Val Val Val Leu Phe Val Thr Thr
          195          200          205
Leu Ala Met Leu Phe Leu Ala Gly Ala Lys Leu Trp Gln Phe Ile Ala
          210          215          220
Ile Ile Gly Met Gly Ile Ser Ala Val Val Leu Leu Ile Leu Ala Glu
225          230          235          240
Pro Tyr Arg Ile Arg Arg Val Thr Ala Phe Trp Asn Pro Trp Glu Asp
          245          250          255
Pro Phe Gly Ser Gly Tyr Gln Leu Thr Gln Ser Leu Met Ala Phe Gly
          260          265          270
Arg Gly Glu Leu Trp Gly Gln Gly Leu Gly Asn Ser Val Gln Lys Leu
          275          280          285
Glu Tyr Leu Pro Glu Ala His Thr Asp Phe Ile Phe Ala Ile Ile Gly
          290          295          300
Glu Glu Leu Gly Tyr Val Gly Val Val Leu Ala Leu Leu Met Val Phe
305          310          315          320
Phe Val Ala Phe Arg Ala Met Ser Ile Gly Arg Lys Ala Leu Glu Ile
          325          330          335
Asp His Arg Phe Ser Gly Phe Leu Ala Cys Ser Ile Gly Ile Trp Phe
          340          345          350
Ser Phe Gln Ala Leu Val Asn Val Gly Ala Ala Ala Gly Met Leu Pro
          355          360          365
Thr Lys Gly Leu Thr Leu Pro Leu Ile Ser Tyr Gly Gly Ser Ser Leu
          370          375          380
Leu Ile Met Ser Thr Ala Ile Met Met Leu Leu Arg Ile Asp Tyr Glu
385          390          395          400
Thr Arg Leu Glu Lys Ala Gln Ala Phe Val Arg Gly Ser Arg
          405          410

```

<210> 454

<211> 355

<212> PRT

<213> Escherichia coli

<400> 454

```

Met Ser Gly Gln Gly Lys Arg Leu Met Val Met Ala Gly Gly Thr Gly
 1          5          10          15
Gly His Val Phe Pro Gly Leu Ala Val Ala His His Leu Met Ala Gln
          20          25          30
Gly Trp Gln Val Arg Trp Leu Gly Thr Ala Asp Arg Met Glu Ala Asp
          35          40          45
Leu Val Pro Lys His Gly Ile Glu Ile Asp Phe Ile Arg Ile Ser Gly
          50          55          60
Leu Arg Gly Lys Gly Ile Lys Ala Leu Ile Ala Ala Pro Leu Arg Ile
          65          70          75          80
Phe Asn Ala Trp Arg Gln Ala Arg Ala Ile Met Lys Ala Tyr Lys Pro
          85          90          95
Asp Val Val Leu Gly Met Gly Gly Tyr Val Ser Gly Pro Gly Gly Leu
          100          105          110
Ala Ala Trp Ser Leu Gly Ile Pro Val Val Leu His Glu Gln Asn Gly
          115          120          125
Ile Ala Gly Leu Thr Asn Lys Trp Leu Ala Lys Ile Ala Thr Lys Val
          130          135          140
Met Gln Ala Phe Pro Gly Ala Phe Pro Asn Ala Glu Val Val Gly Asn
          145          150          155          160
Pro Val Arg Thr Asp Val Leu Ala Leu Pro Leu Pro Gln Gln Arg Leu
          165          170          175
Ala Gly Arg Glu Gly Pro Val Arg Val Leu Val Val Gly Gly Ser Gln
          180          185          190
Gly Ala Arg Ile Leu Asn Gln Thr Met Pro Gln Val Ala Ala Lys Leu
          195          200          205
Gly Asp Ser Val Thr Ile Trp His Gln Ser Gly Lys Gly Ser Gln Gln
          210          215          220
Ser Val Glu Gln Ala Tyr Ala Glu Ala Gly Gln Pro Gln His Lys Val
          225          230          235          240
Thr Glu Phe Ile Asp Asp Met Ala Ala Ala Tyr Ala Trp Ala Asp Val
          245          250          255
Val Val Cys Arg Ser Gly Ala Leu Thr Val Ser Glu Ile Ala Ala Ala
          260          265          270
Gly Leu Pro Ala Leu Phe Val Pro Phe Gln His Lys Asp Arg Gln Gln
          275          280          285
Tyr Trp Asn Ala Leu Pro Leu Glu Lys Ala Gly Ala Ala Lys Ile Ile
          290          295          300
Glu Gln Pro Gln Leu Ser Val Asp Ala Val Ala Asn Thr Leu Ala Gly
          305          310          315          320
Trp Ser Arg Glu Thr Leu Leu Thr Met Ala Glu Arg Ala Arg Ala Ala
          325          330          335
Ser Ile Pro Asp Ala Thr Glu Arg Val Ala Asn Glu Val Ser Arg Val
          340          345          350
Ala Arg Ala
          355

```

<210> 455

<211> 491

<212> PRT

<213> Escherichia coli

<400> 455

```

Met Asn Thr Gln Gln Leu Ala Lys Leu Arg Ser Ile Val Pro Glu Met
 1          5          10          15
Arg Arg Val Arg His Ile His Phe Val Gly Ile Gly Gly Ala Gly Met
          20          25          30
Gly Gly Ile Ala Glu Val Leu Ala Asn Glu Gly Tyr Gln Ile Ser Gly

```

35	40	45
Ser Asp Leu Ala Pro Asn Pro Val Thr Gln Gln Leu Met Asn Leu Gly		
50	55	60
Ala Thr Ile Tyr Phe Asn His Arg Pro Glu Asn Val Arg Asp Ala Ser		
65	70	75
Val Val Val Val Ser Ser Ala Ile Ser Ala Asp Asn Pro Glu Ile Val		
	85	90
Ala Ala His Glu Ala Arg Ile Pro Val Ile Arg Arg Ala Glu Met Leu		
	100	105
Ala Glu Leu Met Arg Phe Arg His Gly Ile Ala Ile Ala Gly Thr His		
	115	120
Gly Lys Thr Thr Thr Thr Ala Met Val Ser Ser Ile Tyr Ala Glu Ala		
130	135	140
Gly Leu Asp Pro Thr Phe Val Asn Gly Gly Leu Val Lys Ala Ala Gly		
145	150	155
Val His Ala Arg Leu Gly His Gly Arg Tyr Leu Ile Ala Glu Ala Asp		
	165	170
Glu Ser Asp Ala Ser Phe Leu His Leu Gln Pro Met Val Ala Ile Val		
	180	185
Thr Asn Ile Glu Ala Asp His Met Asp Thr Tyr Gln Gly Asp Phe Glu		
	195	200
Asn Leu Lys Gln Thr Phe Ile Asn Phe Leu His Asn Leu Pro Phe Tyr		
210	215	220
Gly Arg Ala Val Met Cys Val Asp Asp Pro Val Ile Arg Glu Leu Leu		
225	230	235
Pro Arg Val Gly Arg Gln Thr Thr Thr Tyr Gly Phe Ser Glu Asp Ala		
	245	250
Asp Val Arg Val Glu Asp Tyr Gln Gln Ile Gly Pro Gln Gly His Phe		
	260	265
Thr Leu Leu Arg Gln Asp Lys Glu Pro Met Arg Val Thr Leu Asn Ala		
	275	280
Pro Gly Arg His Asn Ala Leu Asn Ala Ala Ala Val Ala Val Ala		
290	295	300
Thr Glu Glu Gly Ile Asp Asp Glu Ala Ile Leu Arg Ala Leu Glu Ser		
305	310	315
Phe Gln Gly Thr Gly Arg Arg Phe Asp Phe Leu Gly Glu Phe Pro Leu		
	325	330
Glu Pro Val Asn Gly Lys Ser Gly Thr Ala Met Leu Val Asp Asp Tyr		
	340	345
Gly His His Pro Thr Glu Val Asp Ala Thr Ile Lys Ala Ala Arg Ala		
	355	360
Gly Trp Pro Asp Lys Asn Leu Val Met Leu Phe Gln Pro His Arg Phe		
370	375	380
Thr Arg Thr Arg Asp Leu Tyr Asp Asp Phe Ala Asn Val Leu Thr Gln		
385	390	395
Val Asp Thr Leu Leu Met Leu Glu Val Tyr Pro Ala Gly Glu Ala Pro		
	405	410
Ile Pro Gly Ala Asp Ser Arg Ser Leu Cys Arg Thr Ile Arg Gly Arg		
	420	425
Gly Lys Ile Asp Pro Ile Leu Val Pro Asp Pro Ala Arg Val Ala Glu		
	435	440
Met Leu Ala Pro Val Leu Thr Gly Asn Asp Leu Ile Leu Val Gln Gly		
450	455	460
Ala Gly Asn Ile Gly Lys Ile Ala Arg Ser Leu Ala Glu Ile Lys Leu		
465	470	475
Lys Pro Gln Thr Pro Glu Glu Glu Gln His Asp		
	485	490

<210> 456

<211> 306

<212> PRT

<213> Escherichia coli

<400> 456

```

Met Thr Asp Lys Ile Ala Val Leu Leu Gly Gly Thr Ser Ala Glu Arg
 1           5           10           15
Glu Val Ser Leu Asn Ser Gly Ala Ala Val Leu Ala Gly Leu Arg Glu
      20           25           30
Gly Gly Ile Asp Ala Tyr Pro Val Asp Pro Lys Glu Val Asp Val Thr
      35           40           45
Gln Leu Lys Ser Met Gly Phe Gln Lys Val Phe Ile Ala Leu His Gly
      50           55           60
Arg Gly Gly Glu Asp Gly Thr Leu Gln Gly Met Leu Glu Leu Met Gly
65           70           75           80
Leu Pro Tyr Thr Gly Ser Gly Val Met Ala Ser Ala Leu Ser Met Asp
      85           90           95
Lys Leu Arg Ser Lys Leu Leu Trp Gln Gly Ala Gly Leu Pro Val Ala
      100          105          110
Pro Trp Val Ala Leu Thr Arg Ala Glu Phe Glu Lys Gly Leu Ser Asp
      115          120          125
Lys Gln Leu Ala Glu Ile Ser Ala Leu Gly Leu Pro Val Ile Val Lys
      130          135          140
Pro Ser Arg Glu Gly Ser Ser Val Gly Met Ser Lys Val Val Ala Glu
145          150          155          160
Asn Ala Leu Gln Asp Ala Leu Arg Leu Ala Phe Gln His Asp Glu Glu
      165          170          175
Val Leu Ile Glu Lys Trp Leu Ser Gly Pro Glu Phe Thr Val Ala Ile
      180          185          190
Leu Gly Glu Glu Ile Leu Pro Ser Ile Arg Ile Gln Pro Ser Gly Thr
      195          200          205
Phe Tyr Asp Tyr Glu Ala Lys Tyr Leu Ser Asp Glu Thr Gln Tyr Phe
210          215          220
Cys Pro Ala Gly Leu Glu Ala Ser Gln Glu Ala Asn Leu Gln Ala Leu
225          230          235          240
Val Leu Lys Ala Trp Thr Thr Leu Gly Cys Lys Gly Trp Gly Arg Ile
      245          250          255
Asp Val Met Leu Asp Ser Asp Gly Gln Phe Tyr Leu Leu Glu Ala Asn
      260          265          270
Thr Ser Pro Gly Met Thr Ser His Ser Leu Val Pro Met Ala Ala Arg
      275          280          285
Gln Ala Gly Met Ser Phe Ser Gln Leu Val Val Arg Ile Leu Glu Leu
290          295          300
Ala Asp
305

```

<210> 457

<211> 201

<212> PRT

<213> Escherichia coli

<400> 457

```

Met Ala Leu His Asp Glu Asn Val Val Trp His Ser His Pro Val Thr
 1           5           10           15
Val Gln Gln Arg Glu Leu His His Gly His Arg Gly Val Val Leu Trp
      20           25           30
Phe Thr Gly Leu Ser Gly Ser Gly Lys Ser Thr Val Ala Gly Ala Leu
      35           40           45
Glu Glu Ala Leu His Lys Leu Gly Val Ser Thr Tyr Leu Leu Asp Gly
      50           55           60
Asp Asn Val Arg His Gly Leu Cys Ser Asp Leu Gly Phe Ser Asp Ala

```

```

65          70          75          80
Asp Arg Lys Glu Asn Ile Arg Arg Val Gly Glu Val Ala Asn Leu Met
          85          90          95
Val Glu Ala Gly Leu Val Val Leu Thr Ala Phe Ile Ser Pro His Arg
          100          105          110
Ala Glu Arg Gln Met Val Arg Glu Arg Val Gly Glu Gly Arg Phe Ile
          115          120          125
Glu Val Phe Val Asp Thr Pro Leu Ala Ile Cys Glu Ala Arg Asp Pro
          130          135          140
Lys Gly Leu Tyr Lys Lys Ala Arg Ala Gly Glu Leu Arg Asn Phe Thr
145          150          155          160
Gly Ile Asp Ser Val Tyr Glu Ala Pro Glu Ser Ala Glu Ile His Leu
          165          170          175
Asn Gly Glu Gln Leu Val Thr Asn Leu Val Gln Gln Leu Leu Asp Leu
          180          185          190
Leu Arg Gln Asn Asp Ile Ile Arg Ser
          195          200

```

<210> 458

<211> 475

<212> PRT

<213> Escherichia coli

<400> 458

```

Met Asn Thr Ala Leu Ala Gln Gln Ile Ala Asn Glu Gly Gly Val Glu
1          5          10          15
Ala Trp Met Ile Ala Gln Gln His Lys Ser Leu Leu Arg Phe Leu Thr
          20          25          30
Cys Gly Ser Val Asp Asp Gly Lys Ser Thr Leu Ile Gly Arg Leu Leu
          35          40          45
His Asp Thr Arg Gln Ile Tyr Glu Asp Gln Leu Ser Ser Leu His Asn
          50          55          60
Asp Ser Lys Arg His Gly Thr Gln Gly Glu Lys Leu Asp Leu Ala Leu
          65          70          75          80
Leu Val Asp Gly Leu Gln Ala Glu Arg Glu Gln Gly Ile Thr Ile Asp
          85          90          95
Val Ala Tyr Arg Tyr Phe Ser Thr Glu Lys Arg Lys Phe Ile Ile Ala
          100          105          110
Asp Thr Pro Gly His Glu Gln Tyr Thr Arg Asn Met Ala Thr Gly Ala
          115          120          125
Ser Thr Cys Glu Leu Ala Ile Leu Leu Ile Asp Ala Arg Lys Gly Val
          130          135          140
Leu Asp Gln Thr Arg Arg His Ser Phe Ile Ser Thr Leu Leu Gly Ile
          145          150          155          160
Lys His Leu Val Val Ala Ile Asn Lys Met Asp Leu Val Asp Tyr Ser
          165          170          175
Glu Glu Thr Phe Thr Arg Ile Arg Glu Asp Tyr Leu Thr Phe Ala Gly
          180          185          190
Gln Leu Pro Gly Asn Leu Asp Ile Arg Phe Val Pro Leu Ser Ala Leu
          195          200          205
Glu Gly Asp Asn Val Ala Ser Gln Ser Glu Ser Met Pro Trp Tyr Ser
          210          215          220
Gly Pro Thr Leu Leu Glu Val Leu Glu Thr Val Glu Ile Gln Arg Val
          225          230          235          240
Val Asp Ala Gln Pro Met Arg Phe Pro Val Gln Tyr Val Asn Arg Pro
          245          250          255
Asn Leu Asp Phe Arg Gly Tyr Ala Gly Thr Leu Ala Ser Gly Arg Val
          260          265          270
Glu Val Gly Gln Arg Val Lys Val Leu Pro Ser Gly Val Glu Ser Asn
          275          280          285

```

Val Ala Arg Ile Val Thr Phe Asp Gly Asp Arg Glu Glu Ala Phe Ala
 290 295 300
 Gly Glu Ala Ile Thr Leu Val Leu Thr Asp Glu Ile Asp Ile Ser Arg
 305 310 315 320
 Gly Asp Leu Leu Leu Ala Ala Asp Glu Ala Leu Pro Ala Val Gln Ser
 325 330 335
 Ala Ser Val Asp Val Val Trp Met Ala Glu Gln Pro Leu Ser Pro Gly
 340 345 350
 Gln Ser Tyr Asp Ile Lys Ile Ala Gly Lys Lys Thr Arg Ala Arg Val
 355 360 365
 Asp Gly Ile Arg Tyr Gln Val Asp Ile Asn Asn Leu Thr Gln Arg Glu
 370 375 380
 Val Glu Asn Leu Pro Leu Asn Gly Ile Gly Leu Val Asp Leu Thr Phe
 385 390 395 400
 Asp Glu Pro Leu Val Leu Asp Arg Tyr Gln Gln Asn Pro Val Thr Gly
 405 410 415
 Gly Leu Ile Phe Ile Asp Arg Leu Ser Asn Val Thr Val Gly Ala Gly
 420 425 430
 Met Val His Glu Pro Val Ser Gln Ala Thr Ala Ala Pro Ser Glu Phe
 435 440 445
 Ser Ala Phe Glu Leu Glu Leu Asn Ala Leu Val Arg Arg His Phe Pro
 450 455 460
 His Trp Gly Ala Arg Asp Leu Leu Gly Asp Lys
 465 470 475

<210> 459

<211> 127

<212> PRT

<213> Escherichia coli

<400> 459

Met Arg His Arg Lys Ser Gly Arg Gln Leu Asn Arg Asn Ser Ser His
 1 5 10 15
 Arg Gln Ala Met Phe Arg Asn Met Ala Gly Ser Leu Val Arg His Glu
 20 25 30
 Ile Ile Lys Thr Thr Leu Pro Lys Ala Lys Glu Leu Arg Arg Val Val
 35 40 45
 Glu Pro Leu Ile Thr Leu Ala Lys Thr Asp Ser Val Ala Asn Arg Arg
 50 55 60
 Leu Ala Phe Ala Arg Thr Arg Asp Asn Glu Ile Val Ala Lys Leu Phe
 65 70 75 80
 Asn Glu Leu Gly Pro Arg Phe Ala Ser Arg Ala Gly Gly Tyr Thr Arg
 85 90 95
 Ile Leu Lys Cys Gly Phe Arg Ala Gly Asp Asn Ala Pro Met Ala Tyr
 100 105 110
 Ile Glu Leu Val Asp Arg Ser Glu Lys Ala Glu Ala Ala Glu
 115 120 125

<210> 460

<211> 329

<212> PRT

<213> Escherichia coli

<400> 460

Met Gln Gly Ser Val Thr Glu Phe Leu Lys Pro Arg Leu Val Asp Ile
 1 5 10 15
 Glu Gln Val Ser Ser Thr His Ala Lys Val Thr Leu Glu Pro Leu Glu
 20 25 30
 Arg Gly Phe Gly His Thr Leu Gly Asn Ala Leu Arg Arg Ile Leu Leu

35	40	45
Ser Ser Met Pro Gly Cys	Ala Val Thr Glu Val	Glu Ile Asp Gly Val
50	55	60
Leu His Glu Tyr Ser Thr	Lys Glu Gly Val Gln	Glu Asp Ile Leu Glu
65	70	75
Ile Leu Leu Asn Leu Lys	Gly Leu Ala Val Arg	Val Gln Gly Lys Asp
85	90	95
Glu Val Ile Leu Thr Leu	Asn Lys Ser Gly Ile	Gly Pro Val Thr Ala
100	105	110
Ala Asp Ile Thr His Asp	Gly Asp Val Glu Ile	Val Lys Pro Gln His
115	120	125
Val Ile Cys His Leu Thr	Asp Glu Asn Ala Ser	Ile Ser Met Arg Ile
130	135	140
Lys Val Gln Arg Gly Arg	Gly Tyr Val Pro Ala	Ser Thr Arg Ile His
145	150	155
Ser Glu Glu Asp Glu Arg	Pro Ile Gly Arg Leu	Leu Val Asp Ala Cys
165	170	175
Tyr Ser Pro Val Glu Arg	Ile Ala Tyr Asn Val	Glu Ala Ala Arg Val
180	185	190
Glu Gln Arg Thr Asp Leu	Asp Lys Leu Val Ile	Glu Met Glu Thr Asn
195	200	205
Gly Thr Ile Asp Pro Glu	Glu Ala Ile Arg Arg	Ala Ala Thr Ile Leu
210	215	220
Ala Glu Gln Leu Glu Ala	Phe Val Asp Leu Arg	Asp Val Arg Gln Pro
225	230	235
Glu Val Lys Glu Glu Lys	Pro Glu Phe Asp Pro	Ile Leu Leu Arg Pro
245	250	255
Val Asp Asp Leu Glu Leu	Thr Val Arg Ser Ala	Asn Cys Leu Lys Ala
260	265	270
Glu Ala Ile His Tyr Ile	Gly Asp Leu Val Gln	Arg Thr Glu Val Glu
275	280	285
Leu Leu Lys Thr Pro Asn	Leu Gly Lys Lys Ser	Leu Thr Glu Ile Lys
290	295	300
Asp Val Leu Ala Ser Arg	Gly Leu Ser Leu Gly	Met Arg Leu Glu Asn
305	310	315
Trp Pro Pro Ala Ser Ile	Ala Asp Glu	
325		

<210> 461

<211> 206

<212> PRT

<213> Escherichia coli

<400> 461

Met Ala Arg Tyr Leu Gly	Pro Lys Leu Lys Leu Ser	Arg Arg Glu Gly
1	5	10
Thr Asp Leu Phe Leu Lys	Ser Gly Val Arg Ala Ile	Asp Thr Lys Cys
20	25	30
Lys Ile Glu Gln Ala Pro	Gly Gln His Gly Ala Arg	Lys Pro Arg Leu
35	40	45
Ser Asp Tyr Gly Val Gln	Leu Arg Glu Lys Gln Lys	Val Arg Arg Ile
50	55	60
Tyr Gly Val Leu Glu Arg	Gln Phe Arg Asn Tyr Tyr	Lys Glu Ala Ala
65	70	75
Arg Leu Lys Gly Asn Thr	Gly Glu Asn Leu Leu Ala	Leu Leu Glu Gly
85	90	95
Arg Leu Asp Asn Val Val	Tyr Arg Met Gly Phe Gly	Ala Thr Arg Ala
100	105	110
Glu Ala Arg Gln Leu Val	Ser His Lys Ala Ile Met	Val Asn Gly Arg
115	120	125

Val Val Asn Ile Ala Ser Tyr Gln Val Ser Pro Asn Asp Val Val Ser
 130 135 140
 Ile Arg Glu Lys Ala Lys Lys Gln Ser Arg Val Lys Ala Ala Leu Glu
 145 150 155 160
 Leu Ala Glu Gln Arg Glu Lys Pro Thr Trp Leu Glu Val Asp Ala Gly
 165 170 175
 Lys Met Glu Gly Thr Phe Lys Arg Lys Pro Glu Arg Ser Asp Leu Ser
 180 185 190
 Ala Asp Ile Asn Glu His Leu Ile Val Glu Leu Tyr Ser Lys
 195 200 205

<210> 462

<211> 129

<212> PRT

<213> Escherichia coli

<400> 462

Met Ala Lys Ala Pro Ile Arg Ala Arg Lys Arg Val Arg Lys Gln Val
 1 5 10 15
 Ser Asp Gly Val Ala His Ile His Ala Ser Phe Asn Asn Thr Ile Val
 20 25 30
 Thr Ile Thr Asp Arg Gln Gly Asn Ala Leu Gly Trp Ala Thr Ala Gly
 35 40 45
 Gly Ser Gly Phe Arg Gly Ser Arg Lys Ser Thr Pro Phe Ala Ala Gln
 50 55 60
 Val Ala Ala Glu Arg Cys Ala Asp Ala Val Lys Glu Tyr Gly Ile Lys
 65 70 75 80
 Asn Leu Glu Val Met Val Lys Gly Pro Gly Pro Gly Arg Glu Ser Thr
 85 90 95
 Ile Arg Ala Leu Asn Ala Ala Gly Phe Arg Ile Thr Asn Ile Thr Asp
 100 105 110
 Val Thr Pro Ile Pro His Asn Gly Cys Arg Pro Pro Lys Lys Arg Arg
 115 120 125
 Val

<210> 463

<211> 118

<212> PRT

<213> Escherichia coli

<400> 463

Met Ala Arg Ile Ala Gly Ile Asn Ile Pro Asp His Lys His Ala Val
 1 5 10 15
 Ile Ala Leu Thr Ser Ile Tyr Gly Val Gly Lys Thr Arg Ser Lys Ala
 20 25 30
 Ile Leu Ala Ala Ala Gly Ile Ala Glu Asp Val Lys Ile Ser Glu Leu
 35 40 45
 Ser Glu Gly Gln Ile Asp Thr Leu Arg Asp Glu Val Ala Lys Phe Val
 50 55 60
 Val Glu Gly Asp Leu Arg Arg Glu Ile Ser Met Ser Ile Lys Arg Leu
 65 70 75 80
 Met Asp Leu Gly Cys Tyr Arg Gly Leu Arg His Arg Arg Gly Leu Pro
 85 90 95
 Val Arg Gly Gln Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly Pro
 100 105 110
 Arg Lys Pro Ile Lys Lys
 115

<210> 464

<211> 460

<212> PRT

<213> Escherichia coli

<400> 464

```

Met Thr Gln Leu Thr Met Lys Asp Lys Ile Gly Tyr Gly Leu Gly Asp
 1      5      10      15
Thr Ala Cys Gly Phe Val Trp Gln Ala Thr Met Phe Leu Leu Ala Tyr
 20      25      30
Phe Tyr Thr Asp Val Phe Gly Leu Ser Ala Gly Ile Met Gly Thr Leu
 35      40      45
Phe Leu Val Ser Arg Val Leu Asp Ala Val Thr Asp Pro Leu Met Gly
 50      55      60
Leu Leu Val Asp Arg Thr Arg Thr Arg His Gly Gln Phe Arg Pro Phe
 65      70      75      80
Leu Leu Trp Gly Ala Ile Pro Phe Gly Ile Val Cys Val Leu Thr Phe
 85      90      95
Tyr Thr Pro Asp Phe Ser Ala Gln Gly Lys Ile Ile Tyr Ala Cys Val
100      105      110
Thr Tyr Ile Leu Leu Thr Leu Val Tyr Thr Phe Val Asn Val Pro Tyr
115      120      125
Cys Ala Met Pro Gly Val Ile Thr Ala Asp Pro Lys Glu Arg His Ala
130      135      140
Leu Gln Ser Trp Arg Phe Phe Leu Ala Ala Gly Ser Leu Ala Ile
145      150      155      160
Ser Gly Ile Ala Leu Pro Leu Val Ser Ile Ile Gly Lys Gly Asp Glu
165      170      175
Gln Val Gly Tyr Phe Gly Ala Met Cys Val Leu Gly Leu Ser Gly Val
180      185      190
Val Leu Leu Tyr Val Cys Phe Phe Thr Thr Lys Glu Arg Tyr Thr Phe
195      200      205
Glu Val Gln Pro Gly Ser Ser Val Ala Lys Asp Leu Lys Leu Leu Leu
210      215      220
Gly Asn Ser Gln Trp Arg Ile Met Cys Ala Phe Lys Met Met Ala Thr
225      230      235      240
Cys Ser Asn Val Val Arg Gly Gly Ala Thr Leu Tyr Phe Val Lys Tyr
245      250      255
Val Met Asp His Pro Glu Leu Ala Thr Gln Phe Leu Leu Tyr Gly Ser
260      265      270
Leu Ala Thr Met Phe Gly Ser Leu Cys Ser Ser Arg Leu Leu Gly Arg
275      280      285
Phe Asp Arg Val Thr Ala Phe Lys Trp Ile Ile Val Ala Tyr Ser Leu
290      295      300
Ile Ser Leu Leu Ile Phe Val Thr Pro Ala Glu His Ile Ala Leu Ile
305      310      315      320
Phe Ala Leu Asn Ile Leu Phe Leu Phe Val Phe Asn Thr Thr Thr Pro
325      330      335
Leu Gln Trp Leu Met Ala Ser Asp Val Val Asp Tyr Glu Glu Ser Arg
340      345      350
Ser Gly Arg Arg Leu Asp Gly Leu Val Phe Ser Thr Tyr Leu Phe Ser
355      360      365
Leu Lys Ile Gly Leu Ala Ile Gly Gly Ala Val Val Gly Trp Ile Leu
370      375      380
Ala Tyr Val Asn Tyr Ser Ala Ser Ser Ser Val Gln Pro Val Glu Val
385      390      395      400
Leu Thr Thr Ile Lys Ile Leu Phe Cys Val Val Pro Val Val Leu Tyr
405      410      415
Ala Gly Met Phe Ile Met Leu Ser Leu Tyr Lys Leu Thr Asp Ala Arg
420      425      430

```


Val Glu Ala Ile Ser Arg Gln Leu Ile Lys His Arg Ala Ala Gln Gly
 435 440 445
 Glu Ala Val Pro Asp Ala Ala Thr Ala Ala Ser His
 450 455 460

<210> 465
 <211> 536
 <212> PRT
 <213> Escherichia coli

<400> 465
 Met Glu Ile Thr Asn Pro Ile Leu Thr Gly Phe Asn Pro Asp Pro Ser
 1 5 10 15
 Leu Cys Arg Gln Gly Glu Asp Tyr Tyr Ile Ala Thr Ser Thr Phe Glu
 20 25 30
 Trp Phe Pro Gly Val Arg Ile Tyr His Ser Arg Asp Leu Lys Asn Trp
 35 40 45
 Ser Leu Val Ser Thr Pro Leu Asp Arg Val Ser Met Leu Asp Met Lys
 50 55 60
 Gly Asn Pro Asp Ser Gly Gly Ile Trp Ala Pro Cys Leu Ser Tyr Ala
 65 70 75 80
 Asp Gly Lys Phe Trp Leu Leu Tyr Thr Asp Val Lys Ile Val Asp Ser
 85 90 95
 Pro Trp Lys Asn Gly Arg Asn Phe Leu Val Thr Ala Pro Ser Ile Glu
 100 105 110
 Gly Pro Trp Ser Glu Pro Ile Pro Met Gly Asn Gly Gly Phe Asp Pro
 115 120 125
 Ser Leu Phe His Asp Asp Asp Gly Arg Lys Tyr Tyr Ile Tyr Arg Pro
 130 135 140
 Trp Gly Pro Arg His His Ser Asn Pro His Asn Thr Ile Val Leu Gln
 145 150 155 160
 Ala Phe Asp Pro Gln Thr Gly Thr Leu Ser Pro Glu Arg Lys Thr Leu
 165 170 175
 Phe Thr Gly Thr Pro Leu Cys Tyr Thr Glu Gly Ala His Leu Tyr Arg
 180 185 190
 His Ala Gly Trp Tyr Tyr Leu Met Ala Ala Glu Gly Gly Thr Ser Tyr
 195 200 205
 Glu His Ala Val Val Val Leu Arg Ser Lys Asn Ile Asp Gly Pro Tyr
 210 215 220
 Glu Leu His Pro Asp Val Thr Met Met Thr Ser Trp His Leu Pro Glu
 225 230 235 240
 Asn Pro Leu Gln Lys Ser Gly His Gly Ser Leu Leu Gln Thr His Thr
 245 250 255
 Gly Glu Trp Tyr Met Ala Tyr Leu Thr Ser Arg Pro Leu Arg Leu Pro
 260 265 270
 Gly Val Pro Leu Leu Ala Ser Gly Gly Arg Gly Tyr Cys Pro Leu Gly
 275 280 285
 Arg Glu Thr Gly Ile Ala Arg Ile Glu Trp Arg Asp Gly Trp Pro Tyr
 290 295 300
 Val Glu Gly Gly Lys His Ala Gln Leu Thr Val Lys Gly Pro Gln Val
 305 310 315 320
 Ala Glu Gln Pro Ala Ala Val Pro Gly Asn Trp Arg Asp Asp Phe Asp
 325 330 335
 Ala Ser Ser Leu Asp Pro Glu Leu Gln Thr Leu Arg Ile Pro Phe Asp
 340 345 350
 Asp Thr Leu Gly Ser Leu Thr Ala Arg Pro Gly Phe Leu Arg Leu Tyr
 355 360 365
 Gly Asn Asp Ser Leu Asn Ser Thr Phe Thr Gln Ser Thr Val Ala Arg
 370 375 380
 Arg Trp Gln His Phe Ala Phe Arg Ala Glu Thr Arg Met Glu Phe Ser

```

385          390          395          400
Pro Val His Phe Gln Gln Ser Ala Gly Leu Thr Cys Tyr Tyr Asn Ser
          405          410          415
Lys Asn Trp Ser Tyr Cys Phe Val Asp Tyr Glu Glu Gly Gln Gly Arg
          420          425          430
Thr Ile Lys Val Ile Gln Leu Asp His Asn Val Pro Ser Trp Pro Leu
          435          440          445
His Glu Gln Pro Ile Pro Val Pro Glu His Ala Glu Ser Val Trp Leu
          450          455          460
Arg Val Asp Val Asp Thr Leu Val Tyr Arg Tyr Ser Tyr Ser Phe Asp
465          470          475          480
Gly Glu Thr Trp His Thr Val Pro Val Thr Tyr Glu Ala Trp Lys Leu
          485          490          495
Ser Asp Asp Tyr Ile Gly Gly Arg Gly Phe Phe Thr Gly Ala Phe Val
          500          505          510
Gly Leu His Cys Glu Asp Ile Ser Gly Asp Gly Cys Tyr Ala Asp Phe
          515          520          525
Asp Tyr Phe Thr Tyr Glu Pro Val
          530          535

```

<210> 466

<211> 325

<212> PRT

<213> Escherichia coli

<400> 466

```

Met His Met Lys Lys Ile Ile Phe Ala Phe Ile Ile Leu Phe Val Phe
  1          5          10          15
Leu Leu Pro Met Ile Ile Phe Tyr Gln Pro Trp Val Asn Ala Leu Pro
          20          25          30
Ser Thr Pro Arg His Ala Ser Pro Glu Gln Leu Glu Lys Thr Val Arg
          35          40          45
Tyr Leu Thr Gln Thr Val His Pro Arg Ser Ala Asp Asn Ile Asp Asn
          50          55          60
Leu Asn Arg Ser Ala Glu Tyr Ile Lys Glu Val Phe Val Ser Ser Gly
65          70          75          80
Ala Arg Val Thr Ser Gln Asp Val Pro Ile Thr Gly Gly Pro Tyr Lys
          85          90          95
Asn Ile Val Ala Asp Tyr Gly Pro Ala Asp Gly Pro Leu Ile Ile Ile
          100          105          110
Gly Ala His Tyr Asp Ser Ala Ser Tyr Glu Asn Asp Gln Leu Thr
          115          120          125
Tyr Thr Pro Gly Ala Asp Asp Asn Ala Ser Gly Val Ala Gly Leu Leu
          130          135          140
Glu Leu Ala Arg Leu Leu His Gln Gln Val Pro Lys Thr Gly Val Gln
145          150          155          160
Leu Val Ala Tyr Ala Ser Glu Glu Pro Pro Phe Phe Arg Ser Asp Glu
          165          170          175
Met Gly Ser Ala Val His Ala Ala Ser Leu Glu Arg Pro Val Lys Leu
          180          185          190
Met Ile Ala Leu Glu Met Ile Gly Tyr Tyr Asp Ser Ala Pro Gly Ser
          195          200          205
Gln Asn Tyr Pro Tyr Pro Ala Met Ser Trp Leu Tyr Pro Asp Arg Gly
          210          215          220
Asp Phe Ile Ala Val Val Gly Arg Ile Gln Asp Ile Asn Ala Val Arg
225          230          235          240
Gln Val Lys Ala Ala Leu Leu Ser Ser Gln Asp Leu Ser Val Tyr Ser
          245          250          255
Met Asn Thr Pro Gly Phe Ile Pro Gly Ile Asp Phe Ser Asp His Leu
          260          265          270

```

Asn Tyr Trp Gln His Asp Ile Pro Ala Ile Met Ile Thr Asp Thr Ala
 275 280 285
 Phe Tyr Arg Asn Lys Gln Tyr His Leu Pro Gly Asp Thr Ala Asp Arg
 290 295 300
 Leu Asn Tyr Gln Lys Met Ala Gln Val Val Asp Gly Val Ile Thr Leu
 305 310 315 320
 Leu Tyr Asn Ser Lys
 325

<210> 467
 <211> 320
 <212> PRT
 <213> Escherichia coli

<400> 467
 Met Met Ile Lys Thr Arg Phe Ser Arg Trp Leu Thr Phe Phe Thr Phe
 1 5 10 15
 Ala Ala Ala Val Ala Leu Ala Leu Pro Ala Lys Ala Asn Thr Trp Pro
 20 25 30
 Leu Pro Pro Ala Gly Ser Arg Leu Val Gly Glu Asn Lys Phe His Val
 35 40 45
 Val Glu Asn Asp Gly Gly Ser Leu Glu Ala Ile Ala Lys Lys Tyr Asn
 50 55 60
 Val Gly Phe Leu Ala Leu Leu Gln Ala Asn Pro Gly Val Asp Pro Tyr
 65 70 75 80
 Val Pro Arg Ala Gly Ser Val Leu Thr Ile Pro Leu Gln Thr Leu Leu
 85 90 95
 Pro Asp Ala Pro Arg Glu Gly Ile Val Ile Asn Ile Ala Glu Leu Arg
 100 105 110
 Leu Tyr Tyr Tyr Pro Pro Gly Lys Asn Ser Val Thr Val Tyr Pro Ile
 115 120 125
 Gly Ile Gly Gln Leu Gly Gly Asp Thr Leu Thr Pro Thr Met Val Thr
 130 135 140
 Thr Val Ser Asp Lys Arg Ala Asn Pro Thr Trp Thr Pro Thr Ala Asn
 145 150 155 160
 Ile Arg Ala Arg Tyr Lys Ala Gln Gly Ile Glu Leu Pro Ala Val Val
 165 170 175
 Pro Ala Gly Leu Asp Asn Pro Met Gly His His Ala Ile Arg Leu Ala
 180 185 190
 Ala Tyr Gly Gly Val Tyr Leu Leu His Gly Thr Asn Ala Asp Phe Gly
 195 200 205
 Ile Gly Met Arg Val Ser Ser Gly Cys Ile Arg Leu Arg Asp Asp Asp
 210 215 220
 Ile Lys Thr Leu Phe Ser Gln Val Thr Pro Gly Thr Lys Val Asn Ile
 225 230 235 240
 Ile Asn Thr Pro Ile Lys Val Ser Ala Glu Pro Asn Gly Ala Arg Leu
 245 250 255
 Val Glu Val His Gln Pro Leu Ser Glu Lys Ile Asp Asp Asp Pro Gln
 260 265 270
 Leu Leu Pro Ile Thr Leu Asn Ser Ala Met Gln Ser Phe Lys Asp Ala
 275 280 285
 Ala Gln Thr Asp Ala Glu Val Met Gln His Val Met Asp Val Arg Ser
 290 295 300
 Gly Met Pro Val Asp Val Arg Arg His Gln Val Ser Pro Gln Thr Leu
 305 310 315 320

<210> 468
 <211> 494
 <212> PRT

<213> Escherichia coli

<400> 468

```

Met Val Ala Ile His Leu Leu Pro Val Ser Tyr Asn Ser Ala Thr Ser
 1      5      10      15
Thr Val Asn Ile Ser Ala Arg Ile Ile Pro Leu Leu Ile Ile His Gln
 20      25      30
Arg Tyr Lys Ile Pro Met Pro Lys Val Gln Ala Asp Gly Leu Pro Leu
 35      40      45
Pro Gln Arg Tyr Gly Ala Ile Leu Thr Ile Val Ile Gly Ile Ser Met
 50      55      60
Ala Val Leu Asp Gly Ala Ile Ala Asn Val Ala Leu Pro Thr Ile Ala
 65      70      75      80
Thr Asp Leu His Ala Thr Pro Ala Ser Ser Ile Trp Val Val Asn Ala
 85      90      95
Tyr Gln Ile Ala Ile Val Ile Ser Leu Leu Ser Phe Ser Phe Leu Gly
 100     105     110
Asp Met Phe Gly Tyr Arg Arg Ile Tyr Lys Cys Gly Leu Val Val Phe
 115     120     125
Leu Leu Ser Ser Leu Phe Cys Ala Leu Ser Asp Ser Leu Gln Met Leu
 130     135     140
Thr Leu Ala Arg Val Ile Gln Gly Phe Gly Gly Ala Ala Leu Met Ser
 145     150     155     160
Val Asn Thr Ala Leu Ile Arg Leu Ile Tyr Pro Gln Arg Phe Leu Gly
 165     170     175
Arg Gly Met Gly Ile Asn Ser Phe Ile Val Ala Val Ser Ser Ala Ala
 180     185     190
Gly Pro Thr Ile Ala Ala Ala Ile Leu Ser Ile Ala Ser Trp Lys Trp
 195     200     205
Leu Phe Leu Ile Asn Val Pro Leu Gly Ile Ile Ala Leu Leu Leu Ala
 210     215     220
Met Arg Phe Leu Pro Pro Asn Gly Ser Arg Ala Ser Lys Pro Arg Phe
 225     230     235     240
Asp Leu Pro Ser Ala Val Met Asn Ala Leu Thr Phe Gly Leu Leu Ile
 245     250     255
Thr Ala Leu Ser Gly Phe Ala Gln Gly Gln Ser Leu Thr Leu Ile Ala
 260     265     270
Ala Glu Leu Val Val Met Val Val Val Gly Ile Phe Phe Ile Arg Arg
 275     280     285
Gln Leu Ser Leu Pro Val Pro Leu Leu Pro Val Asp Leu Leu Arg Ile
 290     295     300
Pro Leu Phe Ser Leu Ser Ile Cys Thr Ser Val Cys Ser Phe Cys Ala
 305     310     315     320
Gln Met Leu Ala Met Val Ser Leu Pro Phe Tyr Leu Gln Thr Val Leu
 325     330     335
Gly Arg Ser Glu Val Glu Thr Gly Leu Leu Leu Thr Pro Trp Pro Leu
 340     345     350
Ala Thr Met Val Met Ala Pro Leu Ala Gly Tyr Leu Ile Glu Arg Val
 355     360     365
His Ala Gly Leu Leu Gly Ala Leu Gly Leu Phe Ile Met Ala Ala Gly
 370     375     380
Leu Phe Ser Leu Val Leu Leu Pro Ala Ser Pro Ala Asp Ile Asn Ile
 385     390     395     400
Ile Trp Pro Met Ile Leu Cys Gly Ala Gly Phe Gly Leu Phe Gln Ser
 405     410     415
Pro Asn Asn His Thr Ile Ile Thr Ser Ala Pro Arg Glu Arg Ser Gly
 420     425     430
Gly Ala Ser Gly Met Leu Gly Thr Ala Arg Leu Leu Gly Gln Ser Ser
 435     440     445
Gly Ala Ala Leu Val Ala Leu Met Leu Asn Gln Phe Gly Asp Asn Gly
 450     455     460

```

Thr His Val Ser Leu Met Ala Ala Ala Ile Leu Ala Val Ile Ala Ala
 465 470 475 480
 Cys Val Ser Gly Leu Arg Ile Thr Gln Pro Arg Ser Arg Ala
 485 490

<210> 469

<211> 477

<212> PRT

<213> Escherichia coli

<400> 469

Met Lys Val Thr Leu Pro Glu Phe Glu Arg Ala Gly Val Met Val Val
 1 5 10 15
 Gly Asp Val Met Leu Asp Arg Tyr Trp Tyr Gly Pro Thr Ser Arg Ile
 20 25 30
 Ser Pro Glu Ala Pro Val Pro Val Val Lys Val Asn Thr Ile Glu Glu
 35 40 45
 Arg Pro Gly Gly Ala Ala Asn Val Ala Met Asn Ile Ala Ser Leu Gly
 50 55 60
 Ala Asn Ala Arg Leu Val Gly Leu Thr Gly Ile Asp Asp Ala Ala Arg
 65 70 75 80
 Ala Leu Ser Lys Ser Leu Ala Asp Val Asn Val Lys Cys Asp Phe Val
 85 90 95
 Ser Val Pro Thr His Pro Thr Ile Thr Lys Leu Arg Val Leu Ser Arg
 100 105 110
 Asn Gln Gln Leu Ile Arg Leu Asp Phe Glu Glu Gly Phe Glu Gly Val
 115 120 125
 Asp Pro Gln Pro Leu His Glu Arg Ile Asn Gln Ala Leu Ser Ser Ile
 130 135 140
 Gly Ala Leu Val Leu Ser Asp Tyr Ala Lys Gly Ala Leu Ala Ser Val
 145 150 155 160
 Gln Gln Met Ile Gln Leu Ala Arg Lys Ala Gly Val Pro Val Leu Ile
 165 170 175
 Asp Pro Lys Gly Thr Asp Phe Glu Arg Tyr Arg Gly Ala Thr Leu Leu
 180 185 190
 Thr Pro Asn Leu Ser Glu Phe Glu Ala Val Val Gly Lys Cys Lys Thr
 195 200 205
 Glu Glu Glu Ile Val Glu Arg Gly Met Lys Leu Ile Ala Asp Tyr Glu
 210 215 220
 Leu Ser Ala Leu Leu Val Thr Arg Ser Glu Gln Gly Met Ser Leu Leu
 225 230 235 240
 Gln Pro Gly Lys Ala Pro Leu His Met Pro Thr Gln Ala Gln Glu Val
 245 250 255
 Tyr Asp Val Thr Gly Ala Gly Asp Thr Val Ile Gly Val Leu Ala Ala
 260 265 270
 Thr Leu Ala Ala Gly Asn Ser Leu Glu Glu Ala Cys Phe Phe Ala Asn
 275 280 285
 Ala Ala Ala Gly Val Val Val Gly Lys Leu Gly Thr Ser Thr Val Ser
 290 295 300
 Pro Ile Glu Leu Glu Asn Ala Val Arg Gly Arg Ala Asp Thr Gly Phe
 305 310 315 320
 Gly Val Met Thr Glu Glu Glu Leu Lys Leu Ala Val Ala Ala Ala Arg
 325 330 335
 Lys Arg Gly Glu Lys Val Val Met Thr Asn Gly Val Phe Asp Ile Leu
 340 345 350
 His Ala Gly His Val Ser Tyr Leu Ala Asn Ala Arg Lys Leu Gly Asp
 355 360 365
 Arg Leu Ile Val Ala Val Asn Ser Asp Ala Ser Thr Lys Arg Leu Lys
 370 375 380
 Gly Asp Ser Arg Pro Val Asn Pro Leu Glu Gln Arg Met Ile Val Leu

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385          390          395          400
Gly Ala Leu Glu Ala Val Asp Trp Val Val Ser Phe Glu Glu Asp Thr
          405          410          415
Pro Gln Arg Leu Ile Ala Gly Ile Leu Pro Asp Leu Leu Val Lys Gly
          420          425          430
Gly Asp Tyr Lys Pro Glu Glu Ile Ala Gly Ser Lys Glu Val Trp Ala
          435          440          445
Asn Gly Gly Glu Val Leu Val Leu Asn Phe Glu Asp Gly Cys Ser Thr
          450          455          460
Thr Asn Ile Ile Lys Lys Ile Gln Gln Asp Lys Lys Gly
465          470          475

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<210> 470

<211> 946

<212> PRT

<213> Escherichia coli

<400> 470

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Met Lys Pro Leu Ser Ser Pro Leu Gln Gln Tyr Trp Gln Thr Val Val
  1          5          10          15
Glu Arg Leu Pro Glu Pro Leu Ala Glu Glu Ser Leu Ser Ala Gln Ala
          20          25          30
Lys Ser Val Leu Thr Phe Ser Asp Phe Val Gln Asp Ser Val Ile Ala
          35          40          45
His Pro Glu Trp Leu Thr Glu Leu Glu Ser Gln Pro Pro Gln Ala Asp
          50          55          60
Glu Trp Gln His Tyr Ala Ala Trp Leu Gln Glu Ala Leu Cys Asn Val
          65          70          75          80
Ser Asp Glu Ala Gly Leu Met Arg Glu Leu Arg Leu Phe Arg Arg Arg
          85          90          95
Ile Met Val Arg Ile Ala Trp Ala Gln Thr Leu Ala Leu Val Thr Glu
          100          105          110
Glu Ser Ile Leu Gln Gln Leu Ser Tyr Leu Ala Glu Thr Leu Ile Val
          115          120          125
Ala Ala Arg Asp Trp Leu Tyr Asp Ala Cys Cys Arg Glu Trp Gly Thr
          130          135          140
Pro Cys Asn Ala Gln Gly Glu Ala Gln Pro Leu Leu Ile Leu Gly Met
          145          150          155          160
Gly Lys Leu Gly Gly Gly Glu Leu Asn Phe Ser Ser Asp Ile Asp Leu
          165          170          175
Ile Phe Ala Trp Pro Glu His Gly Cys Thr Gln Gly Gly Arg Arg Glu
          180          185          190
Leu Asp Asn Ala Gln Phe Phe Thr Arg Met Gly Gln Arg Leu Ile Lys
          195          200          205
Val Leu Asp Gln Pro Thr Gln Asp Gly Phe Val Tyr Arg Val Asp Met
          210          215          220
Arg Leu Arg Pro Phe Gly Glu Ser Gly Pro Leu Val Leu Ser Phe Ala
          225          230          235          240
Ala Leu Glu Asp Tyr Tyr Gln Glu Gln Gly Arg Asp Trp Glu Arg Tyr
          245          250          255
Ala Met Val Lys Ala Arg Ile Met Gly Asp Ser Glu Gly Val Tyr Ala
          260          265          270
Asn Glu Leu Arg Ala Met Leu Arg Pro Phe Val Phe Arg Arg Tyr Ile
          275          280          285
Asp Phe Ser Val Ile Gln Ser Leu Arg Asn Met Lys Gly Met Ile Ala
          290          295          300
Arg Glu Val Arg Arg Arg Gly Leu Thr Asp Asn Ile Lys Leu Gly Ala
          305          310          315          320
Gly Gly Ile Arg Glu Ile Glu Phe Ile Val Gln Val Phe Gln Leu Ile
          325          330          335

```

Arg Gly Gly Arg Glu Pro Ser Leu Gln Ser Arg Ser Leu Leu Pro Thr
 340 345 350
 Leu Ser Ala Ile Ala Glu Leu His Leu Leu Ser Glu Asn Asp Ala Glu
 355 360 365
 Gln Leu Arg Val Ala Tyr Leu Phe Leu Arg Arg Leu Glu Asn Leu Leu
 370 375 380
 Gln Ser Ile Asn Asp Glu Gln Thr Gln Thr Leu Pro Ser Asp Glu Leu
 385 390 395 400
 Asn Arg Ala Arg Leu Ala Trp Ala Met Asp Phe Ala Asp Trp Pro Gln
 405 410 415
 Leu Thr Gly Ala Leu Thr Ala His Met Thr Asn Val Arg Arg Val Phe
 420 425 430
 Asn Glu Leu Ile Gly Asp Asp Glu Ser Glu Thr Gln Glu Glu Ser Leu
 435 440 445
 Ser Glu Gln Trp Arg Glu Leu Trp Gln Asp Ala Leu Gln Glu Asp Asp
 450 455 460
 Thr Thr Pro Val Leu Ala His Leu Ser Glu Asp Arg Lys Gln Val
 465 470 475 480
 Leu Thr Leu Ile Ala Asp Phe Arg Lys Glu Leu Asp Lys Arg Thr Ile
 485 490 495
 Gly Pro Arg Gly Arg Gln Val Leu Asp His Leu Met Pro His Leu Leu
 500 505 510
 Ser Asp Val Cys Ala Arg Glu Asp Ala Ala Val Thr Leu Ser Arg Ile
 515 520 525
 Thr Ala Leu Leu Val Gly Ile Val Thr Arg Thr Thr Tyr Leu Glu Leu
 530 535 540
 Leu Ser Glu Phe Pro Ala Ala Leu Lys His Leu Ile Ser Leu Cys Ala
 545 550 555 560
 Ala Ser Pro Met Ile Ala Ser Gln Leu Ala Arg Tyr Pro Leu Leu Leu
 565 570 575
 Asp Glu Leu Leu Asp Pro Asn Thr Leu Tyr Gln Pro Thr Ala Thr Asp
 580 585 590
 Ala Tyr Arg Asp Glu Leu Arg Gln Tyr Leu Leu Arg Val Pro Glu Asp
 595 600 605
 Asp Glu Glu Gln Gln Leu Glu Ala Leu Arg Gln Phe Lys Gln Ala Gln
 610 615 620
 Leu Leu Arg Ile Ala Ala Ala Asp Ile Ala Gly Thr Leu Pro Val Met
 625 630 635 640
 Lys Val Ser Asp His Leu Thr Trp Leu Ala Glu Ala Met Ile Asp Ala
 645 650 655
 Val Val Gln Gln Ala Trp Val Gln Met Val Ala Arg Tyr Gly Lys Pro
 660 665 670
 Asn His Leu Asn Glu Arg Glu Gly Arg Gly Phe Ala Val Val Gly Tyr
 675 680 685
 Gly Lys Leu Gly Gly Trp Glu Leu Gly Tyr Ser Ser Asp Leu Asp Leu
 690 695 700
 Ile Phe Leu His Asp Cys Pro Met Asp Ala Met Thr Asp Gly Glu Arg
 705 710 715 720
 Glu Ile Asp Gly Arg Gln Phe Tyr Leu Arg Leu Ala Gln Arg Ile Met
 725 730 735
 His Leu Phe Ser Thr Arg Thr Ser Ser Gly Ile Leu Tyr Glu Val Asp
 740 745 750
 Ala Arg Leu Arg Pro Ser Gly Ala Ala Gly Met Leu Val Thr Ser Ala
 755 760 765
 Glu Ala Phe Ala Asp Tyr Gln Lys Asn Glu Ala Trp Thr Trp Glu His
 770 775 780
 Gln Ala Leu Val Arg Ala Arg Val Val Tyr Gly Asp Pro Gln Leu Thr
 785 790 795 800
 Ala His Phe Asp Ala Val Arg Arg Glu Ile Met Thr Leu Pro Arg Glu
 805 810 815
 Gly Lys Thr Leu Gln Thr Glu Val Arg Glu Met Arg Glu Lys Met Arg

820						825						830					
Ala	His	Leu	Gly	Asn	Lys	His	Arg	Asp	Arg	Phe	Asp	Ile	Lys	Ala	Asp		
835						840						845					
Glu	Gly	Gly	Ile	Thr	Asp	Ile	Glu	Phe	Ile	Thr	Gln	Tyr	Leu	Val	Leu		
850						855						860					
Arg	Tyr	Ala	His	Glu	Lys	Pro	Lys	Leu	Thr	Arg	Trp	Ser	Asp	Asn	Val		
865						870						875					
Arg	Ile	Leu	Glu	Leu	Ala	Gln	Asn	Asp	Ile	Met	Glu	Glu	Gln	Glu	Glu		
885						890						895					
Ala	Met	Ala	Leu	Thr	Arg	Ala	Tyr	Thr	Thr	Leu	Arg	Asp	Glu	Leu	His		
900						905						910					
His	Leu	Ala	Leu	Gln	Glu	Leu	Pro	Gly	His	Val	Ser	Glu	Asp	Cys	Phe		
915						920						925					
Thr	Ala	Glu	Arg	Glu	Leu	Val	Arg	Ala	Ser	Trp	Gln	Lys	Trp	Leu	Val		
930						935						940					
Glu	Glu																
945																	

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<210> 471
<211> 433
<212> PRT
<213> Escherichia coli
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<400> 471																
Met	Ala	Gln	Glu	Ile	Glu	Leu	Lys	Phe	Ile	Val	Asn	His	Ser	Ala	Val	
1				5					10					15		
Glu	Ala	Leu	Arg	Asp	His	Leu	Asn	Thr	Leu	Gly	Gly	Glu	His	His	Asp	
			20					25					30			
Pro	Val	Gln	Leu	Leu	Asn	Ile	Tyr	Tyr	Glu	Thr	Pro	Asp	Asn	Trp	Leu	
		35					40					45				
Arg	Gly	His	Asp	Met	Gly	Leu	Arg	Ile	Arg	Gly	Glu	Asn	Gly	Arg	Tyr	
	50					55					60					
Glu	Met	Thr	Met	Lys	Val	Ala	Gly	Arg	Val	Thr	Gly	Gly	Leu	His	Gln	
65				70						75					80	
Arg	Pro	Glu	Tyr	Asn	Val	Ala	Leu	Ser	Glu	Pro	Thr	Leu	Asp	Leu	Ala	
				85					90					95		
Gln	Leu	Pro	Thr	Glu	Val	Trp	Pro	Asn	Gly	Glu	Leu	Pro	Ala	Asp	Leu	
			100					105					110			
Ala	Ser	Arg	Val	Gln	Pro	Leu	Phe	Ser	Thr	Asp	Phe	Tyr	Arg	Glu	Lys	
		115					120					125				
Trp	Leu	Val	Ala	Val	Asp	Gly	Ser	Gln	Ile	Glu	Ile	Ala	Leu	Asp	Gln	
	130					135					140					
Gly	Glu	Val	Lys	Ala	Gly	Glu	Phe	Ala	Glu	Pro	Ile	Cys	Glu	Leu	Glu	
145				150						155					160	
Leu	Glu	Leu	Leu	Ser	Gly	Asp	Thr	Arg	Ala	Val	Leu	Lys	Leu	Ala	Asn	
				165					170					175		
Gln	Leu	Val	Ser	Gln	Thr	Gly	Leu	Arg	Gln	Gly	Ser	Leu	Ser	Lys	Ala	
			180					185					190			
Ala	Arg	Gly	Tyr	His	Leu	Ala	Gln	Gly	Asn	Pro	Ala	Arg	Glu	Ile	Lys	
		195					200					205				
Pro	Thr	Thr	Ile	Leu	His	Val	Ala	Ala	Lys	Ala	Asp	Val	Glu	Gln	Gly	
		210				215					220					
Leu	Glu	Ala	Ala	Leu	Glu	Leu	Ala	Leu	Ala	Gln	Trp	Gln	Tyr	His	Glu	
225				230						235					240	
Glu	Leu	Trp	Val	Arg	Gly	Asn	Asp	Ala	Ala	Lys	Glu	Gln	Val	Leu	Ala	
			245						250					255		
Ala	Ile	Ser	Leu	Val	Arg	His	Thr	Leu	Met	Leu	Phe	Gly	Gly	Ile	Val	
		260						265					270			
Pro	Arg	Lys	Ala	Ser	Thr	His	Leu	Arg	Asp	Leu	Leu	Thr	Gln	Cys	Glu	
		275					280					285				

Ala Thr Ile Ala Ser Ala Val Ser Ala Val Thr Ala Val Tyr Ser Thr
 290 295 300
 Glu Thr Ala Met Ala Lys Leu Ala Leu Thr Glu Trp Leu Val Ser Lys
 305 310 315 320
 Ala Trp Gln Pro Phe Leu Asp Ala Lys Ala Gln Gly Lys Ile Ser Asp
 325 330 335
 Ser Phe Lys Arg Phe Ala Asp Ile His Leu Ser Arg His Ala Ala Glu
 340 345 350
 Leu Lys Ser Val Phe Cys Gln Pro Leu Gly Asp Arg Tyr Arg Asp Gln
 355 360 365
 Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Ala Gly
 370 375 380
 Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly
 385 390 395 400
 Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe
 405 410 415
 Arg Asn Glu Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys
 420 425 430
 Arg

<210> 472
 <211> 207
 <212> PRT
 <213> Escherichia coli

<400> 472
 Met Leu Asn Lys Leu Ser Leu Leu Leu Lys Asp Ala Gly Ile Ser Leu
 1 5 10 15
 Thr Asp His Gln Lys Asn Gln Leu Ile Ala Tyr Val Asn Met Leu His
 20 25 30
 Lys Trp Asn Lys Ala Tyr Asn Leu Thr Ser Val Arg Asp Pro Asn Glu
 35 40 45
 Met Leu Val Arg His Ile Leu Asp Ser Ile Val Val Ala Pro Tyr Leu
 50 55 60
 Gln Gly Glu Arg Phe Ile Asp Val Gly Thr Gly Pro Gly Leu Pro Gly
 65 70 75 80
 Ile Pro Leu Ser Ile Val Arg Pro Glu Ala His Phe Thr Leu Leu Asp
 85 90 95
 Ser Leu Gly Lys Arg Val Arg Phe Leu Arg Gln Val Gln His Glu Leu
 100 105 110
 Lys Leu Glu Asn Ile Glu Pro Val Gln Ser Arg Val Glu Glu Phe Pro
 115 120 125
 Ser Glu Pro Pro Phe Asp Gly Val Ile Ser Arg Ala Phe Ala Ser Leu
 130 135 140
 Asn Asp Met Val Ser Trp Cys His His Leu Pro Gly Glu Gln Gly Arg
 145 150 155 160
 Phe Tyr Ala Leu Lys Gly Gln Met Pro Glu Asp Glu Ile Ala Leu Leu
 165 170 175
 Pro Glu Glu Tyr Gln Val Glu Ser Val Val Lys Leu Gln Val Pro Ala
 180 185 190
 Leu Asp Gly Glu Arg His Leu Val Val Ile Lys Ala Asn Lys Ile
 195 200 205

<210> 473
 <211> 629
 <212> PRT
 <213> Escherichia coli

<400> 473

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Met Phe Tyr Pro Asp Pro Phe Asp Val Ile Ile Ile Gly Gly Gly His
 1           5           10           15
Ala Gly Thr Glu Ala Ala Met Ala Ala Ala Arg Met Gly Gln Gln Thr
      20           25           30
Leu Leu Leu Thr His Asn Ile Asp Thr Leu Gly Gln Met Ser Cys Asn
      35           40           45
Pro Ala Ile Gly Gly Ile Gly Lys Gly His Leu Val Lys Glu Val Asp
      50           55           60
Ala Leu Gly Gly Leu Met Ala Lys Ala Ile Asp Gln Ala Gly Ile Gln
      65           70           75           80
Phe Arg Ile Leu Asn Ala Ser Lys Gly Pro Ala Val Arg Ala Thr Arg
      85           90           95
Ala Gln Ala Asp Arg Val Leu Tyr Arg Gln Ala Val Arg Thr Ala Leu
      100           105           110
Glu Asn Gln Pro Asn Leu Met Ile Phe Gln Gln Ala Val Glu Asp Leu
      115           120           125
Ile Val Glu Asn Asp Arg Val Val Gly Ala Val Thr Gln Met Gly Leu
      130           135           140
Lys Phe Arg Ala Lys Ala Val Val Leu Thr Val Gly Thr Phe Leu Asp
      145           150           155           160
Gly Lys Ile His Ile Gly Leu Asp Asn Tyr Ser Gly Gly Arg Ala Gly
      165           170           175
Asp Pro Pro Ser Ile Pro Leu Ser Arg Arg Leu Arg Glu Leu Pro Leu
      180           185           190
Arg Val Gly Arg Leu Lys Thr Gly Thr Pro Pro Arg Ile Asp Ala Arg
      195           200           205
Thr Ile Asp Phe Ser Val Leu Ala Gln Gln His Gly Asp Asn Pro Met
      210           215           220
Pro Val Phe Ser Phe Met Gly Asn Ala Ser Gln His Pro Gln Gln Val
      225           230           235           240
Pro Cys Tyr Ile Thr His Thr Asn Glu Lys Thr His Asp Val Ile Arg
      245           250           255
Ser Asn Leu Asp Arg Ser Pro Met Tyr Ala Gly Val Ile Glu Gly Val
      260           265           270
Gly Pro Arg Tyr Cys Pro Ser Ile Glu Asp Lys Val Met Arg Phe Ala
      275           280           285
Asp Arg Asn Gln His Gln Ile Phe Leu Glu Pro Glu Gly Leu Thr Ser
      290           295           300
Asn Glu Ile Tyr Pro Asn Gly Ile Ser Thr Ser Leu Pro Phe Asp Val
      305           310           315           320
Gln Met Gln Ile Val Arg Ser Met Gln Gly Met Glu Asn Ala Lys Ile
      325           330           335
Val Arg Pro Gly Tyr Ala Ile Glu Tyr Asp Phe Phe Asp Pro Arg Asp
      340           345           350
Leu Lys Pro Thr Leu Glu Ser Lys Phe Ile Gln Gly Leu Phe Phe Ala
      355           360           365
Gly Gln Ile Asn Gly Thr Thr Gly Tyr Glu Glu Ala Ala Ala Gln Gly
      370           375           380
Leu Leu Ala Gly Leu Asn Ala Ala Arg Leu Ser Ala Asp Lys Glu Gly
      385           390           395           400
Trp Ala Pro Ala Arg Ser Gln Ala Tyr Leu Gly Val Leu Val Asp Asp
      405           410           415
Leu Cys Thr Leu Gly Thr Lys Glu Pro Tyr Arg Met Phe Thr Ser Arg
      420           425           430
Ala Glu Tyr Arg Leu Met Leu Arg Glu Asp Asn Ala Asp Leu Arg Leu
      435           440           445
Thr Glu Ile Gly Arg Glu Leu Gly Leu Val Asp Asp Glu Arg Trp Ala
      450           455           460
Arg Phe Asn Glu Lys Leu Glu Asn Ile Glu Arg Glu Arg Gln Arg Leu
      465           470           475           480

```

Lys Ser Thr Trp Val Thr Pro Ser Ala Glu Ala Ala Ala Glu Val Asn
 485 490 495
 Ala His Leu Thr Ala Pro Leu Ser Arg Glu Ala Ser Gly Glu Asp Leu
 500 505 510
 Leu Arg Arg Pro Glu Met Thr Tyr Glu Lys Leu Thr Thr Leu Thr Pro
 515 520 525
 Phe Ala Pro Ala Leu Thr Asp Glu Gln Ala Ala Glu Gln Val Glu Ile
 530 535 540
 Gln Val Lys Tyr Glu Gly Tyr Ile Ala Arg Gln Gln Asp Glu Ile Glu
 545 550 555 560
 Lys Gln Leu Arg Asn Glu Asn Thr Leu Leu Pro Ala Thr Leu Asp Tyr
 565 570 575
 Arg Gln Val Ser Gly Leu Ser Asn Glu Val Ile Ala Lys Leu Asn Asp
 580 585 590
 His Lys Pro Ala Ser Ile Gly Gln Ala Ser Arg Ile Ser Gly Val Thr
 595 600 605
 Pro Ala Ala Ile Ser Ile Leu Leu Val Trp Leu Lys Lys Gln Gly Met
 610 615 620
 Leu Arg Arg Ser Ala
 625

<210> 474

<211> 147

<212> PRT

<213> Escherichia coli

<400> 474

Met Ala Asp Ile Thr Leu Ile Ser Gly Ser Thr Leu Gly Gly Ala Glu
 1 5 10 15
 Tyr Val Ala Glu His Leu Ala Glu Lys Leu Glu Glu Ala Gly Phe Thr
 20 25 30
 Thr Glu Thr Leu His Gly Pro Leu Leu Glu Asp Leu Pro Ala Ser Gly
 35 40 45
 Ile Trp Leu Val Ile Ser Ser Thr His Gly Ala Gly Asp Ile Pro Asp
 50 55 60
 Asn Leu Ser Pro Phe Tyr Glu Ala Leu Gln Glu Gln Lys Pro Asp Leu
 65 70 75 80
 Ser Ala Val Arg Phe Gly Ala Ile Gly Ile Gly Ser Arg Glu Tyr Asp
 85 90 95
 Thr Phe Cys Gly Ala Ile Asp Lys Leu Glu Ala Glu Leu Lys Asn Ser
 100 105 110
 Gly Ala Lys Gln Thr Gly Glu Thr Leu Lys Ile Asn Ile Leu Asp His
 115 120 125
 Asp Ile Pro Glu Asp Pro Ala Glu Glu Trp Leu Gly Ser Trp Val Asn
 130 135 140
 Leu Leu Lys
 145

<210> 475

<211> 151

<212> PRT

<213> Escherichia coli

<400> 475

Met Gly Gln Arg Asn Val Ser Leu Met Glu Lys Lys Met Lys Lys Gly
 1 5 10 15
 Thr Val Leu Asn Ser Asp Ile Ser Ser Val Ile Ser Arg Leu Gly His
 20 25 30
 Thr Asp Thr Leu Val Val Cys Asp Ala Gly Leu Pro Ile Pro Lys Ser

```

      35          40          45
Thr Thr Arg Ile Asp Met Ala Leu Thr Gln Gly Val Pro Ser Phe Met
 50          55          60
Gln Val Leu Gly Val Val Thr Asn Glu Met Gln Val Glu Ala Ala Ile
65          70          75          80
Ile Ala Glu Glu Ile Lys His His Asn Pro Gln Leu His Glu Thr Leu
      85          90          95
Leu Thr His Leu Glu Gln Leu Gln Lys His Gln Gly Asn Thr Ile Glu
      100          105          110
Ile Arg Tyr Thr Thr His Glu Gln Phe Lys Gln Gln Thr Ala Glu Ser
      115          120          125
Gln Ala Val Ile Arg Ser Gly Glu Cys Ser Pro Tyr Ala Asn Ile Ile
      130          135          140
Leu Cys Ala Gly Val Thr Phe
145          150

```

<210> 476

<211> 501

<212> PRT

<213> Escherichia coli

<400> 476

```

Met Glu Ala Leu Leu Gln Leu Lys Gly Ile Asp Lys Ala Phe Pro Gly
 1          5          10          15
Val Lys Ala Leu Ser Gly Ala Ala Leu Asn Val Tyr Pro Gly Arg Val
      20          25          30
Met Ala Leu Val Gly Glu Asn Gly Ala Gly Lys Ser Thr Met Met Lys
      35          40          45
Val Leu Thr Gly Ile Tyr Thr Arg Asp Ala Gly Thr Leu Leu Trp Leu
      50          55          60
Gly Lys Glu Thr Thr Phe Thr Gly Pro Lys Ser Ser Gln Glu Ala Gly
65          70          75          80
Ile Gly Ile Ile His Gln Glu Leu Asn Leu Ile Pro Gln Leu Thr Ile
      85          90          95
Ala Glu Asn Ile Phe Leu Gly Arg Glu Phe Val Asn Arg Phe Gly Lys
      100          105          110
Ile Asp Trp Lys Thr Met Tyr Ala Glu Ala Asp Lys Leu Leu Ala Lys
      115          120          125
Leu Asn Leu Arg Phe Lys Ser Asp Lys Leu Val Gly Asp Leu Ser Ile
      130          135          140
Gly Asp Gln Gln Met Val Glu Ile Ala Lys Val Leu Ser Phe Glu Ser
145          150          155          160
Lys Val Ile Ile Met Asp Glu Pro Thr Asp Ala Leu Thr Asp Thr Glu
      165          170          175
Thr Glu Ser Leu Phe Arg Val Ile Arg Glu Leu Lys Ser Gln Gly Arg
      180          185          190
Gly Ile Val Tyr Ile Ser His Arg Met Lys Glu Ile Phe Glu Ile Cys
      195          200          205
Asp Asp Val Thr Val Phe Arg Asp Gly Gln Phe Ile Ala Glu Arg Glu
      210          215          220
Val Ala Ser Leu Thr Glu Asp Ser Leu Ile Glu Met Met Val Gly Arg
225          230          235          240
Lys Leu Glu Asp Gln Tyr Pro His Leu Asp Lys Ala Pro Gly Asp Ile
      245          250          255
Arg Leu Lys Val Asp Asn Leu Cys Gly Pro Gly Val Asn Asp Val Ser
      260          265          270
Phe Thr Leu Arg Lys Gly Glu Ile Leu Gly Val Ser Gly Leu Met Gly
      275          280          285
Ala Gly Arg Thr Glu Leu Met Lys Val Leu Tyr Gly Ala Leu Pro Arg
      290          295          300

```

Thr Ser Gly Tyr Val Thr Leu Asp Gly His Glu Val Val Thr Arg Ser
 305 310 315 320
 Pro Gln Asp Gly Leu Ala Asn Gly Ile Val Tyr Ile Ser Glu Asp Arg
 325 330 335
 Lys Arg Asp Gly Leu Val Leu Gly Met Ser Val Lys Glu Asn Met Ser
 340 345 350
 Leu Thr Ala Leu Arg Tyr Phe Ser Arg Ala Gly Gly Ser Leu Lys His
 355 360 365
 Ala Asp Glu Gln Gln Ala Val Ser Asp Phe Ile Arg Leu Phe Asn Val
 370 375 380
 Lys Thr Pro Ser Met Glu Gln Ala Ile Gly Leu Leu Ser Gly Gly Asn
 385 390 395 400
 Gln Gln Lys Val Ala Ile Ala Arg Gly Leu Met Thr Arg Pro Lys Val
 405 410 415
 Leu Ile Leu Asp Glu Pro Thr Arg Gly Val Asp Val Gly Ala Lys Lys
 420 425 430
 Glu Ile Tyr Gln Leu Ile Asn Gln Phe Lys Ala Asp Gly Leu Ser Ile
 435 440 445
 Ile Leu Val Ser Ser Glu Met Pro Glu Val Leu Gly Met Ser Asp Arg
 450 455 460
 Ile Ile Val Met His Glu Gly His Leu Ser Gly Glu Phe Thr Arg Glu
 465 470 475 480
 Gln Ala Thr Gln Glu Val Leu Met Ala Ala Val Gly Lys Leu Asn
 485 490 495
 Arg Val Asn Gln Glu
 500

<210> 477

<211> 321

<212> PRT

<213> Escherichia coli

<400> 477

Met Thr Thr Gln Thr Val Ser Gly Arg Arg Tyr Phe Thr Lys Ala Trp
 1 5 10 15
 Leu Met Glu Gln Lys Ser Leu Ile Ala Leu Leu Val Leu Ile Ala Ile
 20 25 30
 Val Ser Thr Leu Ser Pro Asn Phe Phe Thr Ile Asn Asn Leu Phe Asn
 35 40 45
 Ile Leu Gln Gln Thr Ser Val Asn Ala Ile Met Ala Val Gly Met Thr
 50 55 60
 Leu Val Ile Leu Thr Ser Gly Ile Asp Leu Ser Val Gly Ser Leu Leu
 65 70 75 80
 Ala Leu Thr Gly Ala Val Ala Ala Ser Ile Val Gly Ile Glu Val Asn
 85 90 95
 Ala Leu Val Ala Val Ala Ala Ala Leu Ala Leu Gly Ala Ala Ile Gly
 100 105 110
 Ala Val Thr Gly Val Ile Val Ala Lys Gly Arg Val Gln Ala Phe Ile
 115 120 125
 Ala Thr Leu Val Met Met Leu Leu Leu Arg Gly Val Thr Met Val Tyr
 130 135 140
 Thr Asn Gly Ser Pro Val Asn Thr Gly Phe Thr Glu Asn Ala Asp Leu
 145 150 155 160
 Phe Gly Trp Phe Gly Ile Gly Arg Pro Leu Gly Val Pro Thr Pro Val
 165 170 175
 Trp Ile Met Gly Ile Val Phe Leu Ala Trp Tyr Met Leu His His
 180 185 190
 Thr Arg Leu Gly Arg Tyr Ile Tyr Ala Leu Gly Gly Asn Glu Ala Ala
 195 200 205
 Thr Arg Leu Ser Gly Ile Asn Val Asn Lys Ile Lys Ile Ile Val Tyr

210	215	220
Ser Leu Cys Gly Leu	Leu Ala Ser Leu Ala Gly	Ile Ile Glu Val Ala
225	230	235
Arg Leu Ser Ser Ala	Gln Pro Thr Ala Gly Thr	Gly Tyr Glu Leu Asp
245	250	255
Ala Ile Ala Ala Val	Val Leu Gly Gly Thr Ser	Leu Ala Gly Gly Lys
260	265	270
Gly Arg Ile Val Gly	Thr Leu Ile Gly Ala Leu	Ile Leu Gly Phe Leu
275	280	285
Asn Asn Gly Leu Asn	Leu Leu Gly Val Ser Ser	Tyr Tyr Gln Met Ile
290	295	300
Val Lys Ala Val Val	Ile Leu Leu Ala Val Leu	Val Asp Asn Lys Lys
305	310	315
Gln		320

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<211> 296

<212> PRT

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<400> 478

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Val Ser Thr Leu Asn	Asn Pro Phe Phe Val Ser	Leu Lys Asp Gly Ala
35	40	45
Gln Lys Glu Ala Asp	Lys Leu Gly Tyr Asn Leu	Val Val Leu Asp Ser
50	55	60
Gln Asn Asn Pro Ala	Lys Glu Leu Ala Asn Val	Gln Asp Leu Thr Val
65	70	75
Arg Gly Thr Lys Ile	Leu Leu Ile Asn Pro Thr	Asp Ser Asp Ala Val
85	90	95
Gly Asn Ala Val Lys	Met Ala Asn Gln Ala Asn	Ile Pro Val Ile Thr
100	105	110
Leu Asp Arg Gln Ala	Thr Lys Gly Glu Val Val	Ser His Ile Ala Ser
115	120	125
Asp Asn Val Leu Gly	Gly Lys Ile Ala Gly Asp	Tyr Ile Ala Lys Lys
130	135	140
Ala Gly Glu Gly Ala	Lys Val Ile Glu Leu Gln	Gly Ile Ala Gly Thr
145	150	155
Ser Ala Ala Arg Glu	Arg Gly Glu Gly Phe Gln	Gln Ala Val Ala Ala
165	170	175
His Lys Phe Asn Val	Leu Ala Ser Gln Pro Ala	Asp Phe Asp Arg Ile
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Lys Gly Leu Asn Val	Met Gln Asn Leu Leu Thr	Ala His Pro Asp Val
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Gln Ala Val Phe Ala	Gln Asn Asp Glu Met Ala	Leu Gly Ala Leu Arg
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Ala Leu Gln Thr Ala	Gly Lys Ser Asp Val Met	Val Val Gly Phe Asp
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Gly Thr Pro Asp Gly	Glu Lys Ala Val Asn Asp	Gly Lys Leu Ala Ala
245	250	255
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 Val Ala Leu Ile Phe Val Asn Gly Glu Gly Glu Asn Val Ile Gly Ile
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 His Ala Gly Ala Asn Ala Ala Leu Ser Pro Ala Leu Val Glu Ala Gln
 115 120 125
 Arg Glu Arg Ile Ala Asn Ala Ser Ala Leu Leu Met Gln Leu Glu Ser
 130 135 140
 Pro Leu Glu Ser Val Met Ala Ala Ala Lys Ile Ala His Gln Asn Lys
 145 150 155 160
 Thr Ile Val Ala Leu Asn Pro Ala Pro Ala Arg Glu Leu Pro Asp Glu
 165 170 175
 Leu Leu Ala Leu Val Asp Ile Ile Thr Pro Asn Glu Thr Glu Ala Glu
 180 185 190
 Lys Leu Thr Gly Ile Arg Val Glu Asn Asp Glu Asp Ala Ala Lys Ala
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 Ala Gln Val Leu His Glu Lys Gly Ile Arg Thr Val Leu Ile Thr Leu
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 Gly Ser Arg Gly Val Trp Ala Ser Val Asn Gly Glu Gly Gln Arg Val
 225 230 235 240
 Pro Gly Phe Arg Val Gln Ala Val Asp Thr Ile Ala Ala Gly Asp Thr
 245 250 255
 Phe Asn Gly Ala Leu Ile Thr Ala Leu Leu Glu Glu Lys Pro Leu Pro
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 Glu Ala Ile Arg Phe Ala His Ala Ala Ala Ala Ile Ala Val Thr Arg
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<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Linker containing T7 terminator

<400> 481

agcttcaaaa aaccctcaa ggaccggtt agagggccca aggggttatg ctagactgca 60

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(54) Title: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION OF E. COLI

(57) Abstract: The sequences of nucleic acids encoding proteins required for E. coli proliferation are disclosed. The nucleic acids can also be used to screen for homologous genes that are required for proliferation in microorganisms other than E. coli. The nucleic acids can also be used to design expression vectors and secretion vectors. The nucleic acids can be used to express proteins or portions thereof, to obtain antibodies capable of specifically binding to the expressed proteins, and to use those expressed proteins as a screen to isolate candidate molecules for rational drug discovery programs. The nucleic acids of the present invention can also be used in various assay systems to screen for antimicrobial agents.

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AMENDED CLAIMS

[received by the International Bureau on 14 January 2002 (14.01.02);
original claims 1-131 replaced by amended claims 1-131 (14 pages)]

1. A purified or isolated nucleic acid sequence consisting essentially of one the sequence of nucleotides of SEQ ID NOs: 1-93, wherein expression of said nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism.

2. The nucleic acid sequence of Claim 1, wherein said nucleic acid sequence is complementary to at least a portion of the nucleotide sequence of the coding strand of a gene whose expression is required for proliferation of a microorganism.

3. The nucleic acid of Claim 1, wherein said nucleic acid sequence has a nucleotide sequence complementary to at least a portion of the nucleotide sequence of an RNA required for proliferation of a microorganism.

4. The nucleic acid of Claim 3, wherein the nucleotide sequence of said RNA encodes more than one gene product.

5. A purified or isolated nucleic acid comprising a fragment of one of the nucleotide sequence of SEQ ID NOs: 1-93, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 and more than 50 consecutive nucleotides of one of the nucleotide sequences of SEQ ID NOs: 1-93.

6. A vector comprising a promoter operably linked to the nucleic acid sequence of Claims 1,2,3,4, or 5.

7. The vector of Claim 6, wherein said promoter is active in a microorganism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species.

8. A host cell containing the vector of Claim 6.

9. A purified or isolated nucleic acid consisting essentially of the coding sequence of one of SEQ ID NOs: 105-112, 119-122, 134-160, 164-171, 179-265, 271-273, 275, and 279-286.

10. A fragment of the nucleic acid of Claim 8, said fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs: 105-112, 119-122, 134-160, 164-171, 179-265, 271-273, 275, and 279-286.

11. A vector comprising a promoter operably linked to the nucleic acid of Claim 9 or Claim 10.

12. A purified or isolated antisense nucleic acid comprising a nucleic acid sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding region, or 3' noncoding region within an operon comprising a proliferation-required gene whose activity or expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93.

13. A purified or isolated nucleic acid comprising a nucleic acid having at least 70% identity to a sequence selected from the group consisting of SEQ ID NOs.: 1-93, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 1-93, the sequences complementary to SEQ ID NOs.: 1-93 and the sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 1-93 as determined using BLASTN version 2.0 with the default parameters.

14. The nucleic acid of Claim 13, wherein said nucleic acid is from an organism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species.

15. A vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93.

16. A host cell containing the vector of Claim 15.

17. The vector of Claim 15, wherein said polypeptide comprises a polypeptide

comprising a sequence selected from the group consisting of SEQ ID NOs: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

18. A purified or isolated polypeptide comprising a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93, or a fragment selected from the group consisting of fragments comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the said polypeptides.

19. The polypeptide of Claim 18, wherein said polypeptide comprises a polypeptide comprising one of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479 or a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

20. A purified or isolated polypeptide comprising a polypeptide having at least 25% identity to a polypeptide whose expression is inhibited by a sequence selected from the group consisting of SEQ ID NOs.: 1-93, or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide whose expression is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-93 as determined using FASTA version 3.0t78 with the default parameters.

21. The polypeptide of Claim 20, wherein said polypeptide has at least 25% identity to a polypeptide comprising one of SEQ ID NOs: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479 or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising one of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479 as determined using FASTA version 3.0t78 with the default parameters.

22. An antibody capable of specifically binding the polypeptide of one of Claims 18-21.

23. A method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93 into a cell and expressing said polypeptide.

24. The method of Claim 23, further comprising the step of isolating said polypeptide.

25. The method of Claim 23, wherein said polypeptide comprises a sequence selected from the group consisting of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

26. A method of inhibiting proliferation of a microorganism comprising inhibiting the

activity or reducing the amount of a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93 or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product.

27. The method of Claim 26, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

28. A method for identifying a compound which influences the activity of a gene product required for proliferation, said gene product comprising a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising:

contacting said gene product with a candidate compound; and

determining whether said compound influences the activity of said gene product.

29. The method of Claim 28, wherein said gene product is a polypeptide and said activity is an enzymatic activity.

30. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a carbon compound catabolism activity.

31. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a biosynthetic activity.

32. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a transporter activity.

33. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a transcriptional activity.

34. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a DNA replication activity.

35. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a cell division activity.

36. A compound identified using the method of Claim 28.

37. The method of Claim 28, wherein said gene product is a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

38. A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising:

(a) providing a target that is a gene or RNA, wherein said target comprises a nucleic acid encoding said gene product;

(b) contacting said target with a candidate compound or nucleic acid; and

(c) measuring an activity of said target.

39. The method of Claim 38, wherein said target is a messenger RNA molecule and said activity is translation of said messenger RNA.

40. The method of Claim 38, wherein said target is a messenger RNA molecule and said activity is transcription of a gene encoding said messenger RNA.

41. The method of Claim 38, wherein said target is a gene and said activity is transcription of said gene.

42. The method of Claim 38, wherein said target is a nontranslated RNA and said activity is processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex.

43. The method of Claim 38, wherein said target gene or RNA encodes a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

44. A compound or nucleic acid identified using the method of Claim 38.

45. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a microorganism, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising the steps of:

(a) expressing a sub-lethal level of an antisense nucleic acid complementary to a nucleic acid encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;

(b) contacting said sensitized cell with a compound; and

(c) determining whether said compound inhibits the growth of said sensitized cell.

46. The method of Claim 45, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

47. The method of Claim 45, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

48. The method of Claim 45, wherein said cell is a Gram negative bacterium.

49. The method of Claim 45, wherein said cell is an *E. coli* cell.

50. The method of Claim 45, wherein said cell is from an organism selected from the

group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species.

51. The method of Claim 45, wherein said antisense nucleic acid is transcribed from an inducible promoter.

52. The method of Claim 51, further comprising the step of contacting said cell with a concentration of inducer which induces said antisense nucleic acid to a sub-lethal level.

53. The method of Claim 45, wherein growth inhibition is measured by monitoring optical density of a culture growth solution.

54. The method of Claim 45, wherein said gene product is a polypeptide.

55. The method of Claim 54, wherein said polypeptide comprises a sequence selected from the group consisting of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

56. The method of Claim 45, wherein said gene product is an RNA.

57. A compound identified using the method of Claim 45.

58. A method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93 or a compound with activity against the product of said gene into a population of cells expressing said gene.

59. The method of Claim 58, wherein said compound is an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, or a proliferation-inhibiting portion thereof.

60. The method of Claim 59, wherein said proliferation inhibiting portion of one of SEQ ID NOs.: 1-93 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive nucleotides of one of SEQ ID NOs.: 1-93.

61. The method of Claim 58, wherein said population is a population selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

62. The method of Claim 58, wherein said population is a population of Gram negative bacteria.

63. The method of Claim 58, wherein said population is a population of *E. coli* cells.

64. The method of Claim 58, wherein said population is a population selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species.

65. The method of Claim 58, wherein said gene encodes a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

66. A preparation comprising an effective concentration of an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable carrier.

67. The preparation of Claim 66, wherein said proliferation-inhibiting portion of one of SEQ ID NOs.: 1-93 comprises at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-93.

68. A method for inhibiting the activity or expression of a gene in an operon required for proliferation wherein the activity or expression of at least one gene in said operon is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising contacting a cell in a cell population with an antisense nucleic acid comprising at least a proliferation-inhibiting portion of said operon.

69. The method of Claim 68, wherein said antisense nucleic acid comprises a sequence selected from the group consisting of SEQ ID NOs.: 1-93 or a proliferation inhibiting portion thereof.

70. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population.

71. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which expresses said antisense nucleic acid into said cell population.

72. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by expressing said antisense nucleic acid from the chromosome of cells in said cell population.

73. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the synthesis of said antisense nucleic acid.

74. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.

75. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide.

76. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell.

77. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid.

78. The method of Claim 68, wherein said antisense nucleic acid is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-93.

79. The method of Claim 68 wherein said antisense nucleic acid is an oligonucleotide.

80. A method for identifying a gene which is required for proliferation of a microorganism comprising:

(a) contacting a microorganism other than *E. coli* with a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-93;

(b) determining whether said nucleic acid inhibits proliferation of said microorganism; and

(c) identifying the gene in said microorganism which is inhibited by said nucleic acid.

81. The method of Claim 80, wherein said microorganism is a Gram negative bacterium.

82. The method of Claim 80 wherein said microorganism is selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida*

pseudotropicalis), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species.

83. The method of Claim 80, further comprising introducing said nucleic acid into a vector functional in said microorganism prior to introducing said inhibitory nucleic acid into said microorganism.

84. A method for identifying a compound having the ability to inhibit proliferation of a microorganism comprising:

(a) identifying in a first microorganism a homolog of a gene or gene product present in a second microorganism which is different than said first microorganism, wherein the activity or level of said gene or gene product is inhibited by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 1-93 ;

(b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said first microorganism;

(c) contacting said first microorganism with a sub-lethal level of said inhibitory nucleic acid, thus sensitizing said first microorganism;

(d) contacting the sensitized microorganism of step (c) with a compound; and

(e) determining whether said compound inhibits proliferation of said sensitized microorganism.

85. The method of Claim 84, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism.

86. The method of Claim 84 wherein step (a) comprises identifying a homologous nucleic acid to a gene or gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-93 or a nucleic acid encoding a homologous polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-93 by using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the

default parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database.

87. The method of Claim 84 wherein said step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying nucleic acids which hybridize to said first gene.

88. The method of Claim 84 wherein the step (a) comprises expressing a nucleic acid selected from the group consisting of SEQ ID NOs. 1-93 in said microorganism.

89. The method of Claim 84, wherein said inhibitory nucleic acid is an antisense nucleic acid.

90. The method of Claim 84, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

91. The method of Claim 84, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

92. The method of Claim 84, wherein the step of contacting the first microorganism with a sub-lethal level of said inhibitory nucleic acid comprises directly contacting said microorganism with said inhibitory nucleic acid.

93. The method of Claim 84, wherein the step of contacting the first microorganism with a sub-lethal level of said inhibitory nucleic acid comprises expressing an antisense nucleic acid to said homolog in said microorganism.

94. The method of Claim 84, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

95. A compound identified using the method of Claim 84.

96. A method of identifying a compound having the ability to inhibit proliferation comprising:

(a) contacting a microorganism other than *E. coli* with a sub-lethal level of a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 1-93 or a portion thereof which inhibits the proliferation of *E. coli*, thus sensitizing said microorganism;

(b) contacting the sensitized microorganism of step (a) with a compound; and

(c) determining whether said compound inhibits proliferation of said sensitized microorganism.

97. The method of Claim 96, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism.

98. A compound identified using the method of Claim 96.
99. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:
- (a) sensitizing a cell by expressing a sub-lethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, in said cell to reduce the activity or amount of said gene product;
 - (b) contacting the sensitized cell with a compound; and
 - (c) determining whether said compound inhibits the growth of said sensitized cell.
100. The method of Claim 99, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.
101. The method of Claim 99, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.
102. The method of Claim 99, wherein said cell is a Gram negative bacterium.
103. The method of Claim 99, wherein said Gram negative bacterium is *E. coli*.
104. The method of Claim 99, wherein said cell is selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, *Yersinia pestis* and any species falling within the genera of any of the above species.
105. The method of Claim 99, wherein said antisense nucleic acid is transcribed from an inducible promoter.
106. The method of Claim 99, further comprising contacting the cell with an agent which

induces expression of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is expressed at a sub-lethal level.

107. The method of Claim 99, wherein inhibition of proliferation is measured by monitoring the optical density of a liquid culture.

108. The method of Claim 99, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479

109. A compound identified using the method of Claim 99.

110. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93;

(b) contacting said cell with a compound; and

(c) determining whether said compound reduces proliferation of said contacted cell.

111. The method of Claim 110, wherein said determining step comprises determining whether said compound reduces proliferation of said contacted cell to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

112. The method of Claim 110, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

113. The method of Claim 110, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises a compound known to inhibit growth or proliferation of a microorganism.

114. The method of Claim 110, wherein said cell contains a mutation which reduces the activity or level of said gene product required for proliferation of said cell.

115. The method of Claim 114, wherein said mutation is a temperature sensitive mutation.

116. The method of Claim 110, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479

117. A compound identified using the method of Claim 110:

118. A method for identifying the biological pathway in which a proliferation-required gene or its gene product lies, wherein said gene or gene product comprises a gene or gene product

whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93, said method comprising:

- (a) expressing a sub-lethal level of an antisense nucleic acid which inhibits the activity of said proliferation-required gene or gene product in a cell;
- (b) contacting said cell with a compound known to inhibit growth or proliferation of a microorganism, wherein the biological pathway on which said compound acts is known; and
- (c) determining whether said cell is sensitive to said compound.

119. The method of Claim 118, wherein said determining step comprises determining whether said cell has a substantially greater sensitivity to said compound than a cell which does not express said sub-lethal level of said antisense nucleic acid and wherein said gene or gene product lies in the same pathway on which said compound acts if said cell expressing said sub-lethal level of said antisense nucleic acid has a substantially greater sensitivity to said compound than said cell which does not express said sub-lethal level of said antisense nucleic acid.

120. The method of Claim 118, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479

121. A method for determining the biological pathway on which a test compound acts comprising:

- (a) expressing a sub-lethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a cell, wherein the activity or expression of said proliferation-required nucleic acid is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93 and wherein the biological pathway in which said proliferation-required nucleic acid or a protein encoded by said proliferation-required polypeptide lies is known,
- (b) contacting said cell with said test compound; and
- (c) determining whether said cell is sensitive to said test compound.

122. The method of Claim 121, wherein said determining step comprises determining whether said cell has a substantially greater sensitivity to said test compound than a cell which does not express said sub-lethal level of said antisense nucleic acid.

123. The method of Claim 121, further comprising:

- (d) expressing a sub-lethal level of a second antisense nucleic acid complementary to a second proliferation-required nucleic acid in a second cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said second cell does not have a substantially greater sensitivity to said test compound than a cell which does not express said sub-lethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological pathway against which the antisense nucleic acid of step (a) acts if said second cell does not have substantially greater sensitivity to said test compound.

124. A purified or isolated nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93.

125. A compound which interacts with a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93 to inhibit proliferation.

126. A compound which interacts with a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-93 to inhibit proliferation.

127. A method for manufacturing an antibiotic comprising the steps of:

screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93; and manufacturing the compound so identified.

128. The method of Claim 127, wherein said screening step comprises performing any one of the methods of Claims 28, 38, 45, 96, 99 and 110.

129. A method for inhibiting proliferation of a microorganism in a subject comprising administering a compound that reduces the activity or level of a gene product required for proliferation of said microorganism, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-93 to said subject.

130. The method of Claim 129 wherein said subject is selected from the group consisting of vertebrates, mammals, avians, and human beings.

131. The method of Claim 129, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 298-305, 312-315, 327-353, 357-364, 372-458, 464-466, 468 and 472-479.

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2 May 2002For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.

(54) Title: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION OF E. COLI

(57) Abstract: The sequences of nucleic acids encoding proteins required for E. coli proliferation are disclosed. The nucleic acids can also be used to screen for homologous genes that are required for proliferation in microorganisms other than E. coli. The nucleic acids can also be used to design expression vectors and secretion vectors. The nucleic acids can be used to express proteins or portions thereof, to obtain antibodies capable of specifically binding to the expressed proteins, and to use those expressed proteins as a screen to isolate candidate molecules for rational drug discovery programs. The nucleic acids of the present invention can also be used in various assay systems to screen for antimicrobial agents.

WO 01/48209 A3

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/34419

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/31 C12N15/11 C12N15/10 C07K14/245

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

SEQUENCE SEARCH, EPO-Internal, WPI Data, PAJ, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EM_PRO 'Online! EMBL; 29 January 1997 (1997-01-29) BLATTNER ET AL.: "Escherichia coli K12 MG1655 section 337 of 400 of the complete genome" retrieved from EBI, accession no. ECAE447 Database accession no. AE000447 XP002181127	5,10,13, 14, 18-21, 124
Y	the whole document	1-131
X	-& DATABASE SWALL 'Online! 1 May 1992 (1992-05-01) BURLAND ET AL.: "60 kDa inner-membrane protein" retrieved from EBI, accession no. 60IM_ECOLI Database accession no. P25714 XP002181128	5,10,13, 14, 18-21, 124
X	the whole document -& DATABASE EM_PRO 'Online!	5,13,14,

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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

A document defining the general state of the art which is not considered to be of particular relevance

C earlier document but published on or after the international filing date

L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

G document member of the same patent family

Date of the actual completion of the international search

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/34419

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>EMBL; 29 January 1997 (1997-01-29) BLATTNER ET AL.: "Escherichia coli K12 MG1655 section 298 of 400 of the complete genome" retrieved from EBI, accession no. ECAE408 Database accession no. AE000408 XP002181129 the whole document -& BLATTNER ET AL.: "THE COMPLETE GENOME SEQUENCE OF ESCHERICHIA COLI K-12" SCIENCE, vol. 277, 5 September 1997 (1997-09-05), pages 1453-1462, XP002923023 the whole document & THE JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 273, no. 46, 13 November 1998 (1998-11-13), pages 30415-30418, & GENOMICS, vol. 16, 1993, pages 551-561, XP000615272 & GENE, vol. 38, 1985, pages 85-93, XP000915093</p>	<p>124</p> <p>1,9</p>
Y	<p>WO 99 02673 A (DUGOURD DOMINIQUE ;WRIGHT JIM A (CA); YOUNG AIPING H (CA); GENESEN) 21 January 1999 (1999-01-21) page 7, line 25 -page 9, line 30; examples 2-6</p>	1-131
X	<p>DATABASE EM_PRO 'Online! EMBL; 19 May 1993 (1993-05-19) BURLAND ET AL.: "E. coli; the region from 81.5 to 84.5 minutes" retrieved from EBI, accession no. ECUW82 Database accession no. L10328 XP002181130 the whole document -& GENOMICS, vol. 16, 1993, pages 551-561, XP000615272</p>	5,10,13, 14,124
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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/34419

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EM_PRO 'Online! EMBL; 30 December 1994 (1994-12-30) PLUNKETT, G: "Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes" retrieved from EBI, accession no. ECUW67 Database accession no. U18997 XP002181132 the whole document</p> <p>---</p>	5,13,14, 124
A	<p>POST L E ET AL: "NUCLEOTIDE SEQUENCE OF THE RIBOSOMAL PROTEIN GENE CLUSTER ADJACENT TO THE GENE FOR RNA POLYMERASE SUBUNIT BETA IN ESCHERICHIA COLI" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE USA,US,NEW YORK, NY, vol. 76, no. 4, 1 April 1979 (1979-04-01), pages 1697-1701, XP000574791 abstract</p> <p>---</p>	1
A	<p>WO 98 21366 A (Q B I ENTERPRISES LTD ;EINAT PAZ (IL); VASQUEZ IASLOP NORA CECILIA) 22 May 1998 (1998-05-22) page 8, line 9 - line 13 page 21, line 30 -page 27, line 35</p> <p>---</p>	1
A	<p>VAN HEESWIJK W C ET AL: "The genes of the glutamine synthetase adenylation cascade are not regulated by nitrogen in Escherichia coli" MOLECULAR MICROBIOLOGY,BLACKWELL SCIENTIFIC, OXFORD,GB, vol. 9, no. 3, 1993, pages 443-457, XP000926027 ISSN: 0950-382X</p> <p>---</p>	
A	<p>LEE N G ET AL: "Molecular cloning and characterization of the nontypable Haemophilus influenzae-2019 rfaE gene required for lipopolysaccharide biosynthesis" INFECTION AND IMMUNITY,AMERICAN SOCIETY FOR MICROBIOLOGY, WASHINGTON,US, vol. 63, no. 3, 1995, pages 818-824, XP000953326 ISSN: 0019-9567</p> <p>---</p>	
A	<p>AUSTIN A E ET AL: "Genetic analysis of lipopolysaccharide core biosynthesis by Escherichia coli k12 insertion mutagenesis of the RFA locus" JOURNAL OF BACTERIOLOGY,WASHINGTON, DC,US, vol. 172, no. 9, September 1990 (1990-09), pages 5312-5325, XP000926028 ISSN: 0021-9193</p> <p>---</p>	

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/34419

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
T	<p>VALVANO M A ET AL: "The rfaE gene from Escherichia coli encodes a bifunctional protein involved in biosynthesis of the lipopolysaccharide core precursor ADP-L-glycero-D-manno-heptose" JOURNAL OF BACTERIOLOGY, WASHINGTON, DC, US, vol. 182, no. 2, January 2000 (2000-01), pages 488-497, XP000926030 ISSN: 0021-9193</p> <p>-----</p>	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/34419

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: —
because they relate to subject matter not required to be searched by this Authority, namely:
see FURTHER INFORMATION sheet PCT/ISA/210
2. ☒ Claims Nos.: —
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

As a result of the prior review under R. 40.2(e) PCT,
part of the additional fees are to be refunded.

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-131 (Seq. Id. Nos. 1, 60, 220 and 413)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☒ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

As far as claims 129-131 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box I.1

Rule 39.1(iv) PCT - Method for treatment of the human or animal body by therapy

Continuation of Box I.2

Present claims 36, 44, 57, 95, 98, 109, and 117 relate to a compound defined by reference to a desirable characteristic or property, namely being identifiable by using the method of claims 28, 38, 45, 84, 96, 99, and 110, respectively. Present claims 125 and 126 relate to a compound defined by reference to a desirable characteristic or property, namely interacting with a gene or gene product or a polypeptide whose activity or expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOS 1-127.

The claims cover all compounds having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for only a very limited number of such compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search has been carried out for those parts of the claims which appear to be clear, supported and disclosed, namely those parts relating to the sequences of claims 1, 9 and 19 .

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-8, 12-14, 45-124, 129-131 all partially

Invention 1:

A purified or isolated nucleic acid sequence, consisting of Seq Id No 1, a vector comprising said sequence, a host cell containing said vector, and their uses.

2. Claims: 1-8, 12-14, 45-124, 129-131 all partially

Inventions 2 to 93:

Idem as invention 1, but for Seq Id Nos 2-93, respectively.

3. Claims: 9-11, 15-44, 125-128 all partially

Invention 94:

A purified or isolated nucleic acid sequence consisting of Seq Id No 106, a vector comprising said sequence, a host cell containing said vector, a polypeptide encoded by said nucleic acid sequence and having Seq Id No 299, and an antibody binding said polypeptide, and their uses.

4. Claims: 9-11, 15-44, 125-128 all partially

Inventions 95 to 231:

Idem as invention 94, but for nucleic acid Seq Id Nos 107-112, 119-122, 134-160, 164-171, 179-265, 271-273, 275, 279-286 and corresponding polypeptide Seq Id Nos 300-305, 312-315, 327-333, 357-364, 372-458, 464-466, 468, 472-479, respectively.

INTERNATIONAL SEARCH REPORT

Information on patent family members

In tional Application No

PCT/US 00/34419

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